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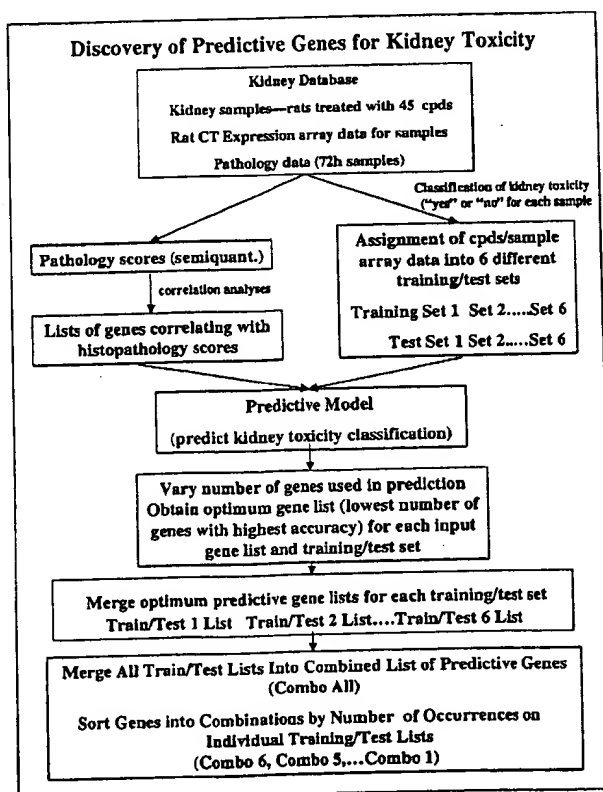
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(54) Title: **KIDNEY TOXICITY PREDICTIVE GENES**

(57) Abstract: The invention provides kidney toxicity predictive genes which can be used to predict kidney toxicity in response to one or more agents.



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# SPECIFICATION

## KIDNEY TOXICITY PREDICTIVE GENES

### Cross Reference to Other Patent Applications

- [01] This application claims priority from U.S. provisional application Serial No. 60/361,128 titled "Kidney Toxicity Predictive Genes", on February 27, 2002, which is hereby incorporated by reference in its entirety.

### Reference to a Sequence Listing and Tables

- [02] This application contains a gene sequence listing and four tables submitted on a compact disc whose file name is "Tables for Burning", created on February 27, 2003, containing 5 files and is herein incorporated by reference in its entirety. The five files are (a) a gene sequencing Table 32 (403 KB), in Microsoft® Word®, (b) Table 38 (785 KB) in Microsoft Excel®, (c) Table 39 (957KB) in Excel, (d) Table 40 (992 KB) in Excel, and (e) Table 45 (57KB) in Excel.

### Background of the Invention

- [03] This invention is in the field of toxicology. More specifically, it relates to kidney toxicity predictive genes and the methods of using such genes to predict kidney toxicity. Molecular biology and genomics technologies have potential to create dramatic advances and improvements for the science of toxicology as for other biological sciences. See, for example, MacGregor, et al. *Fund. Appl. Tox.* 26:156-173, 1995; Rodi et al., *Tox. Pathology* 27:107-110, 1999; Cunningham et al., *Ann. N.Y. Acad. Sci.* 919: 52-67, 2000; Pritchard et al., *Proc. Natl. Acad. Sci. USA* 98:13266-13271, 2001; and Fielden and Zacharewski, *Tox. Sciences* 60: 6-10, 2001.

The advantage of these technologies is that they can provide massive amounts of parallel information and that this information concerns processes and events occurring at the molecular level. This level of information is in dramatic contrast to conventional safety assessment toxicology that, to a large extent, currently relies on subjective evaluation (*e.g.*, in-life observations of behavior, observations of gross abnormalities at necropsy and histopathological examination of stained tissue slides using a microscope). These current methodologies may be largely subjective and in some cases such as histopathological evaluation, they require someone with a high degree of training, experience and skill to make competent evaluations. Furthermore, many of the methodologies require access to organs and tissues that necessitates either killing laboratory animals or surgery to obtain tissue specimens.

[04] Recently, there have been some initial efforts to apply molecular biology and genomics technologies to toxicology. Some efforts have involved application of gene expression measurements. See, for example, U.S. Patent 6,228,589 and WO 01/05804. Analysis of the data has yielded interesting observations of gene expressions that appear to correlate with some toxic effects or mechanisms. See, for example, Mueller et al. *Environmental Health Perspectives* 106(5): 277-230 (1998). However, there has been very little published work in toxicology so far that applies rigorous analytical and statistical techniques to the massive amounts of data available from genomics technologies. The observations, so far, have tended to be phenomenological and focused on individual gene responses rather than determining the generally applicable capabilities of patterns of gene expression to predict toxic effects (see, for example, studies of gene expression altered by exposure to kidney toxicants in Bartosiewicz et al., *J. Pharm. Exp. Ther.* 297: 895-905, 2001; Lieberthal, *Curr. Opin. Nephrol. Hypertens* 7:289-295, 1998; Huang et al., *Tox. Sciences* 63: 196-207, 2001). Even in the larger field of biological sciences, these types of analyses are just beginning to be evidenced in the literature (*e.g.*, Golub et al., *Science* 286: 531-537, 1999).

[05] What is needed are genes and predictive models, which are capable of predicting toxicity response.

## Brief Summary of the Invention

[06] The invention provides kidney toxicity predictive genes and predictive models which are useful to predict toxic responses to one or more agents.

[07] In one aspect, the invention provides methods of predicting kidney toxicity in an individual exposed to an agent which include the steps of: (a) obtaining a biological sample from an individual treated with the agent or treating a biological sample obtained from an individual with the agent or treating *in vitro* cultured cells or explants with the agent; (b) obtaining a gene expression profile from the biological sample or *in vitro* cultured cells or explants; and (c) using the gene expression profile from the biological sample or cells treated with the agent as a test set and a database of gene expression profiles and toxicity classifications as a training set and using kidney toxicity predictive genes and a Predictive Model to determine whether the agent will induce kidney toxicity in the individual or would be predicted to produce kidney toxicity following *in vivo* exposure.

[08] In one embodiment, the predictive model utilizes expression profiles from sets of kidney toxicity predictive gene(s) selected from Combination 6, *infra*, wherein the set is one or more kidney toxicity predictive gene(s). In other embodiments, the predictive model utilizes expression profiles from sets of one or more kidney toxicity predictive gene(s) selected from Combination 5, 4, 3, 2, or 1, wherein the set is one or more kidney toxicity predictive gene(s).

[09] In another aspect, the invention provides methods for determining the presence or absence of a no-observable effect level (NOEL) of an agent by the steps of: (a) obtaining biological samples from individuals treated with the agent at different dose levels or treating a biological sample obtained from an individual with different dose levels of the agent or treating *in vitro* cultured cells or explants with different dose levels of the agent; (b) obtaining gene expression profiles of the samples; and (d) using the gene expression profile from the biological samples as a test set and a database of gene expression profiles and toxicity classifications as a training set and

using kidney toxicity predictive genes and a Predictive Model to determine or predict whether and at which dose levels the agent will induce kidney toxicity. In one embodiment, the predictive model utilizes expression profiles from sets of kidney toxicity predictive gene(s) selected from Combination 6, *infra*, wherein the set is one or more kidney toxicity predictive gene(s). In other embodiments, the predictive model utilizes expression profiles from sets of one or more kidney toxicity predictive gene(s) selected from Combination 5, 4, 3, 2, or 1, wherein the set is one or more kidney toxicity predictive gene(s).

- [10] In another embodiment, the predictive genes and models may be used with an *in vitro* system to identify *in vitro* systems that can be used to accurately predict *in vivo* toxicity and to use the identified *in vitro* systems to accurately predict *in vivo* toxicity.
- [11] In another aspect, the invention provides methods of identifying a kidney toxicity predictive gene in an individual including the steps of: (a) providing a set of candidate toxicity predictive genes; (b) evaluating said genes for their predictive performance with at least one training and test set of data in a predictive model to identify genes which are predictive of kidney toxicity; and (c) testing the performance of predictive genes for their ability to predict kidney toxicity for different training and test sets of data, for prediction of accurate compared to random classification and prediction of test data external to the data used to derive the predictive genes. In one embodiment, the candidate toxicity predictive genes are rat toxicity genes.
- [12] In another aspect, the invention provides methods for determining the presence or absence of a no-observable effect level (NOEL) of an agent by the steps of: (a) obtaining biological samples from individuals treated with the agent at different dose levels or treating a biological sample obtained from an individual with different dose levels of the agent or treating *in vitro* cultured cells or explants with different dose levels of the agent; (b) obtaining gene expression profiles of the samples; and (d) using the gene expression profile from the biological samples as a test set and a database of gene expression profiles and toxicity classifications as a training set and

using kidney toxicity predictive genes and a Predictive Model to determine or predict whether and at which dose levels the agent will induce kidney toxicity. In one embodiment, the predictive model utilizes expression profiles from sets of kidney toxicity predictive gene(s) selected from Combination 6, *infra*, wherein the set is one or more kidney toxicity predictive gene(s). In other embodiments, the predictive model utilizes expression profiles from sets of one or more kidney toxicity predictive gene(s) selected from Combination 5, 4, 3, 2, or 1, wherein the set is one or more kidney toxicity predictive gene(s).

[13] In another aspect, the invention provides a computer program product which includes a set of kidney toxicity predictive genes derived from mining a database having a plurality of gene expression profiles indicative of toxicity. In one embodiment, the set of kidney toxicity predictive genes includes at least one toxicity predictive gene from combination 6, 5, 4, 3, 2, or 1 list.

[14] In another aspect, the invention provides a library of information about kidney toxicity predictive genes produced by the methods disclosed herein.

[15] In another aspect, the invention provides an integrated system for predicting kidney toxicity comprising: an array reader modified to read gene expression profiles from biological samples exposed to a test agent, operably linked to a computer comprising a database file having a plurality of kidney toxicity predictive genes.

## BRIEF DESCRIPTION OF THE DRAWINGS

[16] Figure 1 is a flow diagram illustrating the identification of kidney toxicity predictive genes. The pathway is given for discovery of kidney toxicity predictive genes using the database of expression array data (Rat CT array) and toxicity data for kidney samples from rats treated with various compounds (see Table 1). Gene with expressions correlating with pathology were determined using a variety of correlation statistics (see for example Tables 2 and 3). Predictive model used was

the GeneSpring Predict Parameter Value model that employs a K-nearest neighbor model.

[17] Figure 2 is a graph which shows the percent of overall correct calls as a function of the number of predictivity genes using histopathology correlating genes (Pearson measure) as the input gene list with Training and Test Set A. The percent of overall correct calls is presented as a function of the number of kidney toxicity predictivity genes. The input genes list consisted of 66 genes that showed a statistically significant correlation with the histopathology scores using Pearson's correlation measure ( $r$ -value  $>0.4$ ). Training and Test Set A was used with other model values of 10 nearest neighbors and a p-value ratio cutoff of 0.5. An optimum gene number of 49 was observed (lowest number of genes giving the highest percent overall calls) for this case.

[18] Figure 3 is a flow diagram illustrating how kidney toxicity predictive genes are evaluated for performance. Performance of predictive model is evaluated using 6 sets of training and test data (Rat CT expression array data). The training and test sets have accurate classification assignments (histopathology "yes" or "no" for each sample) or random classifications assignments ("yes" and "no" randomly assigned to samples). The K-nearest neighbor model is used with input being lists of predictive genes, as indicated, and the training and test set data. Four different measures of prediction are considered as indicated.

[19] Figure 4 is a graph that shows the cumulative predictive performance of Combo 6 genes. The mean, minimum and maximum percent accuracy for 6 training and test sets are presented for Combo 6 genes that were used cumulatively in the order given in Table 14.

[20] Figure 5 is a graph that shows the cumulative predictive performance of Combo 5 genes. The mean, minimum and maximum percent accuracy for 6 training and test sets are presented for Combo 5 genes that were used cumulatively in the order given in Table 14.

- [21] Figure 6 is a graph that shows the cumulative predictive performance of Combo 4 genes. The mean, minimum and maximum percent accuracy for 6 training and test sets are presented for Combo 4 genes that were used cumulatively in the order given in Table 14.
- [22] Figure 7 shows the k-means and tree cluster analysis of Combo 6 genes.
- [23] Figure 8 shows the Wards cluster analysis of Combo 6 gene set.
- [24] Figure 9 shows a scanned autoradiogram of a Western blot of serum samples from 8 animals probed with antibodies to clusterin and insulin-like growth factor binding protein 1. Sample information is indicated in the figure. The figure also presents transcriptional differential expression levels of the insulin-like growth factor binding protein 1 gene observed in kidney samples from these animals.

## BRIEF DESCRIPTION OF THE TABLES

- [25] Table 1 lists the compounds, dose levels, kidney pathology and abbreviations in the database.
- [26] Table 2 lists genes whose expression at 24h directly correlates with kidney tubular necrosis at 72h, ranked by Pearson correlation coefficient.
- [27] Table 3 lists genes whose expression at 24h inversely correlates with kidney tubular necrosis at 72h, ranked by Spearman correlation coefficient.
- [28] Table 4 lists the distribution of compounds in individual training and test sets for 24 hour kidney data.
- [29] Table 5 lists the predictive genes for 24 hour expression data.
- [30] Table 6 lists the randomly selected gene subsets from 24 hour combo all (216 genes).

- [31] Table 7 lists the randomly selected gene subsets from 24 h combo 6 gene set (28 genes).
- [32] Table 8 lists the randomly selected gene subsets from 24 h combo 5 gene set (25 genes).
- [33] Table 9 lists the randomly selected gene subsets from 24 h combo 4 gene set (23 genes).
- [34] Table 10 lists the randomly selected gene subsets from array genes excluding combo all set.
- [35] Table 11 lists the kidney toxicity individual sample prediction values for 24 hour data predictive genes (combined list and subsets).
- [36] Table 12 lists the kidney toxicity compound-dose prediction values for 24 hour data predictive genes (combined list and subsets).
- [37] Table 13 lists the kidney toxicity compound prediction values for 24 hour data predictive genes (combined list and subsets).
- [38] Table 14 lists the order of genes used for cumulative analysis of predictive performance of predictive combo gene sets.
- [39] Table 15 lists the individual gene predictions for combo 6.
- [40] Table 16 lists the individual gene predictions for combo 5.
- [41] Table 17 lists kidney toxicity individual sample prediction values for 24 hour data with random gene subsets.
- [42] Table 18 lists the comparison of predictivity for true kidney toxicity classification and random classification using combo gene sets and random subsets and 24 hour data.
- [43] Table 19 lists the distribution of compounds in individual training and test



sets for 6 hour kidney data.

- [44] Table 20 lists the genes whose expression at 6 hours directly correlates with kidney tubular necrosis at 72 hours, ranked by Pearson correlation coefficient.
- [45] Table 21 lists the genes whose expression at 6 hours inversely correlates with kidney tubular necrosis at 72 hours, ranked by Spearman correlation coefficient.
- [46] Table 22 lists the genes whose expression at 6 hours is predictive of kidney toxicity at 72 hours.
- [47] Table 23 lists the kidney toxicity compound-dose prediction values for 6 hour data predictive genes (combined list and subsets).
- [48] Table 24 lists the distribution of compounds in individual training and test sets for the 72 hour kidney data.
- [49] Table 25 lists the genes whose expression at 72 hours directly correlates with kidney tubular necrosis at 72 hours, ranked by Pearson correlation coefficient.
- [50] Table 26 lists the genes whose expression at 72 hours inversely correlates with kidney tubular necrosis at 72 hours, ranked by Spearman correlation coefficient.
- [51] Table 27 lists the genes whose expression at 72 hours is predictive of kidney toxicity at 72 hours.
- [52] Table 28 lists the kidney toxicity compound-dose prediction values for 72 hour data predictive genes (combined list and subsets).
- [53] Table 29 lists the predictive performance of various models.
- [54] Table 30 lists the logistic discrimination coefficients.
- [55] Table 31 lists the prediction of kidney toxicity for samples external to database.
- [56] Table 32 lists the genes predictive for kidney tubular necrosis, sequences,

and accession numbers.

- [57] Table 33 lists the kidney predictive genes (376 genes) organized by time point and combo category.
- [58] Table 34 lists the RCT genes (ESTs) predictive for kidney tubular necrosis: best homology matches.
- [59] Table 35 lists the genes that are predictive at all three time points.
- [60] Table 36 lists the genes that are the most predictive across the time points.
- [61] Table 37 lists the kidney toxicity predictive genes whose protein products are known to be secreted. The genes are from the table listing all the kidney predictive genes at the three time points 6, 24 and 72 hours. The protein products are easier to access since they are secreted into body fluids and are thus more amenable to be quantified. Therefore these proteins could be monitored in body fluids of subjects such as humans and toxicity predictions could be made.
- [62] Table 38 lists the expression data for the 6 hour timepoint.
- [63] Table 39 lists the expression data for the 24 hour timepoint.
- [64] Table 40 lists the expression data for the 72 hour timepoint.
- [65] Table 41 lists the predictive performance of predictive genes organized by occurrence on training/test set lists (combo number) and time point.
- [66] Table 42 lists the summary output of the predictive computer software product.
- [67] Table 43 lists the detailed output of the predictive computer software product.
- [68] Table 44 lists protein marker candidate identification information that includes the gene name, % correct calls, average fold induction for negative histopathology samples, and average fold induction for positive histopathology samples.

[69] Table 45 lists input data used for the predictive computer program product.

## DETAILED DESCRIPTION OF THE INVENTION

[70] This invention relates to methods of predicting whether an agent or other stimulus is capable of inducing kidney toxicity in a recipient organism using predictive molecular toxicology analysis. In particular, the invention provides methods of predicting kidney toxicity that comprise analyzing gene and/or protein expression across a number of kidney toxicity biomarkers disclosed herein for patterns of expression that correlate with and are predictive of kidney tubule necrosis in the recipient organism. This endpoint is significant because mortality in patients is high for acute renal failure and tubular necrosis is associated with many causes such as ischemia, endotoxemia or exposure to nephrotoxins (Ueda et al., *Am. J. Med.* 108: 403-415, 2000).

[71] The invention is based, in part, upon the discovery that modulated transcriptional regulation of relatively small sets of certain genes in response to a test agent can accurately predict the occurrence of kidney toxicity observed at later time points.

[72] Provided herein are multiple sets of kidney toxicity biomarkers which are useful in the practice of the kidney toxicity prediction methods of the invention. In particular, applicants have identified 376 kidney toxicity biomarkers that demonstrate utility in predicting kidney toxicity outcomes. These biomarkers have been thoroughly characterized for their predictive performance, individually as well as in various combinations or subsets thereof. In addition, various optimized subsets of the kidney toxicity biomarkers of the invention are disclosed, which sets have also been thoroughly characterized for predictive performance using the methods of the invention. Among the subsets of kidney toxicity genes provided herein are several which demonstrate prediction accuracies in the vicinity of 95%.

[73] The invention is further described by way of the experimental examples provided herein. These examples demonstrate that small sets of genes (*i.e.*, in some instances, as few as 2 or 3 biomarker genes) may be used to accurately predict kidney toxicity. For example, as further described in the Examples, analysis of mRNA expression of only a few genes can provide an accurate indication of whether a test agent will or will not induce kidney toxicity.

[74] The predictive capacity of the methods of the invention have been verified by (a) comparisons with random classifications, and (b) predictions using data external to the database used to identify the kidney toxicity biomarkers. Moreover, the methods of the invention are capable of distinguishing between agent dose levels which induce toxicity (typically higher doses) and those doses that are non-toxic. This latter feature is an essential component of meaningful toxicological evaluation..

[75] I. General Techniques: The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry, nucleic acid chemistry, and immunology, which are well known to those skilled in the art.. Such techniques are explained fully in the literature, such as, *Molecular Cloning: A Laboratory Manual*, second edition (Sambrook et al., 1989) and *Molecular Cloning: A Laboratory Manual*, third edition (Sambrook and Russel, 2001), (jointly referred to herein as "Sambrook"); *Current Protocols in Molecular Biology* (F.M. Ausubel et al., eds., 1987, including supplements through 2001); *PCR: The Polymerase Chain Reaction*, (Mullis et al., eds., 1994); Harlow and Lane (1988) *Antibodies, A Laboratory Manual*, Cold Spring Harbor Publications, New York; Harlow and Lane (1999) *Using Antibodies: A Laboratory Manual* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (jointly referred to herein as "Harlow and Lane"), Beaucage et al. eds., *Current Protocols in Nucleic Acid Chemistry* John Wiley & Sons, Inc., New York, 2000) and *Casarett and Doull's Toxicology The Basic Science of Poisons*, C. Klaassen, ed., 6th edition (2001).

[76] II. Definitions: Unless otherwise defined, all terms of art, notations and other

scientific terminology used herein are intended to have the meanings commonly understood by those of skill in the art to which this invention pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art. The techniques and procedures described or referenced herein are generally well understood and commonly employed using conventional methodology by those skilled in the art, such as, for example, the widely utilized molecular cloning methodologies described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* 2nd edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with manufacturer defined protocols and/or parameters unless otherwise noted.

- [77] "Toxic" or "toxicity" refers to the result of an agent causing adverse effects, usually by a xenobiotic agent administered at a sufficiently high dose level to cause the adverse effects.
- [78] As used herein, the terms "kidney toxicity biomarker" and "kidney toxicity predictive gene" are used interchangeably and refer to a gene whose expression, measured at the RNA or protein level can predict the likelihood of a kidney toxicity response with accuracy significantly better than would occur by chance. In one embodiment, the kidney toxicity response is tubular necrosis. In other embodiments, the kidney toxicity response can be other toxicity manifestations that elicit similar detectable gene expression changes. These could include other forms of tubular injury, glomerular toxicity and papillary injury.
- [79] A "toxicological response" refers to a cellular, tissue, organ or system level response to exposure to an agent. At the molecular level, this can include, but is not limited to, the differential expression of genes encompassing both the up- and down-regulation of expression of such genes at the RNA and/or protein level; the up- or down-regulation of expression of genes which encode proteins associated with

response to and mitigation of damage, the repair or regulation of cell damage; or changes in gene expression due to changes in populations of cells in the tissue or organ affected in response to toxic damage.

- [80] An "agent" or "compound" is any element to which an individual can be exposed and can include, without limitation, drugs, pharmaceutical compounds, household chemicals, industrial chemicals, environmental chemicals, other chemicals, and physical elements such as electromagnetic radiation.
- [81] The term "biological sample" as used herein refers to substances obtained from an individual. The samples may comprise cells, tissue, parts of tissues, organs, parts of organs, or fluids (e.g., blood, urine or serum). Biological samples include, but are not limited to, those of eukaryotic, mammalian or human origin.
- [82] "Sample" is defined for the purposes of prediction as a biological sample and the gene expression data for that sample. Each sample comes from an individual animal. A toxicity classification may also be associated with the sample.
- [83] "Gene expression" as used herein refers to the relative levels of expression and/or pattern of expression of a gene. In some embodiments, the expression refers to a toxicity gene or toxic response gene. In other embodiments, the expression is of a toxicity predictive gene.
- [84] "Gene expression profile" refers to the relative levels of expression of multiple different genes measured for the same sample. Gene expression profiles may be measured in a sample, such as samples comprising a variety of cell types, different tissues, different organs, or fluids (e.g., blood, urine, spinal fluid, sweat, saliva or serum) by various methods including but not limited to microarray technologies and quantitative and semi-quantitative RT-PCR (e.g., Taqman™) techniques, as well as techniques for measuring expression of proteins.
- [85] "Individual" refers to a vertebrate, including, but not limited to, a human, non-human primate, mouse, hamster, guinea pig, rabbit, cattle sheep, pig, chicken, and dog.

[86] As used herein, the terms "hybridize", "hybridizing", "hybridizes" and the like, used in the context of polynucleotides, are meant to refer to conventional hybridization conditions, such as hybridization in 50% formamide/6X SSC/0.1% SDS/100 µg/ml ssDNA, in which temperatures for hybridization are above 37 degrees Celsius and temperatures for washing in 0.1X SSC/0.1% SDS are above 55 degrees Celsius, and preferably to stringent hybridization conditions. Nucleic acids will hybridize will depend upon factors such as their degree of complementarity as well as the stringency of the hybridization reaction conditions. Stringent conditions can be used to identify nucleic acid duplexes with a high degree of complementarity. Means for adjusting the stringency of a hybridization reaction are well-known to those of skill in the art. See, for example, Sambrook, *et al.*, "Molecular Cloning: A Laboratory Manual," Second Edition, Cold Spring Harbor Laboratory Press, 1989; Ausubel, *et al.*, "Current Protocols In Molecular Biology," John Wiley & Sons, 1996 and periodic updates; and Hames *et al.*, "Nucleic Acid Hybridization: A Practical Approach," IRL Press, Ltd., 1985. In general, conditions that increase stringency (*i.e.*, select for the formation of more closely-matched duplexes) include higher temperature, lower ionic strength and presence or absence of solvents; lower stringency is favored by lower temperature, higher ionic strength, and lower or higher concentrations of solvents.

[87] In the context of amino acid sequence comparisons, the term "identity" is used to express the percentage of amino acid residues at the same relative position which are the same. Also in this context, the term "homology" is used to express the percentage of amino acid residues at the same relative positions which are either identical or are similar, using the conserved amino acid criteria of BLAST analysis, as is generally understood in the art. Further details regarding amino acid substitutions, which are considered conservative under such criteria, are provided.

[88] III. Identification of Kidney Toxicity Biomarkers

A. Generation of Toxicology Gene Expression Biomarkers: The kidney toxicity biomarkers described herein were initially identified utilizing a database

generated from large numbers of *in vivo* experiments, wherein the differential expression of approximately 700 rat genes, measured at various time points, in response to multiple toxic compounds inducing various specific toxic responses, as visualized through microscopic histopathological analysis, was quantified, as described in pending United States Patent Application filed January 29, 2002 (serial number not yet assigned). This quantitative gene expression data, as well as corresponding histopathological information, was then subjected to an analytical approach specifically designed to identify genes which not only correlated with the observed histopathology, but also demonstrated an ability to be used in a model capable of accurately predicting the occurrence of the toxic response associated with the observed histopathology. A complete description of this identification process is presented in the Examples. A flow diagram illustrating how the kidney toxicity biomarkers of the invention were identified is presented in Figure 1.

[89] In addition to the database described and utilized herein, other toxicology gene expression databases may be generated using techniques well known in the art, and used to identify additional kidney toxicity biomarkers, which may also be employed in the practice of the kidney toxicity prediction methods of the invention. Such databases may be generated with test compounds capable of inducing various pathologies indicative of a toxic response in the kidney and/or other organs or systems, over different time periods and under different administration and/or dosing conditions, including without limitation kidney tubule necrosis, glomerular necrosis, glomerular sclerosis and papillary injury. An example of compounds, dose levels, kidney toxicity classifications and histopathology scores used in the Examples which follow is provided in Table 1.

[90] Such databases may be generated using organisms other than the rat, including without limitation, animals of canine, murine, or non-human primate species. In addition, such databases may incorporate data derived from human clinical trials and post-approval human clinical experiences. Various methods for detecting and quantitating the expression of genes and/or proteins in response to



toxic stimuli may be employed in the generation of such databases, as are generally known in the art. For example, microarrays comprising multiple cDNAs or oligonucleotide probes capable of hybridizing to corresponding transcripts of genes of interest may be used to generate gene expression profiles. Additionally, a number of other methods for detecting and quantitating the expression of gene transcripts are known in the art and may be employed, including without limitation, RT-PCR techniques such as TaqMan®, RNase protection, branched chain, etc.

[91] Databases comprising quantitative gene expression information preferably include qualitative and quantitative and/or semi-quantitative information respecting the observed toxicological responses and other conventional toxicology endpoints, such as for example, body and organ weights, serum chemistry and histopathology observations, histopathology scores and/or similar parameters.

[92] B. Identification of Correlating Genes: For the purpose of identifying candidate predictive genes, the database preferably includes histopathology scores for each animal which has been exposed to one or more agent(s). These scores can be assigned based on actual histopathology observations for the tissue and animal or on the basis of effects observed for other animals treated with the same agent and dose level. The scores are numerical scores that reflect the occurrence and severity of histopathological changes. These scores can be adjusted to have similar range to gene expression changes. For example, a score of 1 could be assigned to samples with no changes and scores of 28 assigned to increasingly severe changes. Because the scores are numerical, they are suitable for use with a variety of statistical correlation and similarity measures.

[93] An example of a histopathology scoring system is provided in Example 1. Referring to Figure 1, histopathology scores may be utilized to identify genes which correlate with the observed toxicological response, using any number of statistical correlation and similarity analysis techniques, including without limitation those techniques described or employed in Example 1 (e.g., Pearson, Spearman, change, smooth, distance etc.). Such correlating genes may be used as predictive gene

candidates. Examples of genes whose expression at 24 hours after treatment correlates with histopathology observed at 72h are detailed in Tables 3 and 4. In one embodiment, the correlating gene lists as well as the entire array gene list are used as input gene lists in the GeneSpring™ Predictive Model (otherwise known hereafter as "Predictive Model").

[94] (C) Class Prediction and Classification: Statistical analysis of the database of gene expression profiles can be effected by utilizing commercially available software programs. In one embodiment, GeneSpring™ (Version 4.1, Silicon Genetics, Redwood City, CA) is used. Other software programs which can be used for statistical analysis include, without limitation, SAS software packages (SAS Institute Inc., Cary, NC) and S-PLUS® software (Insightful Corporation, Seattle, WA)

[95] Using GeneSpring™ software, class predictions can be made from the genes in the database, as detailed in Example 1, using one or more training and test sets. In one embodiment, six training sets and six test sets are obtained, as shown in Example 1 (Table 4). Kidney toxicological classifications are entered for the samples in each training and test set. Toxicological classifications can be defined by various pathologies. In one embodiment, the toxicity is defined as kidney tubular necrosis observed 72 hours after treatment with an agent. However, toxicity can manifest in other nephropathologies such as glomerular necrosis or papillary injury.

[96] Once the training sets have been selected, then predicted classifications of the test set samples are obtained by using k-nearest neighbor (or *knn*) voting procedure. The class of each of the *knn* is determined and the test sample is assigned to the class with the largest representation after adjusting for the proportion of classifications in the training set. In one embodiment, adjustments are made to account for different proportions of classes in the training set.

[97] Toxicity can also be observed at various time points after exposure to an agent and is not limited to only 72 hour after treatment. A skilled toxicologist can determine the optimal time after exposure to an agent to observe pathology by either what has been disclosed in the art or a stepwise experimentation with time

increments, for example 2, 4, 6, 12, 18, 24, 36, 48 hours post-exposure or even longer time increments, for example, days, weeks, or months after exposure to the agent.

**[98]** (D) Identification of Predictive Genes: Figure 1 describes the overall process used to identify kidney toxicity predictive genes. In one embodiment, this process was run independently for each time point.

**[99]** The number of genes that are to be used in the Predictive Model can be varied, for example 50, 40, 30, 20, 10, 5, 2, or 1 gene(s) can be used. In a preferred embodiment, at least 50 genes are used.

**[100]** An optimal gene list is generated that generates the best predictive accuracy with the lowest number of genes used. Figure 2 shows an exemplary profile for an optimal gene list.

**[101]** In one embodiment, optimum gene lists for all input gene lists are combined for each training and test set and then these combined lists for all six training and test sets are merged to create an aggregate list of predictive genes. The aggregate list can then be subdivided to smaller lists of genes based on the number of times that the genes occurred on the predictive gene lists for each individual training or test set. These are designated herein as Combo 6, 5, 4, 3, 2, or 1 lists. The genes that were predictive in all 6 training and test sets are designated as Combo 6 and the genes that were predictive in 5 of 6 training and test sets are designated as Combo 5 and so forth. Table 32 presents gene names, accession numbers and sequence information for the kidney toxicity predictive genes found by analysis of the database in the manner described above. Each of these genes has been demonstrated to contribute to predictive performance for at least one input gene list and training/test set and one time point. Table 33 lists the kidney toxicity predictive genes organized by time point and Combo Class. Table 34 lists homologous genes for the RCT sequences that were identified by BLAST search using the GenBank NR database as the target database.

[102] The predictive genes can also be categorized by their occurrence as predictive at different time points. Table 35 lists 53 genes that are on the combined predictive lists of all three time points tested. This list is derived from the list of all the predictive genes measured at 6, 24 and 72 hours that predicted kidney tubular necrosis at 72 hours. Genes that are predictive at multiple time points can be further grouped by their Combo ranking. Table 36 lists 23 genes that are the most predictive across the three time points tested. This list is a subset of the list of 53 genes that are predictive across all three time points 6, 24 and 72 hours. The criteria for inclusion in this table were that the gene be a member of the highest combinations, viz., combinations 6, 5 or 4 in at least 2 out of three time points. The gene expression data of the genes in Table 36 could be expected to be very highly predictive of kidney tubular necrosis. Further, since the predictive strength of these genes is very high across the 3 time points tested, it could be expected that gene expression data derived from these genes even at time points not tested such as any time points falling between 6 and 72 hours or any other time point would be very highly predictive of tubular necrosis. These specific genes could be useful in cases where the dose route or pharmacokinetic properties of a compound may alter the kinetics of predictive gene expression changes.

[103] IV. Evaluation of Predictive Genes for Kidney Toxicity: The predictive genes are evaluated for predictive performance as shown in Figure 3. For each gene list prediction, a table of data was generated using the Predictive Model which included: the test set containing information about the actual call (*i.e.*, "yes" or "no" for kidney toxicity), the predicted call (*i.e.*, "yes" or "no" for kidney toxicity), and the P-value cutoff ratio. Expression data that can be used with the K-nearest neighbor model and predictive genes to enable one skilled in the art to make predictions are given in Tables 38-40.

[104] The combined list of predictive genes or alternatively, Combo 6, 5, 4, 3, 2, or 1 list or subsets thereof was used as input into the Predictive Model. As another verification of the predictive abilities of the genes found to be predictive for kidney toxicity, random lists of genes were generated and also used as input into the

Predictive Model. Example 2 describes the evaluation of the predictive performance of the kidney toxicity predictive genes.

[105] Predictive performance may also be assessed using data from different time points after exposure to the agent. In one embodiment, 24 hour expression data is used. In another embodiment, 6 hour expression data is used, as described in Examples 3 and 4. In another embodiment, 72 hour expression data is used, as described in Example 5 and 6. As shown in Table 41, predictive capability for 24 hour expression data has a high accuracy rate (*i.e.*, 90% accuracy) when the entire predictive gene list is used.

Table 41 Predictive Performance of Predictive Genes Organized by Occurrence on Training/Test Set Lists (Combo number) and Time Point

| Time Point | Gene Set  | Number of Genes | Accuracy**                 | Geometric Mean**           |
|------------|-----------|-----------------|----------------------------|----------------------------|
| 24 h       | Combo All | 216             | <b>0.915</b> (0.861-0.945) | <b>0.810</b> (0.720-0.884) |
| 24 h       | Combo 6   | 28              | <b>0.921</b> (0.867-0.955) | <b>0.837</b> (0.660-0.953) |
| 24 h       | Combo 5   | 25              | <b>0.896</b> (0.829-0.929) | <b>0.821</b> (0.684-0.870) |
| 24 h       | Combo 4   | 23              | <b>0.882</b> (0.829-0.929) | <b>0.776</b> (0.700-0.925) |
| 24 h       | Combo 3   | 19              | <b>0.839</b> (0.778-0.911) | <b>0.740</b> (0.562-0.892) |
| 24 h       | Combo 2   | 45              | <b>0.733</b> (0.641-0.821) | <b>0.552</b> (0.343-0.663) |
| 24 h       | Combo 1   | 76              | <b>0.787</b> (0.667-0.884) | <b>0.645</b> (0.355-0.782) |
| 6h         | Combo All | 176             | <b>0.719</b> (0.571-0.793) | <b>0.610</b> (0.420-0.750) |
| 6h         | Combo 6   | 15              | <b>0.747</b> (0.567-0.800) | <b>0.542</b> (0.000-0.800) |
| 6h         | Combo 5   | 16              | <b>0.536</b> (0.330-0.700) | <b>0.480</b> (0.400-0.650) |
| 6h         | Combo 4   | 19              | <b>0.731</b> (0.607-0.875) | <b>0.584</b> (0.400-0.740) |
| 6h         | Combo 3   | 21              | <b>0.635</b> (0.330-0.830) | <b>0.514</b> (0.350-0.630) |
| 6h         | Combo 2   | 38              | <b>0.607</b> (0.350-0.830) | <b>0.402</b> (0.000-0.600) |
| 6h         | Combo 1   | 67              | <b>0.588</b> (0.420-0.820) | <b>0.509</b> (0.390-0.630) |
| 72 h       | Combo All | 225             | <b>0.882</b> (0.643-0.974) | <b>0.747</b> (0.500-0.913) |
| 72 h       | Combo 6   | 16              | <b>0.808</b> (0.607-0.902) | <b>0.601</b> (0.000-0.869) |
| 72 h       | Combo 5   | 27              | <b>0.742</b> (0.429-0.921) | <b>0.616</b> (0.452-0.803) |
| 72 h       | Combo 4   | 23              | <b>0.828</b> (0.500-0.917) | <b>0.607</b> (0.000-0.839) |
| 72 h       | Combo 3   | 33              | <b>0.705</b> (0.357-0.902) | <b>0.414</b> (0.000-0.649) |
| 72 h       | Combo 2   | 41              | <b>0.661</b> (0.357-0.868) | <b>0.412</b> (0.000-0.690) |
| 72 h       | Combo 1   | 90              | <b>0.783</b> (0.536-0.941) | <b>0.572</b> (0.000-0.896) |

\*\* Means and ranges are given for 6 training and test sets. Unit of prediction was the animal and the predictive classification was for kidney tubular necrosis observed at 72 hours after treatment. Standard prediction measures were used as defined in Materials and Methods of Example 1. These include:

Accuracy = Proportion of total number of predictions that are correct  
Geometric mean = Performance measure that takes into account proportion of positive and negative cases

- [106] Somewhat lower predictive accuracies were observed for the 6h and 72 h data but the prediction was still quite significant. In general, selecting genes from Combo list 6 for use in prediction of kidney toxicity yields higher average accuracy than using genes from Combo list 5 which in turn yields higher average accuracy rates than Combo 4 and so forth for Combo lists 3, 2, and 1. All of the combo lists as well as Combo All list had significantly higher accuracy than using random classifications.
- [107] Predictive performance may also be assessed using subsets of genes from the different Combo lists. As indicated in Examples 2, 4 and 6 randomly selected subsets of the Combo gene lists had very good predictive performance (accuracy better than 80% and approaching 90%) and even individual genes had mean predictive accuracies that were significant (for example, greater than 80%). Cumulative performance of subsets of 24 h data is presented in Figures 4-6. In one embodiment, using 3 genes from Combo list 6 yields about 90% accuracy. However, using different Combo lists may require more genes to reach the same accuracy level, e.g., 8 genes from Combo 5 list, 13 genes from Combo 4 list.
- [108] V. Use of kidney toxicity predictive genes: The kidney toxicity predictive genes disclosed herein and kidney toxicity predictive genes identified by using methods disclosed herein are useful for predicting kidney toxicity in response to exposure to one or more agents.
- [109] The discovery that relatively small sets of different genes have predictive value permits flexible application of these discoveries. The choice of how many and which genes to use can be tailored to a variety of different purposes. Very good predictivity is observed for sets of a few genes (for example as few as three genes of the 24 hour Combo 6 set have mean prediction accuracy of about 90%). These small sets may be particularly advantageous in applications where measurement of

only a few RNA species has considerable advantages in terms of sample processing logistics, speed and cost. These applications would include relatively high throughput screens for predictive capability. An example of this would be an early screen using small samples of primary cells or cultured cell lines that can be processed with automated robotic equipment for treatment and isolation of RNA followed by efficient technologies for measuring expression of a few RNA species such as branched chain technology or RT-PCR. The use of larger numbers of predictive genes provides for redundancy and consequent greater accuracy and precision. Applications using larger numbers of predictive genes might be tests of candidates at later stages of commercial development. An example would be later stages of preclinical development of a therapeutic candidate where *in vivo* samples can be obtained and more comprehensive methods such as microarray measurement of gene expression are appropriate. The larger gene sets can also include different subsets of genes which may offer more insight into potential mechanisms of toxicity and the ability to have refined predictions of long term toxic consequences such as chronic, irreversible toxicity or carcinogenicity.

[110] Some members of the kidney toxicity predictive genes may also be suitable for prediction of toxicity in other organs or may be preferable for predicting toxicity for wider ranges of timepoints or treatment routes or regimens. As an example of the latter, some of the predictive genes are observed at three different timepoints after treatment. These genes may be useful for prediction in cases where the samples come from treatment protocols that have different measurement timepoints or routes of administration than those employed for the database or where the toxicokinetics for a particular agent are known or suspected to be different from those in the database.

[111] In one embodiment, the agent is an agent for which no expression profile has been assessed or stored in the database or library. An animal, *e.g.*, rat, is dosed with such an agent and the gene expression profile(s) is the test set for the Predictive Model. The training set which is used in the Predictive Model in this case can be the entire database of sample array data because the test set data is not present in the

database. As described in Example 8, the prediction can be made with accuracy without requiring the use of histopathology scores for the test set as part of the input into the Predictive Model.

[112] In another embodiment the agent is an agent present in the database but is used at a different dose level or with a different treatment protocol than used in the database. The training set which is used in the Predictive Model in this case can be the entire database of sample array data because the test set data is not present in the database. As described in Example 8, the prediction can be made with accuracy without requiring the use of histopathology scores for the test set as part of the input into the Predictive Model.

[113] In another embodiment, the exposure time of the agent is not 6, 24, or 72 hours or repeat dosing protocols are used. In this case, the skilled artisan can use the toxicity predictive genes from surrounding time points to extrapolate the predicted toxicity without undue experimentation. For example, if the individual has been exposed to the agent for 12 hours, then predictive genes from 6 and 24 hours timepoints are used as guidelines for extrapolating possible predicted toxicity.

[114] In another embodiment, the kidney predictive genes and predictive model can be used to determine the presence or absence of a no-observable toxicity effect level (NOEL). An agent can be used at different treatment levels and expression profiles obtained for each treatment level. The predictive genes and predictive model can be used to determine which dose levels elicit a response that is predicted to be toxic and which dose levels are not toxic. In contrast to conventional endpoints for determining no-effect levels, the use of expression data, predictive genes and predictive models applies a number of quantitative endpoints and criteria instead of subjective endpoints and criteria. This permits more rigorous and precisely defined determination of no effect levels.

[115] In another embodiment, the kidney toxicity predictive genes can be used to detect toxic effects that may be manifested as long lasting or chronic consequences such as irreversible toxicity or carcinogenesis. The predictive genes and model can



be applied to databases where classifications of training and test set samples are made with respect to actual or putative endpoints such as irreversible toxicity or carcinogenicity.

[116] In another embodiment, the predictive genes can be used in a variety of alternative models to predict kidney toxicity. Some of these models do not require the direct use of data in a database but use functions or coefficients derived from the database. In another embodiment, the predictive genes and models may be used to evaluate *in vitro* systems for their ability to reflect *in vivo* toxic events and to use such *in vitro* systems for predicting *in vivo* toxicity. Expression profiles for predictive genes can be created from candidate *in vitro* assays using treatments with agents of known *in vivo* toxicity and for which *in vivo* data on gene expression are available. The expression data and predictive models of this invention can be used to determine whether the *in vitro* assay system has predictive gene expression responses that accurately reflect the *in vivo* situation. Large sets of predictive genes as described in this invention can be tested in such models for their suitability and performance with the candidate *in vitro* systems. This is a superior and novel tool for evaluating and optimizing *in vitro* systems for their ability to reflect and accurately predict *in vitro* responses.

[117] In another embodiment, measurement of the expression levels of the proteins coded for by the predictive genes can be used in conjunction with predictive models to predict kidney toxicity. Among the full set of kidney toxicity predictive genes are various genes known to encode cell surface, secreted and/or shed proteins. This enables the development of methods for predicting toxicity using protein biomarkers. Example 11 presents a process by which candidate protein biomarker genes may be selected from biomarker genes identified from transcription expression. For example, as disclosed in Table 37, there are 23 genes in the master predictive set which are known to encode secreted proteins. As disclosed in Table 43, predictive protein marker candidates may also be selected by categorizing a number of other parameters related to the predictive performance and potential use as protein markers. In Example 11, the utility of this concept has been demonstrated

by testing for serum protein levels of one of the identified biomarkers, insulin-like growth factor binding protein 1. The serum protein levels of this biomarker parallel the kidney transcription levels and distinguish kidney toxic from non-toxic treatments. Thus, in another aspect of the present invention, kidney toxicity predictive assays which detect the expression of one or more of said predictive proteins may be developed. Such assays may have several advantages, such as:

- (1) Ability to use archived tissue specimens such as preserved or embedded tissues that are not suitable for measurement of RNA expression
- (2) Ability to examine predictive protein expression in tissue slides using *in situ* labeling and microscopic observation. This is useful for detecting toxicity predictive signals occurring in very small subpopulations of cells.
- (3) Ability to detect protein markers in specimens that can be readily obtained with little or no invasiveness (*e.g.*, blood, urine, sweat, saliva).
- (4) Reduction in animal use in laboratory studies such that no sacrifice of animals necessary to obtain tissue specimens when toxicity prediction can be made with specimens that can be obtained without animal sacrifice or surgery.
- (5) Application for human use where tissue specimens cannot be obtained or are only obtained with great difficulty.

**[118]** In another embodiment, the identified predictive genes can be considered as potential therapeutic targets when the genes are involved in toxic damage or repair responses whose expression or functional modification may attenuate, ameliorate or eliminate disease conditions or adverse symptoms of disease conditions.

**[119]** In another embodiment, the predictive genes can be organized into clusters of genes that exhibit similar patterns of expression by a variety of statistical procedures commonly used to identify such coordinately expression patterns.

Common functional properties of these clustered genes can be used to provide insight into the functional relationship of the response of these genes to toxic effects. Common genetic properties of these genes (*e.g.*, common regulatory sequences) may provide insight into functional aspects by revealing known or novel similarities in the coding region of the genes. The presence of common known or novel signal transduction systems that regulate expression of the genes can also lead to insight as to the functional properties of the genes. The presence of common known or novel regulatory sequences in the identified predictive genes can also be used to identify toxicity predictive genes that are not present in the current Rat CT array. This can be accomplished by someone skilled in the art who can analyze sequence databases for common regulatory sequences.

**[120]** In yet another embodiment, the kidney toxicity predictive genes can be used to predict toxicity responses in other species, for example, human, non-human primate, mouse, hamster, guinea pig, rabbit, cattle, sheep, pig, chicken, and dog. Some members of the kidney toxicity predictive genes may also be more suitable for prediction of toxicity in species other than the species used to derive the database (rat in the case of the examples provided). One method for identification of such genes is that would be available to someone skilled in the art would be to examine DNA sequence databases to determine whether orthologous sequences to the predictive genes exist in the target species and how close the orthologous sequences are to the predictive gene sequences. One of skill in the art can examine the orthologous sequences for similarity in amino acid coding regions and motifs as well as for similarities in regulatory regions and motifs of the gene.

**[121]** In another embodiment, kidney toxicity predictive genes or gene sequences are used for screening other potential toxicity predictive genes or gene sequences in other species or even within the same species using methods known in the art. See, for example, Sambrook *supra*. Gene sequences which hybridize under stringent conditions to the kidney toxicity predictive gene sequences disclosed herein are selected as potential toxicity predictive genes. Gene sequences which hybridize to the kidney toxicity predictivity gene of this invention can show homology to the kidney

toxicity predictivity genes, preferably at least about 50%, 60%, 70%, 80%, or 90% identical to the kidney toxicity predictivity genes disclosed herein. It is understood that conservative substitutions of amino acids are possible for gene sequences which have some percentage homology with the kidney toxicity predictive gene sequences of this invention. A conservative substitution in a protein is a substitution of one amino acid with an amino acid with similar size and charge. Groups of amino acids known normally to be equivalent are: (a) Ala, Ser, Thr, Pro, and Gly; (b) Asn, Asp, Glu, and Gln; (c) His, Arg, and Lys; (d) Met, Glu, Ile, and Val; and (e) Phe, Tyr, and Trp.

[122] It is also understood that the toxicity predictive genes can be used as guides to predicting toxicity for agents that have been administered via different routes (, intravenous, oral, dermal, inhalation, I, etc.) from the routes that were used to generate the database or to identify the toxicity predictive genes. Furthermore, the invention is not intended to be limiting to agents that have been administered at different dosages than the agents that were used to generate the database or to identify the toxicity predictive genes.

[123] Data described in the examples were generated using the microarray technology disclosed in the Examples. However, the invention is not dependent on using this particular platform. Other similar gene expression analysis technologies may be incorporated in the practice of this invention. These can include, but are not limited to, other arrays containing the predictive genes, RT-PCR (*e.g.*, TaqMan®), branched chain technology, RNAs protection or any other method which quantitatively detects the expression of RNA polynucleotides. The invention can be practiced using these other technologies by generating a database of expression measurements for the predictive genes using samples such as those used in the database described in Example 1. This database can then be used in a model such as the K-nearest neighbor model or can be used to develop any of a number of other models.

[124] The following Examples are provided to illustrate but not to limit the invention

in any manner.

## EXAMPLES

- [125] Example 1 Discovery of Kidney Toxicity Predictive Genes from 24 Hour Expression Data. Materials and Methods: (A) Database of Compounds and Kidney Toxicity: Compounds and treatments list used to construct the kidney database are given in Table 1. This table also provides the evaluation of the kidney toxicity observed as kidney tubular necrosis in samples collected 72 hours after treatment.
- [126] (B) Database of Animal Experiments: Sprague Dawley rats CrI:CD from Charles River, Raleigh, NC were divided into treated rats that receive a specific concentration of the compound (see Table 1) and the control rats that only received the vehicle in which the compound is mixed (*e.g.*, saline).
- [127] At specified timepoints (6h, 24h and 72h) after administration (intraperitoneal route) of the compound, a set number of rats (usually 3 control and 3 treated) were euthanized and tissues collected. Each rat was heavily sedated with an overdose of CO<sub>2</sub> by inhalation and a maximum amount of blood drawn. Exsanguination of the rat by this drawing of blood kills the rat. The method of collecting the tissues is very important and ensures preserving the quality of the mRNA in the tissues. The body of the rat was then opened up and prosectors rapidly removed the tissues (including kidney) and immediately placed them into liquid nitrogen. All of the organs/tissues were completely frozen within 3 minutes of the death of the animal to ensure that mRNA did not degrade. The organs/tissues were then packaged into well-labeled plastic freezer quality bags and stored at -80 degrees until needed for isolation of the mRNA from a portion of the organ/tissue sample.
- [128] (C) Isolating DNA/RNA from animal tissues or cells: Total RNA was isolated from kidney tissue samples using the following materials: Qiagen RNeasy midi kits, 2-mercaptoethanol, liquid N<sub>2</sub>, tissue homogenizer, dry ice Samples were kept on ice when specified.

- [129] If a tissue needed to be broken, then the tissue sample was placed on a double layer of aluminum foil which was then placed within a weigh boat containing a small amount of liquid nitrogen. The aluminum foil was folded around the tissue and then struck by a small foil-wrapped hammer to administer mechanical stress forces.
- [130] About 0.15-0.20 g of kidney tissue was weighed out and placed in a sterile container. To preserve integrity of the RNA, all tissues were kept on dry ice when other samples were being weighed. A RLT (Qiagen®) buffer buffer was added to the sample to aid in the homogenization process. The tissue was homogenized using commercially available homogenizer ( IKA Ultra Turrax T25 homogenizer) with the 7 mm microfine sawtooth shaft and generator (195 mm long with a processing range of 0.25 ml to 20 ml, item # 372718). After homogenization, samples were stored on ice until all samples were homogenized. The homogenized tissue sample was spun to remove nuclei thus reducing DNA contamination. The supernatant of the lysate was then transferred to a clean container containing an equal volume of 70% EtOH in DEPC treated H<sub>2</sub>O and mixed. RNA was isolated by putting the supernatant through an RNeasy spin column, washed, and subsequently eluted. Small quantities of remaining DNA were removed by use of DNase enzyme during the RNA isolation procedure following the instructions provided by Qiagen and alternatively by lithium chloride (LiCl) precipitation following the RNA isolation. The isolated RNA pellet was stored in Rnase-free water or in an RNA storage buffer (10 mM sodium citrate), Ambion Cat #7000. The RNA amount was then quantitated using a spectrophotometer.
- [131] (D) Rat 700 CT chip: Gene expression data was generated from a microarray chip that has a set of toxicologically relevant rat genes which are used to predict toxicological responses. The rat 700 CT gene array is disclosed in U.S. applications 60/264,933; 60/308,161; and pending application filed on January 29, 2002 that claims priority to 60/264,933 and 60/308,161 [Attorney docket 40074-2000600].
- [132] (E) Microarray RT reaction: Fluorescence-labeled first strand cDNA probe was made from the total RNA or mRNA isolated from kidneys of control and treated

rats. This probe was hybridized to microarray slides spotted with DNA specific for toxicologically relevant genes. The materials needed are: total or messenger RNA, primer, Superscript II buffer, dithiothreitol (DTT), nucleotide mix, Cy3 or Cy5 dye, Superscript II (RT), ammonium acetate, 70% EtOH, PCR machine, and ice.

[133] The volume of each sample that would contain 20 $\mu$ g of total RNA (or 2 $\mu$ g of mRNA) was calculated. The amount of DEPC water needed to bring the total volume of each RNA sample to 14  $\mu$ l was also calculated. If RNA was too dilute, the samples were concentrated to a volume of less than 14  $\mu$ l in a speedvac without heat. The speedvac must be capable of generating a vacuum of 0 Milli-Torr so that samples can freeze dry under these conditions. Sufficient volume of DEPC water was added to bring the total volume of each RNA sample to 14  $\mu$ l. Each PCR tube was labeled with the name of the sample or control reaction. The appropriate volume of DEPC water and 8  $\mu$ l of anchored oligo dT mix (stored at -20°C) was added to each tube.

[134] Then the appropriate volume of each RNA sample was added to the labeled PCR tube. The samples were mixed by pipeting. The tubes were kept on ice until all samples are ready for the next step. It is preferable for the tubes to kept on ice until the next step is ready to proceed. The samples were incubated in a PCR machine for 10 minutes at 70°C followed by 4°C incubation period until the sample tubes were ready to be retrieved. The sample tubes were left at 4°C for at least 2 minutes.

[135] The Cy dyes are light sensitive, so any solutions or samples containing Cy-dyes should be kept out of light as much as possible (*e.g.*, cover with foil) after this point in the process. Sufficient amounts of Cy3 and Cy5 reverse transcription mix were prepared for one to two more reactions than would actually be run by scaling up the following:

[136] For labeling with Cy3

8  $\mu$ l 5x First Strand Buffer for Superscript II  
4  $\mu$ l 0.1 M DTT  
2  $\mu$ l Nucleotide Mix  
2  $\mu$ l of 1:8 dilution of Cy3 (*e.g.*, 0.125mM cy3dCTP).

2 ul Superscript II

[137] For labeling with Cy5

8 ul 5x First Strand Buffer for Superscript II

4 ul 0.1 M DTT

2 ul Nucleotide Mix

2 ul of 1:10 dilution of Cy5 (e.g., 0.1mM Cy5dCTP).

2 ul Superscript II

[138] About 18  $\mu$ l of the pink Cy3 mix was added to each treated sample and 18  $\mu$ l of the blue Cy5 mix was added to each control sample. Each sample was mixed by pipeting. The samples were placed in a DNA engine (PTC-200 Petier Thermal Cycler, MJ Research) for 2 hours at 45°C followed by 4°C until the sample tubes were ready to be retrieved.

[139] In addition to the desired cDNA product, the completed RT reaction contained impurities that must be removed. These impurities included excess primers, nucleotides, and dyes. The primary method of removing the impurities was by following the instructions in the QIAquick PCR purification kit (Qiagen cat#120016).

[140] Alternatively, the completed RT reactions were cleaned of impurities by ethanol precipitation and resin bead binding. The samples from DNA engine were transferred to Eppendorf tubes containing 600  $\mu$ l of ethanol precipitation mixture and placed in -80°C freezer for at least 20-30 minutes. These samples were centrifuged for 15 minutes at 20800 x g (14000 rpm in Eppendorf model 5417C) and carefully the supernatant was decanted. A visible pellet was seen (pink/red for Cy3, blue for Cy5). Ice cold 70% EtOH (about 1 ml per tube) was used to wash the tubes and the tubes were subsequently inverted to clean tube and pellet. The tubes were centrifuged for 10 minutes at 20800 x g (14000 rpm in Eppendorf model 5417C), then the supernatant was carefully decanted. The tubes were air dried for about 5 to 10 minutes, protected from light. When the pellets were dried, they were resuspended in 80 ul nanopure water. The cDNA/mRNA hybrid was denatured by heating for 5 minutes at 95°C in a heat block and flash spun. Then the lid of a "Millipore MAHV



N45" 96 well plate was labeled with the appropriate sample numbers. A blue gasket and waste plate (v-bottom 96 well) was attached. About 160  $\mu$ l of Wizard DNA Binding Resin (Promega cat#A1151) was added to each well of the filter plate that was used. Probes were added to the appropriate wells (80  $\mu$ l cDNA samples) containing the Binding Resin. The reaction is mixed by pipeting up and down ~10 times. The plates were centrifuged at 2500 rpm for 5 minutes (Beckman GS-6 or equivalent) and then the filtrate was decanted. About 200  $\mu$ l of 80% isopropanol was added, the plates were spun for 5 minutes at 2500 rpm, and the filtrate was discarded. Then the 80% isopropanol wash and spin step was repeated. The filter plate was placed on a clean collection plate (v-bottom 96 well) and 80  $\mu$ l of Nanopure water, pH 8.0-8.5 was added. The pH was adjusted with NaOH. The filter plate was secured to the collection plate and after 5 minutes was centrifuged for 7 minutes at 2500 rpm.

[141] (F) Purification of Cy –Dye Labeled cDNA: To purify fluorescence-labeled first strand cDNA probes, the following materials were used: Millipore MAHV N45 96 well plate, v-bottom 96 well plate (Costar), Wizard DNA binding Resin, wide orifice pipette tips for 200 to 300  $\mu$ l volumes, isopropanol, nanopure water. It is highly preferable to keep the plates aligned at all times during centrifugation. Misaligned plates lead to sample cross contamination and/or sample loss. It is also important that plate carriers are seated properly in the centrifuge rotor.

[142] The lid of a "Millipore MAHV N45" 96 well plate was labeled with the appropriate sample numbers. A blue gasket and waste plate (v-bottom 96 well) was attached. Wizard DNA Binding Resin (Promega cat#A1151) was shaken immediately prior to use for thorough resuspension. About 160  $\mu$ l of Wizard DNA Binding Resin was added to each well of the filter plate that was used. If this was done with a multi-channel pipette, wide orifice pipette tips would have been used to prevent clogging. It is highly preferable not to touch or puncture the membrane of the filter plate with a pipette tip. Probes were added to the appropriate wells (80  $\mu$ l cDNA samples) containing the Binding Resin. The reaction is mixed by pipeting up and down ~10 times. It is preferable to use regular, unfiltered pipette tips for this step.

The plates were centrifuged at 2500 rpm for 5 minutes (Beckman GS-6 or equivalent) and then the filtrate was decanted. About 200  $\mu$ l of 80% isopropanol was added, the plates were spun for 5 minutes at 2500 rpm, and the filtrate was discarded. Then the 80% isopropanol wash and spin step was repeated. The filter plate was placed on a clean collection plate (v-bottom 96 well) and 80  $\mu$ l of Nanopure water, pH 8.0-8.5 was added. The pH was adjusted with NaOH. The filter plate was secured to the collection plate with tape to ensure that the plate did not slide during the final spin. The plate sat for 5 minutes and was centrifuged for 7 minutes at 2500 rpm. Replicates of samples should be pooled.

[143] (G) Dry-down Process: Concentration of the cDNA probes is preferable so that they can be resuspended in hybridization buffer at the appropriate volume. The volume of the control cDNA (Cy-5) was measured and divided by the number of samples to determine the appropriate amount to add to each test cDNA (Cy-3). Eppendorf tubes were labeled for each test sample and the appropriate amount of control cDNA was allocated into each tube. The test samples (Cy-3) were added to the appropriate tubes. These tubes were placed in a speed-vac to dry down, with foil covering any windows on the speed vac. At this point, heat (45°C) may be used to expedite the drying process. Samples may be saved in dried form at -20°C for up to 14 days.

[144] (H) Microarray Hybridization: To hybridize labeled cDNA probes to single stranded, covalently bound DNA target genes on glass slide microarrays, the following material were used: formamide, SSC, SDS, 2  $\mu$ m syringe filter, salmon sperm DNA (Sigma, cat # D-7656), human Cot-1 DNA (Life Technologies, cat # 15279-011), poly A (40 mer: Life Technologies, custom synthesized), yeast tRNA (Life Technologies, cat # 15401-04), hybridization chambers, incubator, coverslips, parafilm, heat blocks. It is preferable that the array is completely covered to ensure proper hybridization.

[145] About 30  $\mu$ l of hybridization buffer was prepared per cDNA sample (control rat cDNA plus treated rat cDNA). Slightly more than is what is needed should be

made since about 100  $\mu$ l of the total volume made for all hybridizations can be lost during filtration.

| <u>Hybridization Buffer:</u> | <u>for 100 <math>\mu</math>l:</u> |
|------------------------------|-----------------------------------|
| • 50% Formamide              | 50 $\mu$ l formamide              |
| • 5X SSC                     | 25 $\mu$ l 20X SSC                |
| • 0.1% SDS                   | 25 $\mu$ l 0.4% SDS               |

[146] The solution was filtered through 0.2  $\mu$ m syringe filter, then the volume was measured. About 1  $\mu$ l of salmon sperm DNA (10mg/ml) was added per 100  $\mu$ l of buffer.

[147] Alternatively, the hybridization buffer was made up as:

| <u>Hybridization Buffer:</u> | <u>for 101 <math>\mu</math>l:</u> |
|------------------------------|-----------------------------------|
| • 50% Formamide              | 50 $\mu$ l formamide              |
| • 10X SSC                    | 50 $\mu$ l 20X SSC                |
| • 0.2% SDS                   | 1 $\mu$ l 20% SDS                 |

[148] The solution was filtered through 0.2  $\mu$ m syringe filter, then the volume was measured. One microliter of salmon sperm DNA (9.7mg/ml), 0.5  $\mu$ l Human Cot-1 DNA (5  $\mu$ g/ $\mu$ l), 0.5  $\mu$ l poly A (5  $\mu$ g/ $\mu$ l), 0.25  $\mu$ l Yeast tRNA (10  $\mu$ g/ $\mu$ l) was added per 100  $\mu$ l of buffer. The hybridization buffers were compared in validation studies and there was no change in differential gene expression data between the two buffers.

[149] Materials used for hybridization were: 2 Eppendorf tube racks, hybridization chambers (2 arrays per chamber), slides, coverslips, and parafilm. About 30  $\mu$ l of nanopure water was added to each hybridization chamber. Slides and coverslips were cleaned using N<sub>2</sub> stream. About 30  $\mu$ l of hybridization buffer was added to dried probe and vortexed gently for 5 seconds. The probe remained in the dark for 10-15 minutes at room temperature and then was gently vortexed for several seconds and then was flash spun in the microfuge. The probes were boiled or placed in a 95 °C heat block for 5 minutes and centrifuged for 3 min at 20800 x g (14000 rpm, Eppendorf model 5417C). Probes were placed in 70 °C heat block. Each probe remained in this heat block until it was ready for hybridization.

[150] About 25  $\mu$ l was pipeted onto a coverslip. It is highly preferable to avoid the material at the bottom of the tube and to avoid generating air bubbles. This may mean leaving about 1  $\mu$ l remaining in the pipette tip. The slide was gently lowered, face side down, onto the sample so that the coverslip covered that portion of the slide containing the array. Slides were placed in a hybridization chamber (2 per chamber). The lid of the chamber was wrapped with parafilm and the slides were placed in a 42°C humidity chamber in a 42°C incubator. It is preferable to not let probes or slides sit at room temperature for long periods. The slides were incubated for 18-24 hours.

[151] (I) Post-Hybridization Washing: To obtain only single stranded cDNA probes tightly bound to the sense strand of target cDNA on the array, all non-specifically bound cDNA probe should be removed from the array. Removal of all non-specifically bound cDNA probe was accomplished by washing the array and using the following materials: slide holder, glass washing dish, SSC, SDS, and nanopure water. Six glass buffer chambers and glass slide holders were set up with 2X SSC buffer heated to 30-34°C and used to fill up glass dish to 3/4th of volume or enough to submerge the microarrays. The slides were placed in 2X SSC buffer for 2 to 4 minutes while the cover slips fall off. The slides were then moved to 2X SSC, 0.1% SDS and soaked for 5 minutes. The slides were transferred into 0.1X SSC and 0.1% SDS for 5 minutes. Then the slides are transferred to 0.1X SSC for 5 minutes. The slides, still in the slide carrier, were transferred into nanopure water (18 megaohms) for 1 second. To dry the slides, the stainless steel slide carriers were placed on micro-carrier plates and spun in a centrifuge (Beckman GS-6 or equivalent) for 5 minutes at 1000 rpm.

[152] (J) Scanning slides: The washed and dried hybridized slides were scanned on Axon Instruments Inc. GenePix 4000A MicroArray Scanner and the fluorescent readings from this scanner converted into quantitation files (.gpr) on a computer using GenePix software.

[153] II. Array Data, Normalization and Transformation: GeneSpring™ software

(Version 4.1, Silicon Genetics) was used for statistical analyses including identification of genes expressions correlating with histopathology scores, K-means and tree cluster analysis, and predictive modeling using the K-means nearest neighbor (Predict Parameter Values tool).

**[154]** Microarray data were loaded into GeneSpring™ software for analysis as GenePix files as above. Initially, set A training set compounds (see Table 4) data from one microarray was used per animal. Next, set A test set compounds (see Table 4) replicate arrays for each animal were combined into one GenePix file. Specific data loaded into GeneSpring™ software included gene name, GenBank ID control channel mean fluorescence and signal channel mean fluorescence. Expression ratio data (ratio of signal to control fluorescence) were normalized using the 50<sup>th</sup> percentile of the distribution of all genes and control channel. Ratio data were excluded from analysis if the control channel value was <0. For analysis of correlations and predictive values gene expression ratios were transformed as the log of the ratio.

**[155]** Correlation with Histopathology Scores: Histopathology scores for each animal (assigned on a compound-dose basis as indicated in Table 1) were entered with gene expression data by using the GeneSpring™ 'Drawn Gene' function. Correlations between the histopathology scores and gene expression were conducted with the distance measures listed below:

|             |                                   |
|-------------|-----------------------------------|
| standard    | positive and negative correlation |
| smooth      | positive and negative correlation |
| change      | positive correlation              |
| upregulated | positive correlation              |
| Pearson     | positive and negative correlation |
| Spearman    | positive and negative correlation |
| distance    | positive correlation              |

**[156]** These correlation or similarity measures are standard statistical correlation measures that are described in the GeneSpring Advanced Analysis Techniques Manual (Release Data March 13, 2001, Silicon Genetics). Where both positive and negative correlations were obtained combined positive and negative correlating gene lists were also created.

- [157] IV. Class Prediction: The Predict Parameter Values tool in GeneSpring™ software was used for kidney toxicity class prediction. The following is a summary of the procedure used in the GeneSpring predictive software. This is described in GeneSpring Advanced Analysis Techniques Manual (Release Data March 13, 2001, Silicon Genetics) with additional information supplied by Silicon Genetics and a statistical expert. The prediction tool relies on standard statistical procedures that can be implemented in a variety of statistical software packages.
- [158] (IV)(A) Gene Selection: The first step is variable selection of genes to be used for prediction. This entails taking a single gene and a single class (*e.g.*, kidney toxicity) and creating a contingency table. In the table below, columns 1 through  $N$  of the table each represent one possible cutoff point based on the gene expression level (ratio of signal/control) for that class. The number of possible cutoffs is less than or equal to the total number of samples for the class (*e.g.*,  $A$ ). It is possibly less than the total number, since there may be ties in gene expression level. Hence,  $N$ ,  $M$ , and  $X$  may or may not be distinct. In the example, an  $n$ -class problem is illustrated, where  $x$  and  $y$  entries are the class counts at that gene expression cutoff level, for that specific gene and class, either above ("a") or below ("b") the cutoff. "Class1" is the set of all samples (above or below) the cutoff for Class1, and "¬Class1" are all those not in Class1 (above or below) the cutoff, and similarly for the other classes. The class totals in the training set are the total class marginals used to compute Fisher's exact test.
- [159] For a specific gene, and for each class, the best  $p$ -value as calculated by Fisher's Exact Test for independence between one of the pair of columns (*e.g.*, 1a and 1b) and the actual class totals (*e.g.*,  $A$ ) is used to score the gene ( $-\ln(p)$  = the score) for that class. Thus, there are  $N$  (or,  $M$ ,  $Q$  etc.) contingency tables, where the best score of the  $N$  tables is used for that class and gene. If there is a wide disparity between the above and below counts in either the  $a$  or  $b$  column (this is a two-sided Fisher's Exact Test), the smaller the  $p$ -value and the higher the score.
- [160] The genes per class are rank ordered by the most discriminating (highest)

score. The predictivity list is composed of the most discriminating genes per class. Namely, genes are combined that best discriminate class 1 with those that best discriminate class 2 and so on. The genes are selected in rotation of the highest score per class. Duplicate genes are ignored in the rotation and not added to the list, the gene with the next highest score is taken.

[161] The training samples now have only the gene list garnered from the above procedure. As an example, where once the training samples may have had an initial list of 200 genes per sample, they now have only a subset composed of the gene list, for example, 50 (the number of predictivity genes specified) that are selected from the initial list by the gene selections procedure. Thus, each sample is a vector of 50 normalized expression ratios. Since the selection of genes is done in rotation, the list contains 25 genes for one class, and 25 for the other class. The matrix below illustrates the basic features of this gene selection process.

|         |                  |                  |     |                  |                  |                                 |
|---------|------------------|------------------|-----|------------------|------------------|---------------------------------|
| Gene 1  | 1a               | 1b               | ... | Na               | Na               |                                 |
| Class   | Expression above | Expression below | ... | Expression above | Expression below | Actual Class Totals (Marginals) |
| Class1  | x1.1a            | x1.1b            | ... | x1.Na            | x1.Nb            | A                               |
| !Class1 | y1.1a            | y1.1b            | ... | y1.Na            | y1.Nb            | B                               |
| Gene 1  | 1                | 2                | ... | M                |                  |                                 |
| Class2  | x1.2a            | x1.2b            | ... | x1.Ma            |                  | C                               |
| !Class2 | y1.2a            | y1.2b            | ... | y1.Ma            |                  | D                               |
| .       | .                | .                | .   | .                | .                | .                               |
| Gene 1  | 1                | 2                | ... | Qa               | Qb               |                                 |
| Classn  | x1.na            | x1.nb            | ... | x1.Qa            | x1.Qb            | X                               |
| !Classn | y1.na            | y1.nb            | ... | y1.Qa            | y1.Qb            | Y                               |

[162] After the genes to be used in the training set have been selected, the test set is classified based on the *k*-nearest neighbor (*knn*) voting procedure. Using just those genes in the gene list, for each sample in the test set of samples, the *k* nearest neighbors in the training set are found with the Euclidean distance. The class in which each of the *k* nearest neighbors is determined, and the test set sample is assigned to the class with the largest representation in the *k* nearest neighbors after

adjusting for the proportion of classes in the training set.

[163] For example, in a two-class problem, let there be 30 samples of class 1 and 60 samples of class 2 in the training set. With  $k = 9$  say it can be determined that 7 of the nearest neighbors to a sample from the testing set are in class 1. The sample can then be classified as being a member of class 1. If another sample from the test set has a total of 4 nearest neighbors in class 1, after adjusting for the proportion, this sample would be assigned to class 1 rather than class 2, even though the majority vote suggests assignment to class 2.

[164] VI. Decision Threshold: The decision threshold is a mechanism to help clearly define the class into which the sample will fall, and can be set to reject classification if the voting is very close or tied. (Thus,  $k$  can be even for two-class problems without worrying about the tie problem.) A  $p$ -value is calculated for the proportion of neighbors in each class against the proportions found in the training set, again using Fisher's exact test, but now a one-sided test.

[165] For example, let  $k = 11$ , if the proportion of neighbors of class 1 in the test set is  $6/11$ , and the proportion of class 1 in a 100 sample training set is 0.4, the  $p$ -value calculated is 0.29 (half the two-sided test). If the proportion in the training set is 0.1, the  $p$ -value is 0.004. The smaller the  $p$ -value the greater the likelihood that the sample from the testing set belongs to that class.

[166] A  $p$ -value ratio (P-value) is set as a way of setting the level of confidence in individual sample predictions based on the ratio of  $p$ -values for the best class (lowest  $p$ -value) versus the second best class (second lowest  $p$ -value). For example, if the P-value is set at 0.5 and the ratio of  $p$ -values for a particular sample is 0.6, then the predictive model will not make a call for that sample.

[167] VII. Training and Test Data Sets: Data were each separated into 6 training and test sets. The first training and test set was created by allocating one set of data as a training set (Set A training set) and another set of data as a test set (Set A test set). Other training and test sets were created by randomly distributing the



compounds into the sets. This was accomplished by assigning random numbers to lists of compounds that are negative and positive for histopathology, sorting by random number, and then dividing the sorted lists into a specific number of training and test sets. The training and test set assignments are presented in Table 4.

[168] VIII. Kidney Toxicology Classification: Kidney toxicity classifications were entered for training and test set as a parameter column. Toxicity, as defined by observation of kidney tubular necrosis in the kidney at 72 hours after treatment, was entered as a "yes" or "no" for each animal in a compound-dose group. Additionally, a parameter column for random histopathology classification was designated. This was done by randomly assigning the same number of "yes" and "no" calls to the individual animals.

[169] IX. Prediction Output and Initial Data Processing: The "Predict Parameter Value" tool of GeneSpring was used with each of the training and test sets to generate predictions of histopathology classifications of the test sets. Unless otherwise specified a nearest neighbor setting of 10 (default) and P-value ratio cutoff of 0.5 was used. The number of genes used to predict was varied with standard numbers of 50, 40, 30, 20, 10, 5, 2 and 1 genes used. For each number of genes the numbers of correct calls, incorrect calls and non-calls were recorded. Non-calls are cases where no prediction was made because the P-value ratio exceeded the specified P-value ratio cutoff. Calculations were made for overall percent correct calls (number of correct classifications/number of samples), percent correct calls of called samples (number of correct classifications/number of samples with calls) and percent of called samples (samples with calls/number of samples).

[170] For each input list and optimal number of predictive genes (lowest number of genes giving a maximum overall percent of correct calls) additional information was recorded that included the list of specific genes in the optimum predictive set.

[171] X. Results: Expression array data were first examined for the existence of genes whose expression correlated with histopathology scores. Table 1 presents a list of the compounds and dose levels along with the kidney histopathology

classification and histopathology severity scores used for this analysis. For each distance measure the probability was adjusted in increments of 0.05 until at least 50 correlating genes were obtained. Lists of correlating genes were obtained using the distance measures described in Materials and Methods. Example sets of correlating genes are provided in Tables 2 and 3.

[172] The correlating gene lists as well as the entire array gene list were provided as input lists to the GeneSpring Predict Parameter value tool (described in Materials and Methods) that employs a K-means nearest neighbor (*knn*) predictive model. These lists as well as the entire array gene list were used for each of the six training and test sets defined in Materials and Methods to generate predictions of histopathology classifications of the test sets. Input genes for the Predict Parameter Value feature included all 700 genes in the GenePix file (the rat CT Array) which was disclosed in a currently pending application (serial number [Attorney docket no. 40074-2000600]) filed on January 29, 2002, as well as smaller lists of genes whose expressions correlated with histopathology by the correlation measures described previously. The number of genes used to predict are varied with standard numbers of 50, 40, 30, 20, 10, 5, 2 and 1 genes used. The specified number of predictive genes was varied to obtain an optimum number of predictive genes. Figure 2 presents a typical profile for obtaining an optimum gene list.

[173] After this was done for all 6 training and test sets, all gene lists were then merged to create one aggregate list of predictive genes. Each gene on this aggregate list has predictive value for at least one of the training and test sets because it was observed to contribute to an optimum predictivity for a specific training/test set. The aggregate list was subdivided into smaller lists of genes based on the number of times a gene was predictive for an individual training or test set. For example, if 6 training and test sets were used, genes that were predictive in all 6 training and test sets were designated as Combo (combination) 6. Genes that were predictive in only 5 of 6 training and test sets were designated as Combo 5, etc. A list of predictive genes organized by their occurrence in the separate training and test sets is presented in Table 5.

**[174] Example 2 Predictive Properties and Evaluation of Predictive Genes from 24 Hour Expression Data**

(A) Materials and Methods: The database used was as described in Example 1.

**[175]** (B) Array data, normalization procedures and transformations used in these analyses are as described in Example 1. Table 39 presents 24 hour gene expression data for the predictive genes. These data can be used with a k-means nearest neighbor prediction model (as available in GeneSpring or other statistical software packages) to make predictions as described in this example.

**[176]** (C) The Predict Parameter Values tool in GeneSpring™ software was used for kidney toxicity class prediction. A description of this tool and the statistical procedures used is provided in Example 1.

**[177]** (D) The training and test data sets used are those described in Table 4.

**[178]** (E) Kidney toxicology classifications used are described in Table 1. In this analysis randomized classifications (same number of "yes" and "no" classifications distributed randomly among the samples) were used.

**[179]** (F) Prediction Output and Initial Data Processing: For each gene list prediction used for evaluation a table of data generated by the Predict Parameter Values tool in GeneSpring™ software was saved which provided for each sample in the test set the actual call ("yes" or "no" for kidney toxicity), the predicted call ("yes", "no" or no call for kidney toxicity) and the P-value cutoff ratio. This set of data was used to calculate predictive performance measures provided below.

**[180]** (G) Measures of prediction used for these analyses are generally accepted prediction measures for information about actual and predicted classifications done by a classification system (Venables and Ripley, *Modern Applied Statistics with S-Plus*, 3rd edition, Springer, 1994 and Kubat and Matwin, *Proc. 14th International Conference on Machine Learning*, 1997). Results from predictions of a two class case can be described as a two-class matrix:

| Actual | Predicted |          |
|--------|-----------|----------|
|        | Negative  | Positive |
|        | Negative  | a        |
|        | Positive  | b        |
|        |           | c        |
|        |           | d        |

- [181] Standard terms used for prediction are: Accuracy, which is the proportion of total number of predictions that are correct is calculated as:  $(a+d)/(a+b+c+d)$ .
- [182] False positive rate is the proportion of negative cases that are incorrectly classified as positive is calculated as:  $b/a+b$ .
- [183] False negative rate is the proportion of positive cases that are incorrectly classified as negative is calculated as:  $c/c+d$ .
- [184] Geometric-mean is the performance measure that takes into account proportion of positive and negative cases (Kubat et al., *ibid*) is calculated as: the square root of  $TP \cdot TN$ , where  $TP$ =true positive rate ( $d/c+d$ ) and  $TN$ =true negative rate ( $a/a+b$ ). In those cases where no prediction was made because the p-value ratio exceeded the cutoff-value (generally 0.5), the non-call was considered to be incorrect.
- [185] (H) Subsets of randomly selected genes were prepared from the predictive gene sets to test whether such subsets would have predictive value. Assignments of genes to these subsets are presented in Tables 6-10.
- [186] (I) Prediction results for 24 hour expression data using genes identified as predictive are presented in Table 11. These data indicate a very high accuracy in predicting kidney toxicity. Mean accuracy exceeded 0.9 (90% accuracy) for the entire predictive gene list (Combo All) and the Combo 6 gene subset and 0.8 (80% accuracy) for the Combo 5 and 4 subsets. As expected, the predictive performance of the gene sets increased from the lowest occurrence gene list (Combo 1) to the highest occurrence gene list (Combo 6).
- [187] Because these predictions were conducted with multiple training/test set combinations, it is possible to obtain an indication of the variability in prediction rates

and robustness of the prediction capabilities of these gene sets. For the Combo All and Combo 6, 5 and 4 gene sets there was very good predictivity for all training/test sets of data with over 0.8 accuracy as a minimum value for any one training and test set. False positive prediction rates were generally low with means less than 0.1 for Combo All and Combo 6, 5 and 4. Because the proportion of negative classifications was much higher than the proportion of positive (toxic) classifications in these sample sets the false negative rates would be expected to be higher than the false positive rates and this was observed to be the case. Although the false negative rates were higher than the false positive rates, there was still very good prediction of positive responses with mean false negative rates of about 0.3 for Combo All, Combo 6, Combo 5 and Combo 4 gene sets. The geometric mean was used as an indication of predictive performance that includes consideration of the proportion of positive and negative classifications. All gene sets gave geometric mean measures  $>0.5$  and three gene sets (Combo All, Combo 6 and Combo 5) had mean measures  $>0.8$ .

[188] In these analyses, in cases where no prediction was made because the p-value ratio exceeded the cutoff-value (generally 0.5), the non-call was considered to be incorrect.

[189] Prediction results for 24 hour expression data using genes identified as predictive and the predicting unit is compound-dose are presented in Table 12. This prediction unit is probably the most relevant for toxicology prediction. The performance of the genes in predicting compound-dose toxicity is even better than predictions on an individual animal basis. These data indicate a very high accuracy in predicting kidney toxicity. Mean accuracy exceeded 0.9 (90% accuracy) for the entire predictive gene list (Combo All) and Combo 6, 5, 4 and 3 gene lists. As expected, the predictive performance of the gene sets increased from the lowest occurrence gene list (Combo 1) to the highest occurrence gene list (Combo 6). Accuracy was better than 0.8 (80%) for the Combo 2 and Combo 1 lists. Variability in accuracy was low for most of the gene lists with  $>0.8$  minimum accuracy for any single training and test set observed for the Combo All and Combo 6, 5, 4 and 3 gene lists. Particularly noteworthy on the compound-dose level prediction is the low

false-negative rate observed for Combo All, Combo 6 and Combo 5 gene lists. The mean false negative rate was about 0.2 or less for these gene lists. As observed on an individual animal basis the false-positive rate was very low for all gene sets with mean rates of  $<0.12$  for all gene sets.

[190] One noteworthy feature of the predictive ability is the ability to distinguish between effects of a compound at different dose levels. Two compounds, gancyclovir and cyclophosphamide, produced kidney toxicity at the high dose but not at the low dose. The predictive gene sets, particularly the Combo All, Combo 6 and Combo5 sets, accurately predicted toxicity at the high dose level, but not at the low dose level.

[191] Prediction results for 24 hour expression data using genes identified as predictive and the predicting unit is compound are presented in Table 13. In terms of predicting toxicity of compounds the predictive capability was excellent with no compounds missed using the Combo 6 and Combo 5 gene sets and very low false positive rates for all of the gene sets.

[192] Cumulative performance for the Combo gene lists was examined by adding genes one at a time in an order based on predictive weight as calculated by GeneSpring software. This order (and predictive weight) were different for each training set so a mean weight was used to obtain a single gene order for the predictive sets tested. The gene order is presented in Table 14.

[193] Cumulative predictive performance for the Combo 6, Combo 5 and Combo 4 predictive gene sets are presented in Figures 4-6.

[194] The cumulative performance data clearly indicate that very good predictive performance can be achieved with small subsets of the Combo gene sets. For Combo 6, the accuracy reached a plateau level of about 90% at 3 genes. For Combo 5, a similar plateau level was reached with about 8 genes and for Combo 4 the plateau level was reached with about 13 genes. This illustrates the increased predictive power of small sets of genes rather than single genes. The increased

number of genes required to reach a predictive performance plateau of the different Combo sets is consistent with the hierarchy of performance prediction in the Combo sets.

[195] Tables 15 and 16 show the level of predictive accuracy of individual genes of Combo 6 and Combo 5 (The top combo subsets with the highest levels, 92.1% and 89.6%, respectively, of predictive accuracy on an individual sample basis) for 24 hour kidney data.

[196] These tables show that overall, individual genes of both combo groups did not perform as well as the whole combination, as the average predictive accuracy of individual genes of Combo 6 was 67.7% and for Combo 5 was 62.7%. The table also shows that while some of the individual genes of both Combos gave a moderate to good level of predictive accuracy (as high as 79.7% for Combo 6 and as high as 75.6% for Combo 5), the predictive accuracy of individual genes never exceeded the predictive accuracy of the whole combination. The data further support the cumulative gene predictivity conclusion that small subsets of genes have superior predictive power compared to individual genes.

[197] In order to assess the performance of subsets of genes, predictive performance was evaluated for subsets of genes randomly selected from the total combined predictive list (Combo All) and the top Combo sets (as defined in Materials and Methods). Prediction results for 24 hour expression data using randomly selected subsets of genes are presented in Table 17.

[198] These data clearly indicate that subsets of the Combo gene lists have predictive power. The predictive performance, as indicated by several measures including accuracy and geometric mean, increased in parallel with the predictive power of the gene set from which the genes were selected. The predictive power also generally increased as the number of randomly collected genes increased. In the case of the Combo 4, 5 and 6 sets, the 15 gene random subset had predictive performance that was close to that of the entire gene set.

[199] Table 18 compares prediction accuracy for correct classification of kidney toxicity and for the same proportion of positive and negative toxicity calls randomly assigned to the samples (random classification). For each gene set or subset predictions were made using the same six training/test sets as for the other prediction analyses. Additionally, sets of genes were randomly chosen from the array which were not identified on the list of 216 predictive genes at 24 hour (Example 1, Table 10).

[200] It is clear from these data that the predictions with accurate classification are much better than predictions with randomized classification. This means that the predictive results are not simply due to chance and large data sets but are due to significant, meaningful predictive association between the gene expression of the predictive genes and the kidney toxicity. The accuracy numbers for the gene sets selected from a list of all genes on the array minus the predictive genes are much lower than the Combo predictive lists and the random subsets of these predictive lists. This also verifies the predictive power of the identified predictive genes. The fact that the predictive numbers from these subsets are somewhat higher for accurate than random classification is likely due to some residual predictivity in these genes that is not very substantial.

[201] Example 3: Discovery of Kidney Toxicity Predictive Genes from 6 Hour Expression Data: (A) Materials and Methods: Compounds and treatments list used to construct the kidney database are given in Example 1. This table also provides the evaluation of the kidney toxicity observed as kidney tubular necrosis in samples collected 72 hours after treatment. The database is described in detail in Example 1. This Example analyzes expression data from samples collected 6 hours after treatment. Array data, normalization and transformation procedures used were as described in Example 1. Procedures and methods for obtaining gene lists correlating with histopathology scores were as described in Example 1 with scores as in Example 1. The Predict Parameter Values tool in GeneSpring™ software used for kidney toxicity class prediction is described in detail in Material and Methods of Example 1.



- [202] (B) Training and Test Data Sets: Data were each separated into 6 training and test sets. The first training and test set was created by allocating one set of data as a training set (Set A training set) and another set of data as a test set (Set A test set). Other training and test sets were created by randomly distributing the compounds into the sets. This was accomplished by assigning random numbers to lists of compounds that are negative and positive for histopathology, sorting by random number, and then dividing the sorted lists into a specific number of training and test sets. The training and test set assignments are presented in Table 19.
- [203] (C) Kidney toxicity classifications were entered for training and test set as a parameter column. Toxicity, as defined by observation of kidney tubular necrosis in the kidney at 72 hours after treatment, was entered as a "yes" or "no" for each animal in a compound-dose group. Additionally, a parameter column for random histopathology classification was designated. This was done by randomly assigning "yes" and "no" calls to the individual animals. The total number of "yes" and "no" calls was maintained the same as in the correct classification, so that the proportion of "yes" and no calls was the same in all the training and test sets.
- [204] (D) Prediction Output and Initial Data Processing: The "Predict Parameter Value" tool of GeneSpring was used with each of the training and test sets to generate predictions of histopathology classifications of the test sets. Unless otherwise specified a nearest neighbor setting of 10 (default) and P-value ratio cutoff of 0.5 was used. The number of genes used to predict was varied with standard numbers of 50, 40, 30, 20, 10, 5, 2 and 1 genes used. For each number of genes the numbers of correct calls, incorrect calls and non-calls were recorded. Non-calls are cases where no prediction was made because the P-value ratio exceeded the specified P-value ratio cutoff. Calculations were made for overall percent correct calls (number of correct classifications/number of samples), percent correct calls of called samples (number of correct classifications/number of samples with calls) and percent of called samples (samples with calls/number of samples).
- [205] For each input list and optimal number of predictive genes (lowest number of

genes giving a maximum overall percent of correct calls) additional information was recorded that included the list of specific genes in the optimum predictive set.

[206] (E) Results: Expression array data were first examined for the existence of genes whose expression correlated with histopathology scores. Materials and Methods of Example 1 presents a list of the compounds and dose levels along with the kidney histopathology classification and histopathology severity scores used for this analysis. For each distance measure the probability was adjusted in increments of 0.05 until at least 50 correlating genes were obtained. Lists of correlating genes were obtained using the distance measures described in Materials and Methods. Example sets of correlating genes are provided in Tables 20 and 21. The correlating gene lists as well as the entire array gene list were provided as input lists to the GeneSpring Predict Parameter value tool (described in Materials and Methods) that employs a K-means nearest neighbor (*knn*) predictive model. These lists as well as the entire array gene list were used for each of the six training and test sets defined in Materials and Methods to generate predictions of histopathology classifications of the test sets. Input genes for the Predict Parameter Value feature included all 700 genes in the GenePix file (the rat CT Array) as well as smaller lists of genes whose expressions correlated with histopathology by the correlation measures described previously. The number of genes used to predict are varied with standard numbers of 50, 40, 30, 20, 10, 5, 2 and 1 genes used. The specified number of predictive genes was varied to obtain an optimum number of predictive genes.

[207] After this was done for all 6 training and test sets, all gene lists were then merged to create one aggregate list of predictive genes. Each gene on this aggregate list has predictive value for at least one of the training and test sets because it was observed to contribute to an optimum predictivity for a specific training/test set. The aggregate list was subdivided into smaller lists of genes based on the number of times a gene was predictive for an individual training or test set. For example, if 6 training and test sets were used, genes that were predictive in all 6 training and test sets were designated as Combo (combination) 6. Genes that were predictive in only 5 of 6 training and test sets were designated as Combo 5, etc.

- [208] A list of predictive genes organized by their occurrence in the separate training and test sets is presented in Table 22.
- [209] Example 4 Predictive Properties and Evaluation of Predictive Genes from 6 Hour Expression Data: (A) Materials and Methods: The database used was as described in Example 1. Array data, normalization procedures and transformations used in these analyses are as described in Example 1. Table 38 presents 6 hour gene expression data for the predictive genes. These data can be used with a k-means nearest neighbor prediction model (as available in GeneSpring or other statistical software packages) to make predictions as described in this example. The Predict Parameter Values tool in GeneSpring™ software was used for kidney toxicity class prediction. A description of this tool and the statistical procedures used is provided in Example 1.
- [210] (B) Training and Test Data Sets: The training and test data sets used are those described in Table 19.
- [211] (C) Kidney Toxicology Classification: Kidney toxicology classifications used are described in Example 1. In this analysis randomized classifications (same number of "yes" and "no" classifications distributed randomly among the samples) were used.
- [212] (D) Prediction Output and Initial Data Processing: For each gene list prediction used for evaluation a table of data generated by the Predict Parameter Values tool in GeneSpring™ software was saved which provided for each sample in the test set the actual call ("yes" or "no" for kidney toxicity), the predicted call ("yes", "no" or no call for kidney toxicity) and the P-value cutoff ratio. This set of data was used to calculate predictive performance measures provided below.
- [213] (E) Prediction Measures: Measures of prediction used for these analyses are generally accepted prediction measures for information about actual and predicted classifications done by a classification system (Venables and Ripley, *ibid* and Kubat and Matwin, *ibid*). Results from predictions of a two class case can be described as

a two-class matrix as described above.

- [214] (F) Results: Prediction results for 6 hour expression data using genes identified as predictive and the predicting unit is compound-dose are presented in Table 23. This prediction unit is probably the most relevant for toxicology prediction. The performance of the genes in predicting compound-dose toxicity is even better than predictions on an individual animal basis.
- [215] These data indicate some accuracy in predicting kidney toxicity. Mean accuracy exceeded 0.7 (70% accuracy) for the entire predictive gene list (Combo All) and Combo 6 and 5 gene lists. As expected, the predictive performance of the gene sets generally increased from the lowest occurrence gene list (Combo 1) to the highest occurrence gene list (Combo 6) with the exception of the Combo 5 list. Mean false negative values were in the range of 0.4-0.6 as were the geometric mean measures.
- [216] Example 5 Discovery of Kidney Toxicity Predictive Genes from 72 Hour Expression Data: (A) Materials and Methods: Compounds and treatments list used to construct the kidney database are given in Example 1. This table also provides the evaluation of the kidney toxicity observed as kidney tubular necrosis in samples collected 72 hours after treatment. The Database is described in detail in Example 1. This Example analyzes expression data from samples collected 6 hours after treatment. Array data, normalization and transformation procedures used were as described in Example 1. Procedures and methods for obtaining gene lists correlating with histopathology scores were as described in Example 1 with scores as in Example 1. The Predict Parameter Values tool in GeneSpring™ software used for kidney toxicity class prediction is described in detail in Material and Methods of Example 1.
- [217] (B) Training and Test Data Sets: Data were each separated into 6 training and test sets. The first training and test set was created by allocating one set of data as a training set (Set A training set) and another set of data as a test set (Set A test set). Other training and test sets were created by randomly distributing the

compounds into the sets. This was accomplished by assigning random numbers to lists of compounds that are negative and positive for histopathology, sorting by random number, and then dividing the sorted lists into a specific number of training and test sets.

The training and test set assignments are presented in the following Table 24.

- [218]** (C) Kidney Toxicology Classification: Kidney toxicity classifications were entered for training and test set as a parameter column. Toxicity, as defined by observation of kidney tubular necrosis in the kidney at 72 hours after treatment, was entered as a "yes" or "no" for each animal in a compound-dose group. Additionally, a parameter column for random histopathology classification was designated. This was done by randomly assigning "yes" and "no" calls to the individual animals. The total number of "yes" and "no" calls was maintained the same as in the correct classification, so that the proportion of "yes" and no calls was the same in all the training and test sets.
- [219]** (D) Prediction Output and Initial Data Processing: The "Predict Parameter Value" tool of GeneSpring was used with each of the training and test sets to generate predictions of histopathology classifications of the test sets. Unless otherwise specified a nearest neighbor setting of 10 (default) and P-value ratio cutoff of 0.5 was used. The number of genes used to predict was varied with standard numbers of 50, 40, 30, 20, 10, 5, 2 and 1 genes used. For each number of genes the numbers of correct calls, incorrect calls and non-calls were recorded. Non-calls are cases where no prediction was made because the P-value ratio exceeded the specified P-value ratio cutoff. Calculations were made for overall percent correct calls (number of correct classifications/number of samples), percent correct calls of called samples (number of correct classifications/number of samples with calls) and percent of called samples (samples with calls/number of samples).
- [220]** For each input list and optimal number of predictive genes (lowest number of genes giving a maximum overall percent of correct calls) additional information was recorded that included the list of specific genes in the optimum predictive set.

**[221]** (E) Results: Expression array data were first examined for the existence of genes whose expression correlated with histopathology scores. Materials and Methods of Example 1 presents a list of the compounds and dose levels along with the kidney histopathology classification and histopathology severity scores used for this analysis. For each distance measure the probability was adjusted in increments of 0.05 until at least 50 correlating genes were obtained. Lists of correlating genes were obtained using the distance measures described in Materials and Methods. Example sets of correlating genes are provided in Tables 25-26. The correlating gene lists as well as the entire array gene list were provided as input lists to the GeneSpring Predict Parameter value tool (described in Materials and Methods) that employs a K-means nearest neighbor (*knn*) predictive model. These lists as well as the entire array gene list were used for each of the six training and test sets defined in Materials and Methods to generate predictions of histopathology classifications of the test sets. Input genes for the Predict Parameter Value feature included all 700 genes in the GenePix file (the Rat CT Array) as well as smaller lists of genes whose expressions correlated with histopathology by the correlation measures described previously. The number of genes used to predict are varied with standard numbers of 50, 40, 30, 20, 10, 5, 2 and 1 genes used. The specified number of predictive genes was varied to obtain an optimum number of predictive genes.

**[222]** After this was done for all 6 training and test sets, all gene lists were then merged to create one aggregate list of predictive genes. Each gene on this aggregate list has predictive value for at least one of the training and test sets because it was observed to contribute to an optimum predictivity for a specific training/test set. The aggregate list was subdivided into smaller lists of genes based on the number of times a gene was predictive for an individual training or test set. For example, if 6 training and test sets were used, genes that were predictive in all 6 training and test sets were designated as Combo (combination) 6. Genes that were predictive in only 5 of 6 training and test sets were designated as Combo 5, etc.

**[223]** A list of predictive genes organized by their occurrence in the separate training and test sets is presented in Table 27.

- [224] Example 6: Predictive Properties and Evaluation of Predictive Genes from 72 Hour Expression Data: (A) Materials and Methods: The Database used was as described in Example 1. Array data, normalization procedures and transformations used in these analyses are as described in Example 1. Table 40 presents 72 hour gene expression data for the predictive genes. These data can be used with a k-means nearest neighbor prediction model (as available in GeneSpring or other statistical software packages) to make predictions as described in this example. The Predict Parameter Values tool in GeneSpring™ software was used for kidney toxicity class prediction. A description of this tool and the statistical procedures used is provided in Example 1. The training and test data sets used are those described in Example 1.
- [225] (B) Kidney Toxicology Classification: Kidney toxicology classifications used are described in Example 1. In this analysis randomized classifications (same number of "yes" and "no" classifications distributed randomly among the samples) were used.
- [226] (C) Prediction Output and Initial Data Processing: For each gene list prediction used for evaluation a table of data generated by the Predict Parameter Values tool in GeneSpring™ software was saved which provided for each sample in the test set the actual call ("yes" or "no" for kidney toxicity), the predicted call ("yes", "no" or no call for kidney toxicity) and the P-value cutoff ratio. This set of data was used to calculate predictive performance measures provided below.
- [227] (D) Prediction Measures: Measures of prediction used for these analyses are generally accepted prediction measures for information about actual and predicted classifications done by a classification system (Venables and Ripley, *ibid* and Kubat and Matwin, *ibid*). Results from predictions of a two class case can be described above.
- [228] (E) Results: Prediction results for 72 hour expression data using genes identified as predictive and the predicting unit is compound-dose are presented in Table 28. This prediction unit is probably the most relevant for toxicology prediction.

The performance of the genes in predicting compound-dose toxicity is even better than predictions on an individual animal basis.

**[229]** These data indicate a high accuracy in predicting kidney toxicity. Mean accuracy exceeded 0.85 (85% accuracy) for the entire predictive gene list (Combo All) and 0.8 (80% accuracy) for the Combo 6 and 4 subsets. False positive prediction rates were generally low for Combo All (mean less than 0.1) as well as the other Combos except Combo 2 (means 0.138 – 0.228). Because the proportion of negative classifications was much higher than the proportion of positive (toxic) classifications in these sample sets the false negative rates would be expected to be higher than the false positive rates and this was observed to be the case. The geometric mean was used as an indication of predictive performance that includes consideration of the proportion of positive and negative classifications. Combo All, Combo 6, Combo 5, and Combo 4 gave geometric mean measures >0.6.

**[230]** Example 7 Alternate Models for Predicting Kidney Toxicity: (A) Materials and Methods: The database used for evaluation of these models was the 24 hour expression data for kidney samples described above. Expression data was for the Combo 6 set of predictive genes as described herein. Due to heteroscedasticity (*i.e.*, the variance increases proportionately more than the mean increases) of the gene expression ratio data, a log transformation of the data is often considered. In general untransformed data was used but for some models log transformed data was used for comparison. Six training and testing sets were used that are the same as described in Example 1.

**[231]** (B) Predictive Modeling: The predictive task with the kidney toxicology gene expression data is a two-class classification problem, where the two classes of possible responses are defined by either kidney toxicity histopathology (*yes*) or absence of kidney toxicity histopathology (*no*). This is an uneven class problem in that the class of *yes* responses is roughly 20 percent of the data or less in the database tested. A discrimination function is used to classify a training set. This function is cross-validated with a testing set, often repeatedly to quantify the mean



and variation of the classification error. There are numerous common discrimination functions, and a comparative study of the performance of these functions is useful in determining the best classifier. Additional measures are then used to compare the performance of the classifiers. Since the classes are of significantly uneven sizes, use a geometric mean measure (*GMM*) was used to compare models, namely, the square root of the product of the true positives and the true negatives.

[232] Common discrimination methods are Fisher's linear discriminant, quadratic discriminant (mahalanobis distance), *k*-nearest neighbors (*knn*), logistic discriminant (MacLachlan, 1992), classification trees (or more generally known as recursive partitioning) (Breiman et al., 1984; Clark and Pregibon, 1993; Quinlan and Kaufman, 1988), and neural network classifiers (Ripley, 1996). Most are formula-based such as linear and quadratic discriminant, whereas others are rule-based, such as recursive partitioning, or algorithmically based, such as *knn*. *knn* is also database dependent in that a database containing training set is needed to perform nearest neighbor search and classification.

[233] (C) Classifier Models: A variety of common classification techniques were evaluated. As an extension of the *k*-means nearest neighbor (*knn*) model a simple hybrid classifier was designed and tested, using the *knn* results, to transform the *knn* model into a database independent model. This model is termed a *centroid* model. The centroid model uses the correctly identified test data results from *knn* and locates a centroid of the subset of *k* samples that are of the same class for each correctly identified test sample. The centroid is assigned the correct class, and with new test data, a sample is assigned the class of its nearest centroid.

[234] In addition to the *knn* and centroid models described above, tree, centroid, logistic, and neural network models were employed. The neural network is a simple, feed-forward network, allowing skip layers, and with an entropy fitting criterion. Linear classifiers perform poorly with respect to this data and quadratic classifiers perform modestly, so their results are not presented.

[235] (D) Cross Validation of the Models: Six training and testing sets were used to cross-validate *knn*. Gene selection ranking was then performed on each training set. A number of different gene sets were used for each of the six sets and the best GMM value was chosen to represent the performance of the model. Trees were pruned via ten-fold internal cross-validation (*i.e.*, using subsets of the training set) for each training set, and then the tree was used to predict the testing set. A GMM was thus calculated for each testing set. Trees perform the gene selection via pruning, and anywhere from one to five genes were selected for each tree. The centroid model is five-fold cross-validated using random subsets of the testing set. The mean of the GMM of each of the validation runs is used as the performance measure. The top five discriminating genes are used in the centroid models. The logistic discrimination uses a stepwise backwards selection process to determine the gene set during the training phase. Three to six genes are typically selected via this process. A single performance is then obtained using the corresponding testing set. A neural network is trained on each training set and then validated on the corresponding testing set. All 28 genes in the data set are used with the neural network model.

[236] (E) Results: Model performance is presented in Table 29. The *knn* model performed the best overall. If the best common gene selection is used, *knn* is still the best, though the performance mean is more in line with the logistic and centroid models. Logistic and centroid models perform the next best overall, and either could be used successfully with a less than 25 percent misclassification error, if a database independent solution is preferred. Log transformations of the data produced mixed results when used with logistic and neural network models, suggesting that such a transformation has little impact. Tree and neural network models perform the poorest respectively on average; however, all of the models perform well for this type of data on at least some of the training and testing pairs, with the equivalent of a less than 20 percent misclassification error. The *knn*, centroid and neural network models could be improved by a more thorough gene selection scheme.

[237] Table 30 presents logistic discrimination coefficients derived from this analysis. These coefficients may be used in a logistic discriminant model to obtain

predictions of kidney toxicity when expression values for the indicated genes are determined using appropriate samples and an appropriate microarray expression detection system such as the Rat CT array used to develop the Database.

[238] Similarly, the classification model for all of the data using a classification tree in S-Plus software provided the following rule for predicting toxicity: if  $Gadd45 < 1.474$  AND Tissue inhibitor of metalloproteinases 1  $< 1.786$ , then "No" (not toxic), otherwise "Yes" Toxic.

[239] For this model and rule, the internal performance with the entire database was a total 7 of 241 samples were misclassified, with a misclassification error 0.03. A total of 2 of 38 of the yes class (toxic) are misclassified and 5 of 203 no class (not toxic) are misclassified. This is equivalent to a 0.053 and 0.025 misclassification error, respectively. The geometric mean performance measure is 0.961267. This model rule can be applied to obtain predictions of kidney toxicity when expression values for the indicated genes are determined using appropriate samples and an appropriate microarray expression detection system such as the Rat CT array used to develop the Database.

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- [240]        Example 8 Use of Predictive Genes to Predict Kidney Toxicity for Samples External to the Database: (A) Materials and Methods: (A)(1) Animal Treatment and Tissue Harvest: Male Sprague-Dawley rats in groups of 3 were treated by intraperitoneal injection with test compounds (cephalosporidine, 1500 mg/kg and cisplatin, 20 mg/kg) or only with the vehicle in which the compound was mixed. At specified timepoints (6h and 24h) the rats were euthanized and tissues collected. Kidney tissues were immediately placed into liquid nitrogen and frozen within 3 minutes of the death of the animal to ensure that mRNA did not degrade. The tissues were sent blinded to be evaluated. The organs/tissues are then packaged into well-labeled plastic freezer quality bags and stored at -80 degrees until needed for isolation of the mRNA from a portion of the organ/tissue sample.
- [241]        (A)(2) Gene Expression Measurement: Isolation of RNA, preparation of cDNA labeled probes and hybridizations procedures were as described in Example 1 Materials and Methods. Probes were hybridized to the rat CT Chip which is the same array as used for the database.
- [242]        (B) Data Analysis: Array data from the samples was loaded into GeneSpring software using the same procedures as used for the database. No kidney toxicity parameters were entered for these samples. The Predict Parameter Value tool was used to make toxicity predictions using different Combo Gene sets from the 24 hour data and the entire database as the training set. Other values used were 10 nearest neighbors and a p-value ratio cutoff of 0.5.
- [243]        (C) RESULTS: Table 31 presents predictions for samples that were external to the database used to derive the predictive genes. The samples were kidney samples from replicate animals treated with cephaloridine and cisplatin. One of these compounds (cisplatin) is also represented in the database (at a different dose

level) and the other compound, cephaloridine, is not in the database. Histopathology conducted on the kidney samples verified that these treatments induced kidney tubular necrosis. Each of the Combo gene sets correctly predicted that these samples had expression patterns indicative of kidney toxicity.

**[244]** These results demonstrate clearly that the discovered sets of predictive genes in conjunction with the database and K-means nearest neighbor model can accurately predict toxicity from microarray data that is external to the database. Because the database consists mostly of non-toxic samples the prediction of toxicity for these samples is significantly different from what would be expected from chance. It is also noteworthy that three different sets of predictive genes are capable of making accurate predictions.

**[245]** Example 9 Clustering Analysis to Identify Coordinantly Behaving Subset of Predictive Genes

(A) Materials and Methods

(A)(1) Gene Expression Data: Gene expression data used for cluster analysis were the 24 hour kidney expression data of the 28 genes of the Combo 6 predictive gene set. These data are shown in Table 39.

**[246]** (B) Cluster Analysis: Cluster analysis tools used in these analyses included K-means and gene tree features of GeneSpring software and Wards clustering algorithm in S-Plus statistical analysis software.

**[247]** (C) Results: Figure 7 presents combined results of K-means and gene-tree hierarchical clustering analysis. Combo 6 (28 genes) was clustered using K-means (number of cluster 10, maximum iteration 100, similarity measure Pearson) and Gene tree (separation ratio 0.5, minimum distance 0.001, similarity measure Pearson). The k-means clusters are colored according to the corresponding set 1 to set 10. The gene names on the display from top to bottom correspond to left to right cluster bars.

**[248]** Wards cluster analysis results are shown in Figure 8. Cluster tree for Combo

6 genes are shown with the best cut line indicating 7 clusters. Gene names corresponding to numbers are indicated in tabular form below the diagram.

**[249]**            Example 10. Use of Expression Profiles of Predictive Genes in a Computer Program Product to Predict Renal Toxicity

(A) Materials and Methods

(A1) Overview of Computer Program Product: A computer program product produces a prediction of the occurrence of a kidney toxicity using input gene expression data from test samples. The model and data for the computer program have been primarily validated using Phase-1 Rat CT arrays and Phase-1 Rat CT expression data in the Phase-1 TOXBank database as described in previous examples. In other embodiments, expression data from other expression platforms (such as TaqMan using Syber Green technology) may also be used in the computer program product. Those skilled in the art are capable of developing and validating scaling factors to adjust for differences in differential gene expression sensitivity and responsiveness among different platforms used in the computer program product.

**[250]**            The computer program product uses the Predictive Model as described in the previous examples. The computer program product contains an encrypted training data set that includes differential gene expression values and an endpoint classification for each sample in the training set. The computer program product samples are from the same timepoint (e.g., gene expression measured at 24 hours after dosing) and the classification is binary for the specific endpoint (e.g., kidney tubular necrosis or no kidney tubular necrosis). The computer program product also contains encrypted lists of the Combo sets of predictive genes (also called Predictagen sets). Inputs to the Predictive Model of the computer program product are the  $k$  value for number of nearest neighbors and the type of distance measure to

be used in the model. Data inputs for the Predictive Model include the Combo list(s) of predictive genes and training set as encrypted "plug-in" files and specification of a test data file(s) that has expression data.

[251] The initial prediction is made after calculating the probability that the tabulated votes are different from the proportion of votes in the training set for each classification. A statistical test (hypergeometric mean distribution) is run for each classification and  $p$ -values are calculated. The classification prediction would be that class that has the highest  $p$ -value. A classification cutoff procedure is used that uses the  $p$ -value ratio ( $1 - p_0/p_1$  where  $p_0$  is the  $p$ -value for the not predicted class and  $p_1$  is the  $p$ -value for the predicted class). If the  $p$ -value ratio does not exceed a specified cutoff value (input to the computer program product by the user) then a prediction is not made. The Prediction Machine can be used with multiple Predictagen sets with the classifications,  $p$ -values and  $p$ -value ratios calculated as above. In this case an overall prediction is made by combining the predictions of the individual Predictagen sets. Each Predictagen set is weighted by a performance number. The overall certainty for this combined prediction is calculated by a paired value  $t$ -test using the  $p$ -value ratio and  $(1-p\text{-value ratio})$  for each Predictagen set as a pair of values. The certitude is  $1-p$  where  $p$  is the value for the paired value  $t$ -test.

[252] (A2) Computer Program Product Input: Encrypted training data is included as a plug-in module for the software. User input includes specification of encrypted Predictagen gene lists and samples for prediction (files with gene expression data). Additional specifications are distance measure to be used in the knn model (currently Euclidean), number of neighbors and a certitude cutoff ( $p$ -value ratio cutoff).

[253] (A3) Program Operation: The program is executed as follows. First, on the Prediction tab the 'Load Predictagens' button is clicked on to load the desired predictagen(s). In this example, the 24 hour kidney Predictagen is loaded. Next, a predictagen in the Predictagen sets list box is highlighted and the 'Make Predictor' button is clicked on (in this example, 24 hour kidney). If necessary, the predictor is highlighted and the 'Configure' button is clicked on to set parameter values. Next, the

'Load Samples' button is clicked on. Sample data is loaded as text files in the format shown in Table 44. Samples from the Samples list box using the left mouse button are then selected, and the CTRL key is simultaneously selected to make multiple selections. In this example, 3 kidney samples from rats treated with 25 mg/kg paraquat and 3 kidney samples from rats treated with 80 mg/kg phenobarbital are selected. The samples were treated and processed for gene expression analysis as described in the previous examples. The 'Add to predictor' button is then clicked on, and the 'Predict' button is then clicked on to generate the program's output.

[254] On the Output tab, the 'Summary', 'Detail', or 'Full' radio buttons are selected to control the amount of information displayed about the prediction. The 'Tabular Report' checkbox is checked to put the output in a format that can be loaded into Excel as tab-delimited text. The 'Save', 'Copy', 'Print', and 'Clear' buttons are selected to save the output, copy the output to the clipboard, print the output, or clear the output window prior to another prediction.

[255] (A4) Computer Program Product Output: The summary view displays sample information, the call (kidney tubular necrosis or negative), and the overall certitude. The detail view presents the individual calls and 1-*p*-value ratio for each Predictagen, in addition to summary view information. The full view presents, for each sample and Predictagen gene list, the specific nearest neighbors and their classification (votes) along with the hypergeometric mean *p* values for each classification. At the end of this information detail view information is presented.

[256] (B) Test Data: Table 43 displays the test set of gene expression data used to generate predictions. The table shows the correct classification of kidney samples that have histopathology (kidney tubular necrosis) or no histopathology.

[257] (C) Results: Table 42 displays the summary output of the computer program after loading. Two out of three of the paraquat samples (sample #s 16477 and 16479) were correctly predicted for rat kidney tubular necrosis (with certitudes of 0.472 and 0.796). Three out of three of the phenobarbital samples were correctly predicted as negative for kidney tubular necrosis. Table 43 displays the detailed



output of the computer program, which shows the individual performances of the 24 hour kidney Combo sets and the overall certitude score.

**[258]**           Example 11 Selection and Validation of Protein Biomarker Candidates.

Protein marker candidates can be selected from biomarker genes using a number of parameters. Table 44 presents biomarker genes sorted in order of their mean individual gene predictive performance (percent correct calls) for all genes exhibiting  $\geq 60\%$  percent correct calls. Each gene was then evaluated for evidence whether it codes for a protein. This is clearly a key criterion for a protein marker. The next parameters evaluated were the relative transcriptional response in toxic versus non-toxic samples. If protein levels are proportional to RNA levels then these columns indicate the relative potential magnitude of the protein marker in toxic and non-toxic samples. The better marker candidates should be those genes exhibiting the larger differences in RNA expression. A number of additional criteria can be considered included protein MW, occurrence of the protein in tissues other than the target tissue and availability of antibodies which will recognize the protein. One important criterion may also be whether the protein is secreted. The last column in Table 44 indicates that 3 of the proteins are known to be secreted. Table 37 lists proteins known to be secreted derived from the total list of predictive genes. The property of secretion may be useful in identification of proteins which could be biomarkers in serum or possibly other matrices such as urine or saliva.

**[259]**           Protein markers can be rapidly evaluated by testing for levels of the identified marker candidates using any of a number of analytical techniques for measuring specific protein levels such as Western blots or ELISA assays. Samples for analysis may be selected from a tissue bank such as that described in Example 1. Selection for analysis would include samples from toxic treatments and samples from non-toxic treatments. Quantitative protein marker data can be analyzed using the same approaches described in Example 2 for evaluation and validation of predictive performance of the protein markers.

**[260]**           Experimental data demonstrating application of this concept and

identification and validation of a protein marker were developed using antibodies to clusterin and insulin-like growth factor binding protein 1. These genes were selected from the list of genes on Table 44 based on available antibodies. Insulin-like growth factor binding protein 1 is known to be secreted. Serum sample protein from four pairs of animals (2 pairs treated with non-toxic compounds and 2 pairs treated with kidney-toxic compounds) were analyzed using Western blot methods known to those skilled in the art. The Western blot was probed with antibodies to insulin-like growth factor binding protein 1 and clusterin.

[261] A scanned autoradiogram of results is presented in Figure 9. Clusterin appeared to be approximately equal abundance in the samples. Insulin-like growth factor binding protein 1 protein levels clearly appeared to be proportional to the gene expression levels observed in kidneys of these animals and were clearly elevated in the kidney-toxic treatments compared to the non-toxic treatments. The insulin-like growth factor binding protein 1 protein levels in serum were correlative at the individual animal level with the transcription factor signals. These data clearly indicate that predictive markers identified through transcript measurement and analysis can also be predictive protein markers.

[262] It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent or patent application were specifically and individually indicated to be so incorporated by reference.

Table 1 Compounds, Dose Levels, Kidney  
Pathology and Abbreviations in the database

| Compound                 | Dose Level | Abbreviation | Kidney*<br>Tubular Necrosis | Score** |
|--------------------------|------------|--------------|-----------------------------|---------|
| 1-naphthylisothiocyanate | 15mg/kg    | ANIT 15      | no                          | 1       |
| 1-naphthylisothiocyanate | 60mg/kg    | ANIT 60      | no                          | 1       |
| 5-fluorouracil           | 13 mg/kg   | 5-FU 13      | no                          | 1       |
| 5-fluorouracil           | 50 mg/kg   | 5-FU 50      | no                          | 1       |
| acetaminophen            | 250 mg/kg  | APAP 250     | no                          | 1       |
| acetaminophen            | 1000 mg/kg | APAP 1000    | no                          | 1       |
| amphotericin B           | 5 mg/kg    | AMPB 5       | no                          | 1       |
| amphotericin B           | 20 mg/kg   | AMPB 20      | no                          | 1       |
| azathioprine             | 50 mg/kg   | AZA 50       | no                          | 1       |
| azathioprine             | 200 mg/kg  | AZA 200      | no                          | 1       |
| benzene                  | 0.25 ml/kg | BEN 250      | no                          | 1       |
| benzene                  | 1 ml/kg    | BEN 1000     | no                          | 1       |
| benzo[a]pyrene           | 30 mg/kg   | BAP 30       | no                          | 1       |
| bromobenzene             | 0.2 ml/kg  | BRB 200      | no                          | 1       |
| bromobenzene             | 0.8 ml/kg  | BRB 800      | no                          | 1       |
| busulfan                 | 14 mg/kg   | BUS 14       | no                          | 1       |
| cadmium chloride         | 1 mg/kg    | CAD 1        | no                          | 1       |
| cadmium chloride         | 2 mg/kg    | CAD 2        | no                          | 1       |
| cadmium chloride         | 4 mg/kg    | CAD 4        | yes (6h)                    | 3       |
| carbon tetrachloride     | 0.25 ml/kg | CCL4 250     | no                          | 1       |
| carbon tetrachloride     | 1 ml/kg    | CCL4 1000    | no                          | 1       |
| carmustine               | 16 mg/kg   | CAR 16       | no                          | 1       |
| chloroform               | 0.25 ml/kg | CHCL3 250    | yes                         | 3       |
| chloroform               | 0.5 ml/kg  | CHCL3 500    | yes                         | 5       |
| chlorpromazine           | 8 mg/kg    | CHLOR 8      | no                          | 1       |
| chlorpromazine           | 30 mg/kg   | CHLOR 30     | no                          | 1       |
| cisplatin                | 2.5 mg/kg  | CIS 2.5      | yes                         | 6       |
| cisplatin                | 10 mg/kg   | CIS 10       | yes                         | 8       |
| clofibrate               | 75 mg/kg   | CLO 75       | no                          | 1       |
| clofibrate               | 250 mg/kg  | CLO 250      | no                          | 1       |
| clozapine                | 45 mg/kg   | CLOZ 45      | no                          | 1       |
| clozapine                | 180 mg/kg  | CLOZ 180     | no                          | 1       |
| carboxy methyl cellulose | 30 mg/kg   | CMC 30       | no                          | 1       |
| cycloheximide            | 0.5 mg/kg  | CHEX 0.5     | no                          | 1       |
| cycloheximide            | 2 mg/kg    | CHEX 2       | no                          | 1       |
| cyclophosphamide         | 25 mg/kg   | CPHOS 25     | no                          | 1       |
| cyclophosphamide         | 100 mg/kg  | CPHOS 100    | yes                         | 2       |
| cyclosporin A            | 20 mg/kg   | CYCA 20      | no                          | 1       |
| cyclosporin A            | 80 mg/kg   | CYCA 80      | no                          | 1       |
| dexamethasone            | 8 mg/kg    | DEX 8        | no                          | 1       |
| dexamethasone            | 30 mg/kg   | DEX 30       | no                          | 1       |
| diflunisal               | 25 mg/kg   | DIF 25       | no                          | 1       |
| diflunisal               | 100 mg/kg  | DIF 100      | no                          | 1       |
| dimethylnitrosamine      | 20 mg/kg   | DMN 20       | no                          | 1       |

|                       |            |          |     |   |
|-----------------------|------------|----------|-----|---|
| doxorubicin           | 12 mg/kg   | DOX 12   | no  | 1 |
| erythromycin estolate | 40 mg/kg   | ERY 40   | no  | 1 |
| erythromycin estolate | 160 mg/kg  | ERY 160  | no  | 1 |
| estradiol             | 0.1 mg/kg  | EST 0.1  | no  | 1 |
| estradiol             | 0.4 mg/kg  | EST 0.4  | no  | 1 |
| ethanol               | 2.5 ml/kg  | ETH 2500 | no  | 1 |
| gancyclovir           | 50 mg/kg   | GAN 50   | no  | 1 |
| gancyclovir           | 200 mg/kg  | GAN 200  | yes | 3 |
| gentamicin            | 38 mg/kg   | GEN 38   | no  | 1 |
| gentamicin            | 150 mg/kg  | GEN 150  | no  | 1 |
| hydroxyurea           | 250 mg/kg  | HYD 250  | yes | 2 |
| hydroxyurea           | 1000 mg/kg | HYD 1000 | yes | 4 |
| isoniazid             | 50 mg/kg   | ISON 50  | no  | 1 |
| isoniazid             | 200 mg/kg  | ISON 200 | no  | 1 |
| ketoconazole          | 20 mg/kg   | KETO 20  | no  | 1 |
| ketoconazole          | 80 mg/kg   | KETO 80  | no  | 1 |
| lipopolysaccharide    | 2 mg/kg    | LPS 2    | yes | 4 |
| lipopolysaccharide    | 8 mg/kg    | LPS 8    | yes | 8 |
| methotrexate          | 1.3 mg/kg  | MET 1.3  | no  | 1 |
| methotrexate          | 5 mg/kg    | MET 5    | no  | 1 |
| naloxone              | 45 ml/kg   | NAL 45   | no  | 1 |
| naloxone              | 180 mg/kg  | NAL 180  | no  | 1 |
| phenobarbital         | 20 mg/kg   | PBARB 20 | no  | 1 |
| phenobarbital         | 80 mg/kg   | PBARB 80 | no  | 1 |
| phenylhydrazine       | 20 mg/kg   | PHEN 20  | no  | 1 |
| phenylhydrazine       | 80 mg/kg   | PHEN 80  | no  | 1 |
| polyethylene glycol   | 5 ml/kg    | PEG 5000 | no  | 1 |
| puromycin             | 38 mg/kg   | PUR 38   | no  | 1 |
| puromycin             | 150 mg/kg  | PUR 150  | no  | 1 |
| quinidine             | 25 mg/kg   | QUIN 25  | no  | 1 |
| quinidine             | 100 mg/kg  | QUIN 100 | no  | 1 |
| streptozotocin        | 20 mg/kg   | STRZ 20  | no  | 1 |
| streptozotocin        | 75 mg/kg   | STRZ 75  | no  | 1 |
| tamoxifen             | 50 mg/kg   | TAM 50   | no  | 1 |
| tamoxifen             | 200 mg/kg  | TAM 200  | no  | 1 |
| tetracycline          | 50 mg/kg   | TET 50   | yes | 2 |
| tetracycline          | 150 mg/kg  | TET 150  | yes | 4 |
| theophylline          | 25 mg/kg   | THEO 25  | no  | 1 |
| theophylline          | 100 mg/kg  | THEO 100 | no  | 1 |

\* Values in parentheses indicate that array data are only available for indicated time points

\*\* Histopathology tubular necrosis severity scores. 1= not remarkable; 2 and higher indicate histopathology of increasing severity

Table 2 List of Genes, Whose Expression at 24h Directly Correlates with Kidney Tubular Necrosis at 72h, Ranked by Pearson Correlation Coefficient

| Gene   | Correlation Coefficient |
|--|-------------------------|
| Gadd153                                      | 0.692123                |
| Gadd45                                       | 0.6542049               |
| Insulin-like growth factor binding protein 1 | 0.6465685               |
| PAR interacting protein                      | 0.6218616               |
| RCT-144                                      | 0.6188912               |
| Calpactin I heavy chain                      | 0.610469                |
| Tissue inhibitor of metalloproteinases-1     | 0.5927494               |
| 60S ribosomal protein L6 (alternate clone 1) | 0.5900929               |
| RCT-68                                       | 0.5799504               |
| Cathepsin L                                  | 0.5752138               |
| RCT-49                                       | 0.5744045               |
| IgE binding protein                          | 0.5633063               |
| Dynein light chain 1                         | 0.561974                |
| Clusterin                                    | 0.5537873               |
| 60S ribosomal protein L6                     | 0.5526743               |
| Interleukin-1 beta                           | 0.5508332               |
| Cathepsin L, sequence 2                      | 0.5458164               |
| Superoxide dismutase Mn                      | 0.5432356               |
| Matrix metalloproteinase-1                   | 0.5432082               |
| Ribosomal protein S8                         | 0.5429754               |
| RCT-274                                      | 0.5399542               |
| RCT-179                                      | 0.5396944               |
| Ubiquitin D (Ubd)                            | 0.5390609               |
| Thymosin beta-10                             | 0.5375005               |
| Multidrug resistant protein-1                | 0.5359658               |
| Ribosomal protein S9                         | 0.5295026               |
| Uncoupling protein 2                         | 0.5272409               |
| Multidrug resistant protein-3                | 0.5255124               |
| Beta-tubulin, class I                        | 0.5235234               |
| RCT-145                                      | 0.5214936               |
| CD44 metastasis suppressor gene              | 0.521281                |
| RCT-109                                      | 0.5141034               |
| Alpha-tubulin                                | 0.5105499               |
| Ribosomal protein L13A                       | 0.5068002               |
| Zinc finger protein                          | 0.4949505               |
| Ferritin H-chain                             | 0.493831                |
| RCT-50                                       | 0.4927958               |
| RCT-198                                      | 0.483781                |
| RCT-158                                      | 0.4823461               |

|   |           |
|---|-----------|
| c-myc   | 0.4734444 |
| RCT-60  | 0.4707905 |
| Beta-actin, sequence 2                              | 0.4689375 |
| Canalicular multispecific organic anion transporter | 0.459423  |
| MHC class I antigen RT1.A1(f) alpha-chain           | 0.458286  |
| Calgranulin B1                                      | 0.4560673 |
| Osteopontin   | 0.4508689 |
| Complement component C3                             | 0.4491239 |
| Ubiquitin conjugating enzyme (RAD 6 homologue)      | 0.446513  |
| RCT-152   | 0.4463049 |
| Alpha-fibrinogen                                    | 0.4461847 |
| RCT-293   | 0.4419801 |
| Organic cation transporter 3                        | 0.4411987 |
| Keratinocyte growth factor                          | 0.4402586 |
| RCT-24  | 0.4377164 |
| RCT-18  | 0.4342767 |
| RCT-241   | 0.4299609 |
| RCT-138   | 0.4268714 |
| DNA topoisomerase I                                 | 0.4262425 |
| RCT-149   | 0.4230694 |
| RCT-192   | 0.4214455 |
| RCT-127   | 0.4187711 |
| RCT-126   | 0.4119079 |
| RCT-258   | 0.4112586 |
| RCT-91  | 0.4109416 |
| Ceruloplasmin                                       | 0.402974  |
| Vacuole membrane protein 1                          | 0.400575  |

Table 3 List of Genes, Whose Expression at 24h Inversely Correlates with Kidney Tubular Necrosis at 72h, Ranked by Spearman Correlation Coefficient

| Gene                                       | Correlation Coefficient |
|--|-------------------------|
| RCT-42                                     | -0.25083                |
| Membrane bound cytochrome b5               | -0.25275                |
| RCT-132                                    | -0.25352                |
| RCT-99                                     | -0.25374                |
| Four repeat ion channel                    | -0.25412                |
| RCT-62                                     | -0.25524                |
| RCT-137                                    | -0.25548                |
| AT-1                                       | -0.25881                |
| UDP-glucuronosyltransferase 2B             | -0.26029                |
| Calgranulin B4                             | -0.26618                |
| Methylacyl-CoA racemase alpha              | -0.26791                |
| Cyclin D1                                  | -0.27006                |
| Organic anion transporting polypeptide 1   | -0.27038                |
| Cystatin C                                 | -0.27304                |
| Matrin F/G                                 | -0.27305                |
| RCT-181                                    | -0.27455                |
| RCT-25                                     | -0.27625                |
| RCT-143                                    | -0.27626                |
| RCT-93                                     | -0.28389                |
| Protein tyrosine phosphatase alpha         | -0.28421                |
| RCT-79                                     | -0.28485                |
| Caspase 2                                  | -0.28686                |
| Vascular endothelial growth factor         | -0.28716                |
| Glutathione S-transferase Ya               | -0.28785                |
| Senescence marker protein-30               | -0.29192                |
| RCT-178                                    | -0.29272                |
| Organic anion transporter K1               | -0.29329                |
| RCT-256                                    | -0.2943                 |
| 25-DX                                      | -0.29444                |
| RCT-22                                     | -0.29564                |
| Sarcoplasmic reticulum calcium ATPase      | -0.2974                 |
| RCT-280                                    | -0.29749                |
| RCT-148                                    | -0.30758                |
| Arginosuccinate synthetase 1               | -0.30894                |
| RCT-142                                    | -0.31028                |
| RCT-260                                    | -0.31039                |
| Apoptosis-regulating basic protein         | -0.31798                |
| Organic anion transporter 3                | -0.32302                |
| Ornithine aminotransferase                 | -0.32748                |
| Hemoglobin alpha 1 chain (alternate clone) | -0.33449                |

|  |          |
|--|----------|
| Cytochrome P450 2A3  | -0.33951 |
| Hemoglobin alpha 1 chain   | -0.34347 |
| Selenoprotein P  | -0.34685 |
| Cytochrome P450 2C23   | -0.34696 |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II)                   | -0.34712 |
| RCT-38   | -0.34982 |
| Iron-responsive element-binding protein                                    | -0.3572  |
| RCT-10   | -0.36278 |
| Epidermal growth factor  | -0.36487 |
| Sodium/glucose cotransporter 1   | -0.36594 |
| Calgranulin B2   | -0.36604 |
| Cytochrome c oxidase subunit II  | -0.36678 |
| RCT-89   | -0.37036 |
| Acyl-CoA dehydrogenase, medium chain                                       | -0.37526 |
| RCT-39   | -0.37793 |
| RCT-34   | -0.37992 |
| Malate dehydrogenase, cytosolic  | -0.38206 |
| D-dopachrome tautomerase   | -0.38497 |
| RCT-87   | -0.3857  |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II) (alternate clone) | -0.40004 |
| RCT-101  | -0.40144 |
| RCT-69   | -0.40543 |
| Thiopurine methyltransferase   | -0.41035 |
| Very long-chain acyl-CoA synthetase  | -0.41248 |
| Fatty acyl-CoA oxidase   | -0.42391 |
| RCT-287  | -0.4351  |
| Dimethylarginine dimethylaminohydrolase                                    | -0.4413  |
| RCT-182  | -0.44238 |
| RCT-291  | -0.4606  |
| 3-hydroxyisobutyrate dehydrogenase   | -0.48712 |



Table 4 Distribution of Compounds\* in Individual Training and Test Sets  
for 24 Hour Kidney Data

Training and Test Set A

| Training Set A<br>Negative** | Training Set A<br>Positive | Test Set A<br>Negative | Test Set A<br>Positive |
|------------------------------|----------------------------|------------------------|------------------------|
| AMPB                         | CIS                        | ANIT                   | CHCL3                  |
| AZA                          | HYD                        | 5-FU                   | CPHOS                  |
| CAD                          | LPS                        | APAP                   | GAN                    |
| CHLOR                        | TET                        | BEN                    |                        |
| CLO                          |                            | BAP                    |                        |
| CYCA                         |                            | BRB                    |                        |
| DEX                          |                            | BUS                    |                        |
| DIF                          |                            | CCL4                   |                        |
| DOX                          |                            | CAR                    |                        |
| ERY                          |                            | CLOZ                   |                        |
| EST                          |                            | CMC                    |                        |
| ETH                          |                            | CHEX                   |                        |
| GEN                          |                            | DMN                    |                        |
| MET                          |                            | ISON                   |                        |
| PHEN                         |                            | KETO                   |                        |
| PUR                          |                            | NAL                    |                        |
| TAM                          |                            | PBARB                  |                        |
| TET                          |                            | PEG                    |                        |
|                              |                            | QUIN                   |                        |
|                              |                            | STRZ                   |                        |
|                              |                            | THEO                   |                        |

Training and Test Set 1

| Training Set 1 Negative | Training Set 1<br>Positive | Test Set 1 Negative | Test Set 1 Positive |
|-------------------------|----------------------------|---------------------|---------------------|
| AMPB                    | CPHOS                      | 5-FU                | CHCL3               |
| ANIT                    | GAN                        | APAP                | CIS                 |
| AZA                     | LPS                        | BEN                 | HYD                 |
| BAP                     | TET                        | BRB                 |                     |
| CAD                     |                            | BUS                 |                     |
| CAR                     |                            | CLOZ                |                     |
| CCL4                    |                            | CMC                 |                     |
| CHEX                    |                            | DIF                 |                     |
| CHLOR                   |                            | DMN                 |                     |
| CLO                     |                            | DOX                 |                     |
| CYCA                    |                            | ERY                 |                     |
| DEX                     |                            | ETH                 |                     |

|       |  |      |  |
|-------|--|------|--|
| EST   |  | NAL  |  |
| GEN   |  | PEG  |  |
| ISON  |  | PUR  |  |
| KETO  |  | STRZ |  |
| MET   |  | TAM  |  |
| PBARB |  |      |  |
| PHEN  |  |      |  |
| QUIN  |  |      |  |
| THEO  |  |      |  |

Training and Test Set 2

| Training Set 2 Negative | Training Set 2 Positive | Test Set 2 Negative | Test Set 2 Positive |
|-------------------------|-------------------------|---------------------|---------------------|
| AMPB                    | CHCL3                   | 5-FU                | CPHOS               |
| APAP                    | CIS                     | ANIT                | LPS                 |
| AZA                     | GAN                     | BRB                 | TET                 |
| BAP                     | HYD                     | CAD                 |                     |
| BEN                     |                         | CHEX                |                     |
| BUS                     |                         | CHLOR               |                     |
| CAR                     |                         | CLOZ                |                     |
| CCL4                    |                         | CMC                 |                     |
| CLO                     |                         | DEX                 |                     |
| CYCA                    |                         | DMN                 |                     |
| DIF                     |                         | GEN                 |                     |
| DOX                     |                         | NAL                 |                     |
| ERY                     |                         | PUR                 |                     |
| EST                     |                         | QUIN                |                     |
| ETH                     |                         | STRZ                |                     |
| ISON                    |                         | TAM                 |                     |
| KETO                    |                         | THEO                |                     |
| MET                     |                         |                     |                     |
| PBARB                   |                         |                     |                     |
| PEG                     |                         |                     |                     |
| PHEN                    |                         |                     |                     |

Training and Test Set 3

| Training Set 3 Negative | Training Set 3 Positive | Test Set 3 Negative | Test Set 3 Positive |
|-------------------------|-------------------------|---------------------|---------------------|
| ANIT                    | CHCL3                   | 5-FU                | CPHOS               |
| APAP                    | CIS                     | AMPB                | LPS                 |
| BEN                     | GAN                     | AZA                 | TET                 |
| BUS                     | HYD                     | BAP                 |                     |
| CAD                     |                         | BRB                 |                     |
| CAR                     |                         | CCL4                |                     |
| CHLOR                   |                         | CHEX                |                     |
| CLO                     |                         | CYCA                |                     |

|      |  |       |  |
|------|--|-------|--|
| CLOZ |  | DIF   |  |
| CMC  |  | DOX   |  |
| DEX  |  | ERY   |  |
| DMN  |  | GEN   |  |
| EST  |  | ISON  |  |
| ETH  |  | PBARB |  |
| KETO |  | PHEN  |  |
| MET  |  | PUR   |  |
| NAL  |  | STRZ  |  |
| PEG  |  |       |  |
| QUIN |  |       |  |
| TAM  |  |       |  |
| THEO |  |       |  |

Training and Test Set 4

| Training Set 4<br>Negative | Training Set 4<br>Positive | Test Set 4<br>Negative | Test Set 4 Positive |
|----------------------------|----------------------------|------------------------|---------------------|
| 5-FU                       | CHCL3                      | AMPB                   | CPHOS               |
| APAP                       | CIS                        | ANIT                   | HYD                 |
| BEN                        | GAN                        | AZA                    | LPS                 |
| CAR                        | TET                        | BAP                    |                     |
| CHEX                       |                            | BRB                    |                     |
| CHLOR                      |                            | BUS                    |                     |
| CLO                        |                            | CAD                    |                     |
| CLOZ                       |                            | CCL4                   |                     |
| CMC                        |                            | DEX                    |                     |
| CYCA                       |                            | ERY                    |                     |
| DIF                        |                            | EST                    |                     |
| DMN                        |                            | ETH                    |                     |
| DOX                        |                            | KETO                   |                     |
| GEN                        |                            | PBARB                  |                     |
| ISON                       |                            | QUIN                   |                     |
| MET                        |                            | TAM                    |                     |
| NAL                        |                            | THEO                   |                     |
| PEG                        |                            |                        |                     |
| PHEN                       |                            |                        |                     |
| PUR                        |                            |                        |                     |
| STRZ                       |                            |                        |                     |

Training and Test Set 5

| Training Set 5<br>Negative | Training Set 5<br>Positive | Test Set 5<br>Negative | Test Set 5 Positive |
|----------------------------|----------------------------|------------------------|---------------------|
|----------------------------|----------------------------|------------------------|---------------------|

|       |       |      |       |
|-------|-------|------|-------|
| AZA   | CPHOS | 5-FU | CHCL3 |
| BAP   | GAN / | AMPB | CIS   |
| BRB   | HYD   | ANIT | TET   |
| BUS   | LPS   | APAP |       |
| CAR   |       | BEN  |       |
| CHEX  |       | CAD  |       |
| CHLOR |       | CCL4 |       |
| CLO   |       | CMC  |       |
| CLOZ  |       | DEX  |       |
| CYCA  |       | ERY  |       |
| DIF   |       | EST  |       |
| DMN   |       | ETH  |       |
| DOX   |       | GEN  |       |
| KETO  |       | ISON |       |
| NAL   |       | MET  |       |
| PBARB |       | QUIN |       |
| PEG   |       | THEO |       |
| PHEN  |       |      |       |
| PUR   |       |      |       |
| STRZ  |       |      |       |
| TAM   |       |      |       |

\* For abbreviations please see Table 1 (Compound, Dose, Abbreviation, etc.)

\*\* Negative= Compounds that did not elicit histopathology (score=1)

Positive= Compounds that did elicit histopathology (score of 2 or greater)

Table 5 Predictive Genes for 24 Hour Expression Data

| Gene Name   | Combination Category* |
|---|-----------------------|
| 60S ribosomal protein L6 (alternate clone 1)        | 6                     |
| Alpha-tubulin                                       | 6                     |
| Calpactin I heavy chain                             | 6                     |
| Cathepsin L   | 6                     |
| Cathepsin L, sequence 2                             | 6                     |
| CDK108  | 6                     |
| Clusterin   | 6                     |
| c-myc   | 6                     |
| Dynein light chain 1                                | 6                     |
| Gadd153   | 6                     |
| Gadd45  | 6                     |
| Insulin-like growth factor binding protein 1        | 6                     |
| PAR interacting protein                             | 6                     |
| RCT-109   | 6                     |
| RCT-144   | 6                     |
| RCT-145   | 6                     |
| RCT-152   | 6                     |
| RCT-158   | 6                     |
| RCT-198   | 6                     |
| Vacuole membrane protein 1                          | 6                     |
| RCT-24  | 6                     |
| RCT-241   | 6                     |
| RCT-271   | 6                     |
| RCT-68  | 6                     |
| Ribosomal protein L13A                              | 6                     |
| Ribosomal protein S8                                | 6                     |
| Tissue inhibitor of metalloproteinases-1            | 6                     |
| Uncoupling protein 2                                | 6                     |
| 60S ribosomal protein L6                            | 5                     |
| Alpha-fibrinogen                                    | 5                     |
| Beta-actin, sequence 2                              | 5                     |
| Beta-tubulin, class I                               | 5                     |
| Canalicular multispecific organic anion transporter | 5                     |
| Carbonic anhydrase III, sequence 2                  | 5                     |
| Heme binding protein 23                             | 5                     |
| IgE binding protein                                 | 5                     |
| Keratinocyte growth factor                          | 5                     |
| MHC class I antigen RT1.A1(f) alpha-chain           | 5                     |
| Multidrug resistant protein-3                       | 5                     |
| Osteopontin   | 5                     |
| RCT-126   | 5                     |
| RCT-179   | 5                     |

|  |   |
|--|---|
| RCT-182  | 5 |
| Calgranulin B1   | 5 |
| RCT-258  | 5 |
| RCT-274  | 5 |
| RCT-49   | 5 |
| RCT-50   | 5 |
| RCT-60   | 5 |
| Proliferating cell nuclear antigen gene                                    | 5 |
| Ribosomal protein S9   | 5 |
| Thymosin beta-10   | 5 |
| Zinc finger protein  | 5 |
| Preproalbumin, sequence 2 (alternate clone 1)                              | 4 |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk)        | 4 |
| CD44 metastasis suppressor gene  | 4 |
| Ceruloplasmin  | 4 |
| Connexin-32  | 4 |
| Epidermal growth factor  | 4 |
| Ferritin H-chain   | 4 |
| Hypoxanthine-guanine phosphoribosyltransferase                             | 4 |
| Interleukin-1 beta   | 4 |
| Matrix metalloproteinase-1   | 4 |
| Multidrug resistant protein-1  | 4 |
| Organic cation transporter 3   | 4 |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II)                   | 4 |
| RCT-138  | 4 |
| RCT-180  | 4 |
| RCT-240  | 4 |
| RCT-287  | 4 |
| RCT-293  | 4 |
| RCT-38   | 4 |
| Pyruvate kinase, muscle  | 4 |
| Ref-1  | 4 |
| Superoxide dismutase Mn  | 4 |
| Ubiquitin conjugating enzyme (RAD 6 homologue)                             | 4 |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II) (alternate clone) | 3 |
| Annexin V  | 3 |
| Aspartoacylase   | 3 |
| Calreticulin   | 3 |
| Cathepsin S  | 3 |
| Dimethylarginine dimethylaminohydrolase                                    | 3 |
| Ecto-ATPase  | 3 |
| Methylacyl-CoA racemase alpha  | 3 |
| p53  | 3 |
| RCT-10   | 3 |
| RCT-149  | 3 |

|  |   |
|--|---|
| RCT-192  | 3 |
| RCT-196  | 3 |
| RCT-22   | 3 |
| RCT-256  | 3 |
| Ubiquitin D (Ubd)  | 3 |
| RCT-34   | 3 |
| RCT-8  | 3 |
| RCT-89   | 3 |
| Activin receptor type II                                 | 2 |
| Casein-alpha   | 2 |
| CDK102   | 2 |
| Cellular nucleic acid binding protein (CNBP)             | 2 |
| Complement component C3                                  | 2 |
| Defender against cell death-1                            | 2 |
| DNA topoisomerase I                                      | 2 |
| Elongation factor-1 alpha                                | 2 |
| Fatty acyl-CoA oxidase                                   | 2 |
| Fetuin beta (Fetub)                                      | 2 |
| Glucose transporter 1                                    | 2 |
| Glycine methyltransferase                                | 2 |
| Histidine-rich glycoprotein                              | 2 |
| Hypoxia-inducible factor 1 alpha                         | 2 |
| Insulin-like growth factor binding protein 3             | 2 |
| Malate dehydrogenase, cytosolic                          | 2 |
| N-hydroxy-2-acetylaminofluorene sulfotransferase (ST1C1) | 2 |
| Organic anion transporter 3                              | 2 |
| Organic anion transporting polypeptide 1                 | 2 |
| Ornithine aminotransferase                               | 2 |
| RCT-127  | 2 |
| RCT-155  | 2 |
| RCT-162  | 2 |
| Calgranulin B4   | 2 |
| Calgranulin B5   | 2 |
| RCT-242  | 2 |
| RCT-244  | 2 |
| RCT-246  | 2 |
| RCT-260  | 2 |
| RCT-280  | 2 |
| RCT-291  | 2 |
| RCT-292  | 2 |
| RCT-42   | 2 |
| RCT-84   | 2 |
| RCT-88   | 2 |
| RCT-91   | 2 |
| RCT-92   | 2 |

|   |   |
|---|---|
| Proteasome activator 28 alpha   | 2 |
| Ribosomal protein L27   | 2 |
| Selenoprotein P   | 2 |
| Senescence marker protein-30  | 2 |
| Stathmin  | 2 |
| Thioredoxin-1 (Trx1)  | 2 |
| Vascular cell adhesion molecule 1 (VCAM-1)                            | 2 |
| Vesicular monoamine transporter (VMAT)                                | 2 |
| 14-3-3 zeta   | 1 |
| Acyl-CoA dehydrogenase, medium chain                                  | 1 |
| Adrenodoxin reductase   | 1 |
| Alcohol dehydrogenase 1   | 1 |
| Alpha-2-macroglobulin   | 1 |
| Arginosuccinate synthetase 1  | 1 |
| Bcl-2   | 1 |
| Calnexin  | 1 |
| Carbonyl reductase  | 1 |
| Cholesterol esterase  | 1 |
| Cytochrome P450 14DM  | 1 |
| Cytochrome P450 2A3   | 1 |
| Cytochrome P450 2C11  | 1 |
| Cytochrome P450 2C23  | 1 |
| DNA binding protein inhibitor ID2                                     | 1 |
| eIF-4E  | 1 |
| Equilibrative nitrobenzylthioinosine-sensitive nucleoside transporter | 1 |
| Fibrinogen gamma chain  | 1 |
| Gamma-glutamyl transpeptidase   | 1 |
| Glucose-6-phosphate dehydrogenase                                     | 1 |
| Glucose-regulated protein 78  | 1 |
| Heme oxygenase  | 1 |
| HMG CoA reductase   | 1 |
| Iron-responsive element-binding protein                               | 1 |
| Low density lipoprotein receptor                                      | 1 |
| Macrophage inflammatory protein-1 alpha                               | 1 |
| Macrophage metalloelastase  | 1 |
| Mitogen activated protein kinase (P38)                                | 1 |
| Monocyte chemotactic protein receptor (CCR2)                          | 1 |
| Mullerian inhibiting substance  | 1 |
| Na/K ATPase alpha-1   | 1 |
| N-cadherin  | 1 |
| Nerve growth factor receptor  | 1 |
| Organic anion transporter K1  | 1 |
| Organic cation transporter 2  | 1 |
| Peroxisomal multifunctional enzyme type II                            | 1 |
| Peroxisome proliferator activated receptor alpha                      | 1 |



|   |   |
|---|---|
| RCT 165   | 1 |
| RCT 252   | 1 |
| RCT-101   | 1 |
| RCT-111   | 1 |
| Protein O-mannosyltransferase 1 (Pomt1)                             | 1 |
| RCT-129   | 1 |
| Apoptosis-regulating basic protein                                  | 1 |
| RCT-140   | 1 |
| RCT-147   | 1 |
| RCT-153   | 1 |
| RCT-164   | 1 |
| RCT-166   | 1 |
| RCT-18  | 1 |
| RCT-181   | 1 |
| RCT-185   | 1 |
| RCT-206   | 1 |
| RCT-220   | 1 |
| RCT-221   | 1 |
| Inositol polyphosphate multikinase (Ipmk)                           | 1 |
| RCT-268   | 1 |
| RCT-276   | 1 |
| RCT-279   | 1 |
| RCT-31  | 1 |
| RCT-36  | 1 |
| RCT-43  | 1 |
| RCT-61  | 1 |
| RCT-72  | 1 |
| RCT-76  | 1 |
| Renal organic anion transporter                                     | 1 |
| Retinoid X receptor alpha   | 1 |
| Retinol dehydrogenase type III                                      | 1 |
| Retinol-binding protein (RBP)                                       | 1 |
| Sarcoplasmic reticulum calcium ATPase                               | 1 |
| Sulfotransferase K2   | 1 |
| Superoxide dismutase Cu/Zn  | 1 |
| T-cell cyclophilin  | 1 |
| Thiol-specific antioxidant (natural killer cell-enhancing factor B) | 1 |
| Thiopurine methyltransferase  | 1 |
| Thrombin receptor (PAR-1)   | 1 |

\* Combination category is the number of training/test set gene list occurrences.

Table 6 Randomly Selected Gene Subsets from 24 H Combo All (216 Genes)\*

| Rand 5 (1)                                | Rand 5 (2)                                    |
|---|---|
| CDK108                                    | Preproalbumin, sequence 2 (alternate clone 1) |
| Ferritin H-chain                          | Adrenodoxin reductase                         |
| Histidine-rich glycoprotein               | RCT-111                                       |
| RCT-182                                   | RCT-198                                       |
| Inositol polyphosphate multikinase (lpmk) | RCT-206                                       |

| Rand 10 (1)                                  | Rand 10 (2)                               |
|--|---|
| Cathepsin S                                  | Bcl-2                                     |
| Cellular nucleic acid binding protein (CNBP) | Cytochrome P450 2A3                       |
| Cholesterol esterase                         | Defender against cell death-1             |
| DNA binding protein inhibitor ID2            | Ferritin H-chain                          |
| DNA topoisomerase I                          | MHC class I antigen RT1.A1(f) alpha-chain |
| Iron-responsive element-binding protein      | RCT-221                                   |
| RCT-126                                      | RCT-267                                   |
| Apoptosis-regulating basic protein           | RCT-287                                   |
| RCT-211                                      | RCT-49                                    |
| RCT-88                                       | Tissue inhibitor of metalloproteinases-1  |

| Rand 15 (1)                                  | Rand 15 (2)  |
|--|--|
| Cellular nucleic acid binding protein (CNBP) | Glucose transporter 1                                    |
| Gamma-glutamyl transpeptidase                | Organic anion transporter K1                             |
| Glucose transporter 1                        | Pancreatic secretory trypsin inhibitor type II (PSTI-II) |
| Glucose-regulated protein 78                 | RCT-111  |
| Hypoxia-inducible factor 1 alpha             | RCT-127  |
| Multidrug resistant protein-3                | RCT-152  |
| Organic cation transporter 3                 | RCT-214  |
| Peroxisomal multifunctional enzyme type II   | RCT-240  |
| RCT-126                                      | RCT-274  |
| RCT-242                                      | RCT-279  |
| RCT-280                                      | RCT-292  |
| RCT-287                                      | RCT-34   |
| RCT-88                                       | RCT-8  |
| Retinol dehydrogenase type III               | T-cell cyclophilin                                       |
| Superoxide dismutase Cu/Zn                   | Vesicular monoamine transporter (VMAT)                   |

\* Genes were randomly selected from the Combo All list of predictive genes (216 genes) assigning a random number to each gene, sorting by the random number and selecting the appropriate number of sorted genes.

Table 7 Randomly Selected Gene Subsets from 24 H Combo 6 Gene Set (28 Genes)\*

| Rand 5 (1)              | Rand 5 (2)                               |
|-------------------------|--|
| Calpactin I heavy chain | Cathepsin L, sequence 2                  |
| Clusterin               | RCT-152                                  |
| Dynein light chain 1    | RCT-271                                  |
| RCT-109                 | RCT-68                                   |
| Ribosomal protein L13A  | Tissue inhibitor of metalloproteinases-1 |

| Rand 10 (1)                              | Rand 10 (2)                |
|--|----------------------------|
| Alpha-tubulin                            | Cathepsin L                |
| Cathepsin L                              | PAR interacting protein    |
| Cathepsin L, sequence 2                  | RCT-144                    |
| c-myc                                    | RCT-198                    |
| Dynein light chain 1                     | Vacuole membrane protein 1 |
| Gadd153                                  | RCT-24                     |
| RCT-109                                  | RCT-241                    |
| RCT-152                                  | RCT-271                    |
| RCT-198                                  | Ribosomal protein L13A     |
| Tissue inhibitor of metalloproteinases-1 | Uncoupling protein 2       |

| Rand 15 (1)                                  | Rand 15 (2)                                  |
|--|--|
| 60S ribosomal protein L6 (alternate clone 1) | 60S ribosomal protein L6 (alternate clone 1) |
| Calpactin I heavy chain                      | Cathepsin L                                  |
| Cathepsin L                                  | Cathepsin L, sequence 2                      |
| CDK108                                       | Dynein light chain 1                         |
| Clusterin                                    | Gadd153                                      |
| Dynein light chain 1                         | Insulin-like growth factor binding protein 1 |
| Gadd153                                      | PAR interacting protein                      |
| Gadd45                                       | RCT-109                                      |
| RCT-109                                      | RCT-145                                      |
| RCT-152                                      | RCT-152                                      |
| Vacuole membrane protein 1                   | RCT-198                                      |
| RCT-241                                      | RCT-24                                       |
| RCT-68                                       | RCT-241                                      |
| Tissue inhibitor of metalloproteinases-1     | RCT-68                                       |
| Uncoupling protein 2                         | Tissue inhibitor of metalloproteinases-1     |

\* Genes were randomly selected from the Combo All list of predictive genes (216 genes) assigning a random number to each gene, sorting by the random number and selecting the appropriate number of sorted genes.

Table 8 Randomly Selected Gene Subsets from 24 H Combo 5 Gene Set (25 genes)\*

| Rand 5 (1)  | Rand 5 (2)              |
|---|-------------------------|
| Canalicular multispecific organic anion transporter | Beta-tubulin, class I   |
| IgE binding protein                                 | Heme binding protein 23 |
| RCT-211   | Osteopontin             |
| RCT-258   | RCT-211                 |
| Zinc finger protein                                 | RCT-60                  |

| Rand 10 (1)                               | Rand 10 (2)                               |
|---|---|
| Beta-actin, sequence 2                    | 60S ribosomal protein L6                  |
| Beta-tubulin, class I                     | Beta-tubulin, class I                     |
| Carbonic anhydrase III, sequence 2        | Carbonic anhydrase III, sequence 2        |
| IgE binding protein                       | IgE binding protein                       |
| MHC class I antigen RT1.A1(f) alpha-chain | MHC class I antigen RT1.A1(f) alpha-chain |
| RCT-126                                   | Multidrug resistant protein-3             |
| RCT-258                                   | RCT-182                                   |
| RCT-50                                    | RCT-274                                   |
| RCT-60                                    | RCT-50                                    |
| Ribosomal protein S9                      | Ribosomal protein S9                      |

| Rand 15 (1)   | Rand 15 (2)                        |
|---|------------------------------------|
| Beta-actin, sequence 2                              | Alpha-fibrinogen                   |
| Canalicular multispecific organic anion transporter | Carbonic anhydrase III, sequence 2 |
| Carbonic anhydrase III, sequence 2                  | Heme binding protein 23            |
| Heme binding protein 23                             | IgE binding protein                |
| IgE binding protein                                 | Keratinocyte growth factor         |
| Keratinocyte growth factor                          | Multidrug resistant protein-3      |
| Multidrug resistant protein-3                       | RCT-126                            |
| Osteopontin   | RCT-179                            |
| RCT-179   | RCT-182                            |
| RCT-211   | RCT-258                            |
| RCT-258   | RCT-274                            |
| RCT-60  | RCT-49                             |
| Proliferating cell nuclear antigen gene             | RCT-60                             |
| Ribosomal protein S9                                | Ribosomal protein S9               |
| Zinc finger protein                                 | Thymosin beta-10                   |

\* Genes were randomly selected from the Combo All list of predictive genes (216 genes) assigning a random number to each gene, sorting by the random number and selecting the appropriate number of sorted genes.

Table 9 Randomly Selected Gene Subsets from 24 H Combo 4 Gene Set (23 genes)\*

| Rand 5 (1)                                     | Rand 5 (2)   |
|--|--|
| Hypoxanthine-guanine phosphoribosyltransferase | Hypoxanthine-guanine phosphoribosyltransferase           |
| Matrix metalloproteinase-1                     | Multidrug resistant protein-1                            |
| Multidrug resistant protein-1                  | Pancreatic secretory trypsin inhibitor type II (PSTI-II) |
| RCT-240  | RCT-38   |
| RCT-293  | Ref-1  |

| Rand 10 (1)   |
|---|
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk) |
| Ceruloplasmin   |
| Matrix metalloproteinase-1  |
| RCT-138   |
| RCT-240   |
| RCT-293   |
| RCT-38  |
| Pyruvate kinase, muscle   |
| Superoxide dismutase Mn   |
| Ubiquitin conjugating enzyme (RAD 6 homologue)                      |

| Rand 10 (2)   |
|---|
| Organic cation transporter 3  |
| Preproalbumin, sequence 2 (alternate clone 1)                       |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk) |
| Ceruloplasmin   |
| Hypoxanthine-guanine phosphoribosyltransferase                      |
| Multidrug resistant protein-1                                       |
| RCT-180   |
| RCT-240   |
| RCT-287   |
| Pyruvate kinase, muscle   |

| Rand 15 (1)   |
|---|
| Preproalbumin, sequence 2 (alternate clone 1)                       |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk) |
| CD44 metastasis suppressor gene                                     |
| Epidermal growth factor   |
| Hypoxanthine-guanine phosphoribosyltransferase                      |
| Interleukin-1 beta  |

|  |
|--|
| Matrix metalloproteinase-1                     |
| Multidrug resistant protein-1                  |
| Organic cation transporter 3                   |
| RCT-180  |
| RCT-240  |
| RCT-38   |
| Pyruvate kinase, muscle                        |
| Superoxide dismutase Mn                        |
| Ubiquitin conjugating enzyme (RAD 6 homologue) |

|   |
|---|
| Rand 15 (2)   |
| Preproalbumin, sequence 2 (alternate clone 1)                       |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk) |
| CD44 metastasis suppressor gene                                     |
| Connexin-32   |
| Epidermal growth factor   |
| Matrix metalloproteinase-1  |
| Multidrug resistant protein-1                                       |
| Organic cation transporter 3  |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II)            |
| RCT-287   |
| RCT-293   |
| Pyruvate kinase, muscle   |
| Ref-1   |
| Superoxide dismutase Mn   |
| Ubiquitin conjugating enzyme (RAD 6 homologue)                      |

\* Genes were randomly selected from the Combo All list of predictive genes (216 genes) assigning a random number to each gene, sorting by the random number and selecting the appropriate number of sorted genes.

Table 10 Randomly Selected Gene Subsets from Array Genes Excluding Combo All Set\*

| Rand 5 (1)              | Rand 5 (2)                                   |
|-------------------------|--|
| Argininosuccinate lyase | { RCT-247 }                                  |
| RCT-115                 | Inter-alpha-inhibitor H4 heavy chain (Itih4) |
| RCT-37                  | RCT-290                                      |
| RCT-9                   | RCT-96                                       |
| Phosphoglycerate kinase | Very long-chain acyl-CoA dehydrogenase       |

| Rand 10 (1)                              | Rand 10 (2)                              |
|--|--|
| AT-1                                     | Aryl sulfotransferase                    |
| Cellular retinoic acid binding protein 2 | BAK                                      |
| Ornithine decarboxylase                  | Cyclooxygenase 2                         |
| Peroxisomal 3-ketoacyl-CoA thiolase 1    | L-gulono-gamma-lactone oxidase           |
| RCT-107                                  | Metallothionein 1                        |
| RCT-117                                  | Osteoactivin                             |
| RCT-130                                  | RCT-12                                   |
| RCT-134                                  | Protein kinase C alpha                   |
| RCT-137                                  | Putative membrane fatty acid transporter |
| RCT-175                                  | RAC protein kinase beta                  |

| Rand 15 (1)                                   | Rand 15 (2)                                      |
|---|--|
| Adrenomedullin                                | Alpha 1-antitrypsin                              |
| AT-4  | BAK  |
| Calpain 2                                     | Bile salt export pump (sister of p-glycoprotein) |
| Cyclin G                                      | C4b-binding protein                              |
| Cytochrome P450 17A                           | Choline kinase                                   |
| Endogenous retroviral sequence, 5' and 3' LTR | Cyclin dependent kinase 2                        |
| NADPH cytochrome P450 oxidoreductase          | Extracellular-signal-regulated kinase 1          |
| Paraoxonase 1                                 | Glutathione S-transferase P1                     |
| RCT-102                                       | Histone 2A                                       |
| RCT-143                                       | RCT-25   |
| RCT-208                                       | RCT-57   |
| RCT-225                                       | RCT-66   |



|               |                             |
|---------------|-----------------------------|
| RCT-253       | RCT-7                       |
| RCT-52        | RCT-87                      |
| Urate oxidase | Poly(ADP-ribose) polymerase |

\* Genes were randomly selected from the entire array list of genes excluding the Combo  
All 216 predictive genes by assigning a random number to each gene, sorting by the  
random number and selecting the appropriate number of sorted genes.

Table 11 Kidney Toxicity Individual Sample Prediction Values for 24 Hour Data  
Predictive Genes (Combined List and Subsets)

| Gene Set  | Number   | Prediction Measure*        |                            |                            |                            |
|-----------|----------|----------------------------|----------------------------|----------------------------|----------------------------|
|           | of Genes | Accuracy**                 | False Positive**           | False Negative**           | Geometric Mean**           |
| Combo All | 216      | <b>0.915</b> (0.861-0.945) | <b>0.046</b> (0.012-0.108) | <b>0.310</b> (0.200-0.467) | <b>0.810</b> (0.720-0.884) |
| Combo 6   | 28       | <b>0.921</b> (0.867-0.955) | <b>0.062</b> (0.031-0.108) | <b>0.300</b> (0.050-0.533) | <b>0.837</b> (0.660-0.953) |
| Combo 5   | 25       | <b>0.896</b> (0.829-0.929) | <b>0.073</b> (0.044-0.122) | <b>0.269</b> (0.200-0.467) | <b>0.821</b> (0.684-0.870) |
| Combo 4   | 23       | <b>0.882</b> (0.829-0.929) | <b>0.087</b> (0.010-0.145) | <b>0.325</b> (0.000-0.467) | <b>0.776</b> (0.700-0.925) |
| Combo 3   | 19       | <b>0.839</b> (0.778-0.911) | <b>0.127</b> (0.054-0.215) | <b>0.358</b> (0.133-0.667) | <b>0.740</b> (0.562-0.892) |
| Combo 2   | 45       | <b>0.733</b> (0.641-0.821) | <b>0.215</b> (0.113-0.349) | <b>0.586</b> (0.400-0.867) | <b>0.552</b> (0.343-0.663) |
| Combo 1   | 76       | <b>0.787</b> (0.667-0.884) | <b>0.171</b> (0.054-0.322) | <b>0.464</b> (0.333-0.867) | <b>0.645</b> (0.355-0.782) |

\* Prediction measures are given as means and range of values (in parentheses) for six training/test sets using 24 hour array data and gene lists. Unit of prediction was the animal and the predictive classification was for kidney tubular necrosis observed at 72 hours after treatment.

\*\* Standard prediction measures were used as defined in Materials and Methods. These include:

|                     |  |
|---------------------|--|
| Accuracy            | =Proportion of total number of predictions that are correct                            |
| False positive rate | =Proportion of negative cases that are incorrectly classified as positive              |
| False negative rate | =Proportion of positive cases that are incorrectly classified as negative              |
| Geometric mean      | =Performance measure that takes into account proportion of positive and negative cases |

Table12 Kidney Toxicity Compound-Dose Prediction Values for 24 Hour Data  
Predictive Genes (Combined List and Subsets)

| Gene Set  | Number of Genes | Accuracy**                 | Prediction Measure*<br>False Positive** | False Negative**           | Geometric Mean**           |
|-----------|-----------------|----------------------------|---|----------------------------|----------------------------|
| Combo All | 216             | <b>0.932</b> (0.889-0.950) | <b>0.048</b> (0.000-0.097)              | <b>0.206</b> (0.000-0.500) | <b>0.859</b> (0.688-0.967) |
| Combo 6   | 28              | <b>0.950</b> (0.889-1.000) | <b>0.041</b> (0.000-0.065)              | <b>0.161</b> (0.000-0.400) | <b>0.894</b> (0.749-0.973) |
| Combo 5   | 25              | <b>0.945</b> (0.861-1.000) | <b>0.041</b> (0.000-0.097)              | <b>0.189</b> (0.000-0.400) | <b>0.878</b> (0.736-0.984) |
| Combo 4   | 23              | <b>0.909</b> (0.889-0.950) | <b>0.059</b> (0.000-0.107)              | <b>0.378</b> (0.000-0.600) | <b>0.751</b> (0.622-0.945) |
| Combo 3   | 19              | <b>0.915</b> (0.892-0.974) | <b>0.067</b> (0.030-0.125)              | <b>0.200</b> (0.000-0.500) | <b>0.857</b> (0.688-0.985) |
| Combo 2   | 45              | <b>0.849</b> (0.757-0.892) | <b>0.105</b> (0.061-0.188)              | <b>0.489</b> (0.167-1.000) | <b>0.608</b> (0.000-0.868) |
| Combo 1   | 76              | <b>0.847</b> (0.778-0.895) | <b>0.117</b> (0.053-0.194)              | <b>0.408</b> (0.167-0.750) | <b>0.712</b> (0.487-0.863) |

\* Prediction measures are given as means and range of values (in parentheses) for six training/test sets using 24 hour array data and gene lists. Unit of prediction was compound-dose level and the predictive classification was for kidney tubular necrosis observed at 72 hours after treatment. Prediction for compound-dose was based on a majority of individual animal calls. In cases where there were an equal number of opposing calls or no calls a no-call was assigned to the compound-dose level.

\*\* Standard prediction measures were used as defined in Materials and Methods. As described in Materials and Methods in cases where no prediction was made because the p-value ratio exceeded the cutoff-value (generally 0.5) the non-call was considered to be incorrect.

Table 13 Kidney Toxicity Compound Prediction Values for 24 Hour Data Predictive Genes (Combined List and Subsets)

| Gene Set  | Number of Genes | Accuracy**                 | Prediction Measure*<br>False Positive** | False Negative**           | Geometric Mean**           |
|-----------|-----------------|----------------------------|---|----------------------------|----------------------------|
| Combo All | 216             | <b>0.944</b> (0.900-1.000) | <b>0.057</b> (0.000-0.118)              | <b>0.056</b> (0.000-0.333) | <b>0.941</b> (0.797-1.000) |
| Combo 6   | 28              | <b>0.968</b> (0.950-1.000) | <b>0.037</b> (0.000-0.059)              | <b>0.000</b> (0.000-0.000) | <b>0.981</b> (0.970-1.000) |
| Combo 5   | 25              | <b>0.968</b> (0.950-1.000) | <b>0.037</b> (0.000-0.059)              | <b>0.000</b> (0.000-0.000) | <b>0.981</b> (0.970-1.000) |
| Combo 4   | 23              | <b>0.921</b> (0.875-0.950) | <b>0.047</b> (0.000-0.118)              | <b>0.278</b> (0.000-0.667) | <b>0.816</b> (0.563-0.970) |
| Combo 3   | 19              | <b>0.928</b> (0.850-0.950) | <b>0.077</b> (0.048-0.176)              | <b>0.056</b> (0.000-0.333) | <b>0.931</b> (0.797-0.970) |
| Combo 2   | 45              | <b>0.881</b> (0.750-0.950) | <b>0.086</b> (0.048-0.235)              | <b>0.333</b> (0.000-1.000) | <b>0.706</b> (0.000-0.970) |
| Combo 1   | 76              | <b>0.904</b> (0.850-1.000) | <b>0.067</b> (0.000-0.118)              | <b>0.278</b> (0.000-0.667) | <b>0.810</b> (0.563-1.000) |

\* Prediction measures are given as means and range of values (in parentheses) for six training/test sets using 24 hour array data and gene lists. Unit of prediction was the compound and the predictive classification was for kidney tubular necrosis observed at 72 hours after treatment. Compounds were considered toxic if any compound-dose level for that compound was predicted as toxic.

\*\* Standard prediction measures were used as defined in Materials and Methods. As described in Materials and Methods in cases where no prediction was made because the p-value ratio exceeded the cutoff-value (generally 0.5) the non-call was considered to be incorrect.

Table 14 Order of Genes Used for Cumulative Analysis of Predictive Performance of Predictive Combo Gene Sets\*

| Combo 6 Gene Set                             |
|--|
| Gadd45                                       |
| Gadd153                                      |
| Clusterin                                    |
| Cathepsin L                                  |
| PAR interacting protein                      |
| Tissue inhibitor of metalloproteinases-1     |
| Insulin-like growth factor binding protein 1 |
| Cathepsin L, sequence 2                      |
| Dynein light chain 1                         |
| RCT-68                                       |
| Calpactin I heavy chain                      |
| Alpha-tubulin                                |
| 60S ribosomal protein L6 (alternate clone 1) |
| Vacuole membrane protein 1                   |
| RCT-241                                      |
| RCT-144                                      |
| RCT-271                                      |
| RCT-24                                       |
| RCT-145                                      |
| Uncoupling protein 2                         |
| c-myc  |
| CDK108                                       |
| Ribosomal protein S8                         |
| RCT-152                                      |
| RCT-158                                      |
| Ribosomal protein L13A                       |
| RCT-109                                      |
| RCT-198                                      |

| Combo 5 Gene Set                   |
|------------------------------------|
| RCT-182                            |
| Carbonic anhydrase III, sequence 2 |
| RCT-258                            |
| 60S ribosomal protein L6           |
| RCT-274                            |

|   |
|---|
| Multidrug resistant protein-3                       |
| Osteopontin   |
| Beta-actin, sequence 2                              |
| Beta-tubulin, class I                               |
| Zinc finger protein                                 |
| Canalicular multispecific organic anion transporter |
| Keratinocyte growth factor                          |
| Alpha-fibrinogen                                    |
| Ribosomal protein S9                                |
| RCT-60  |
| RCT-179   |
| Thymosin beta-10                                    |
| Proliferating cell nuclear antigen gene             |
| IgE binding protein                                 |
| RCT-211   |
| RCT-49  |
| RCT-50  |
| Heme binding protein 23                             |
| MHC class I antigen RT1.A1(f) alpha-chain           |
| RCT-126   |

|   |
|---|
| Combo 4 Gene Set  |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II)            |
| RCT-240   |
| Epidermal growth factor   |
| Matrix metalloproteinase-1  |
| RCT-287   |
| Connexin-32   |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk) |
| Superoxide dismutase Mn   |
| Pyruvate kinase, muscle   |
| Ferritin H-chain  |
| Multidrug resistant protein-1                                       |
| RCT-293   |
| Interleukin-1 beta  |
| Organic cation transporter 3  |
| Preproalbumin, sequence 2 (alternate clone 1)                       |
| CD44 metastasis suppressor gene                                     |
| Ubiquitin conjugating enzyme (RAD 6 homologue)                      |

|  |
|--|
| RCT-38   |
| Ref-1  |
| Ceruloplasmin                                  |
| Hypoxanthine-guanine phosphoribosyltransferase |
| RCT-138  |
| RCT-180  |

\* Genes are listed in the order in which they were used for cumulative analysis of predictive performance

Table 15 Individual Gene Predictions: Combo 6

| Gene Name                                    | Overall Correct Calls |              |              |              |
|--|-----------------------|--------------|--------------|--------------|
|  | Mean                  | s.d.         | min          | max          |
| 60S ribosomal protein L6 (alternate clone 1) | 71.4%                 | 6.6%         | 60.2%        | 80.4%        |
| Alpha-tubulin                                | 65.2%                 | 9.7%         | 54.6%        | 78.6%        |
| Calpactin I heavy chain                      | 62.5%                 | 8.2%         | 50.0%        | 73.2%        |
| Cathepsin L                                  | 76.0%                 | 4.6%         | 70.9%        | 83.3%        |
| Cathepsin L, sequence 2                      | 76.7%                 | 6.3%         | 67.3%        | 83.9%        |
| CDK108                                       | 58.7%                 | 25.5%        | 20.4%        | 82.1%        |
| Clusterin                                    | 75.3%                 | 10.8%        | 55.6%        | 84.9%        |
| c-myc  | 67.7%                 | 10.1%        | 55.2%        | 80.2%        |
| Dynein light chain 1                         | 74.6%                 | 4.4%         | 69.4%        | 80.2%        |
| Gadd153                                      | 70.8%                 | 13.7%        | 54.3%        | 87.5%        |
| Gadd45                                       | 69.9%                 | 11.1%        | 61.2%        | 91.1%        |
| Insulin-like growth factor binding protein 1 | 67.4%                 | 5.3%         | 61.9%        | 74.6%        |
| PAR interacting protein                      | 66.4%                 | 8.9%         | 53.3%        | 75.9%        |
| RCT-109                                      | 69.8%                 | 4.3%         | 61.2%        | 72.3%        |
| RCT-144                                      | 58.4%                 | 32.8%        | 9.3%         | 91.3%        |
| RCT-145                                      | 76.2%                 | 8.9%         | 65.0%        | 89.7%        |
| RCT-152                                      | 64.9%                 | 22.7%        | 20.4%        | 81.0%        |
| RCT-158                                      | 67.6%                 | 3.9%         | 61.3%        | 72.2%        |
| RCT-198                                      | 66.1%                 | 8.3%         | 55.3%        | 78.1%        |
| Vacuole membrane protein 1                   | 60.8%                 | 21.3%        | 40.0%        | 87.5%        |
| RCT-24                                       | 65.4%                 | 11.1%        | 50.9%        | 82.1%        |
| RCT-241                                      | 79.9%                 | 6.4%         | 73.3%        | 92.1%        |
| RCT-271                                      | 57.2%                 | 15.2%        | 37.3%        | 76.8%        |
| RCT-68                                       | 64.5%                 | 8.5%         | 56.2%        | 79.5%        |
| Ribosomal protein L13A                       | 55.8%                 | 15.4%        | 27.0%        | 71.4%        |
| Ribosomal protein S8                         | 58.5%                 | 18.8%        | 20.4%        | 70.5%        |
| Tissue inhibitor of metalloproteinases-1     | 74.0%                 | 11.7%        | 56.5%        | 87.5%        |
| Uncoupling protein 2                         | 73.7%                 | 4.4%         | 67.0%        | 78.1%        |
| <b>Average Individual Combo 6</b>            | <b>67.7%</b>          | <b>11.4%</b> | <b>51.3%</b> | <b>80.9%</b> |
| <b>Minimum Individual Combo 6</b>            | <b>55.8%</b>          | <b>3.9%</b>  | <b>9.3%</b>  | <b>70.5%</b> |
| <b>Maximum Individual Combo 6</b>            | <b>79.9%</b>          | <b>32.8%</b> | <b>73.3%</b> | <b>92.1%</b> |



Table 16 Individual Gene Predictions: Combo 5

| Gene Name   | Overall Correct Calls |              |              |              |
|---|-----------------------|--------------|--------------|--------------|
|   | Mean                  | s.d.         | min          | max          |
| 60S ribosomal protein L6                            | 75.6%                 | 5.3%         | 69.1%        | 82.1%        |
| Alpha-fibrinogen                                    | 62.2%                 | 19.6%        | 27.6%        | 80.4%        |
| Beta-actin, sequence 2                              | 65.8%                 | 23.2%        | 19.0%        | 81.0%        |
| Beta-tubulin, class I                               | 58.4%                 | 20.5%        | 21.9%        | 74.6%        |
| Canalicular multispecific organic anion transporter | 59.7%                 | 6.9%         | 52.8%        | 69.1%        |
| Carbonic anhydrase III, sequence 2                  | 59.2%                 | 23.7%        | 22.9%        | 81.8%        |
| Heme binding protein 23                             | 55.8%                 | 24.9%        | 8.7%         | 76.8%        |
| IgE binding protein                                 | 60.0%                 | 22.2%        | 15.9%        | 77.3%        |
| Keratinocyte growth factor                          | 63.2%                 | 6.8%         | 55.2%        | 70.6%        |
| MHC class I antigen RT1.A1(f) alpha-chain           | 54.0%                 | 9.8%         | 40.0%        | 66.4%        |
| Multidrug resistant protein-3                       | 66.8%                 | 5.1%         | 60.7%        | 73.8%        |
| Osteopontin   | 75.3%                 | 21.0%        | 33.3%        | 88.4%        |
| RCT-126   | 47.0%                 | 9.1%         | 39.0%        | 61.9%        |
| RCT-179   | 67.2%                 | 10.1%        | 56.3%        | 85.7%        |
| RCT-182   | 49.9%                 | 29.4%        | 21.3%        | 86.6%        |
| RCT-211   | 55.9%                 | 8.0%         | 45.6%        | 67.5%        |
| RCT-258   | 72.5%                 | 15.1%        | 42.9%        | 82.7%        |
| RCT-274   | 69.8%                 | 9.0%         | 58.3%        | 83.3%        |
| RCT-49  | 61.2%                 | 19.2%        | 27.0%        | 79.4%        |
| RCT-50  | 58.2%                 | 16.6%        | 25.7%        | 72.3%        |
| RCT-60  | 64.7%                 | 12.1%        | 43.7%        | 78.6%        |
| Proliferating cell nuclear antigen gene             | 70.5%                 | 11.9%        | 52.4%        | 84.9%        |
| Ribosomal protein S9                                | 72.9%                 | 9.4%         | 59.0%        | 83.9%        |
| Thymosin beta-10                                    | 67.8%                 | 7.9%         | 59.1%        | 82.5%        |
| Zinc finger protein                                 | 55.0%                 | 14.7%        | 35.2%        | 78.6%        |
| <b>Average Combo 5</b>                              | <b>62.7%</b>          | <b>14.5%</b> | <b>39.7%</b> | <b>78.0%</b> |
| <b>Minimum Individual Combo 6</b>                   | <b>47.0%</b>          | <b>5.1%</b>  | <b>8.7%</b>  | <b>61.9%</b> |
| <b>Maximum Individual Combo 6</b>                   | <b>75.6%</b>          | <b>29.4%</b> | <b>69.1%</b> | <b>88.4%</b> |

Table 17 Kidney Toxicity Individual Sample Prediction Values  
for 24 Hour Data with Random Gene Subsets

| Gene Set  | Random Subset* |                     | Prediction Measure** |                      |                     |
|-----------|----------------|---------------------|----------------------|----------------------|---------------------|
|           |                | Accuracy***         | False Positive***    | False Negative***    | Geometric Mean***   |
| Combo All | 5 genes (1)    | 0.581 (0.324-0.778) | 0.416 (0.180-0.700)  | 0.453 (0.350-0.5330) | 0.556 (0.374-0.658) |
| Combo All | 5 genes (2)    | 0.651 (0.476-0.812) | 0.334 (0.155-0.578)  | 0.489 (0.300-0.933)  | 0.542 (0.227-0.712) |
| Combo All | 10 genes (1)   | 0.740 (0.593-0.875) | 0.239 (0.099-0.441)  | 0.375 (0.200-0.533)  | 0.681 (0.591-0.842) |
| Combo All | 10 genes (2)   | 0.836 (0.786-0.929) | 0.101 (0.031-0.172)  | 0.278 (0.000-0.533)  | 0.630 (0.250-0.804) |
| Combo All | 15 genes (1)   | 0.823 (0.718-0.884) | 0.167 (0.072-0.349)  | 0.278 (0.000-0.533)  | 0.763 (0.644-0.913) |
| Combo All | 15 genes (2)   | 0.790 (0.713-0.911) | 0.153 (0.031-0.269)  | 0.522 (0.400-0.650)  | 0.633 (0.535-0.719) |
| Combo All | All 216 genes  | 0.915 (0.861-0.945) | 0.046 (0.012-0.108)  | 0.310 (0.200-0.467)  | 0.810 (0.720-0.884) |
|           |                |                     |                      |                      |                     |
| Combo 6   | 5 genes (1)    | 0.799 (0.713-0.845) | 0.177 (0.078-0.33)   | 0.317 (0.000-0.533)  | 0.733 (0.645-0.862) |
| Combo 6   | 5 genes (2)    | 0.757 (0.629-0.902) | 0.222 (0.082-0.367)  | 0.336 (0.133-0.550)  | 0.713 (0.616-0.857) |
| Combo 6   | 10 genes (1)   | 0.893 (0.861-0.944) | 0.073 (0.031-0.118)  | 0.300 (0.200-0.400)  | 0.805 (0.744-0.878) |
| Combo 6   | 10 genes (2)   | 0.872 (0.806-0.929) | 0.096 (0.031-0.157)  | 0.317 (0.150-0.400)  | 0.784 (0.740-0.847) |
| Combo 6   | 15 genes (1)   | 0.910 (0.886-0.955) | 0.043 (0.010-0.086)  | 0.350 (0.267-0.467)  | 0.787 (0.710-0.852) |
| Combo 6   | 15 genes (2)   | 0.914 (0.883-0.964) | 0.050 (0.000-0.075)  | 0.292 (0.200-0.467)  | 0.819 (0.718-0.862) |
| Combo 6   | All 28 genes   | 0.921 (0.867-0.955) | 0.062 (0.031-0.108)  | 0.300 (0.050-0.533)  | 0.837 (0.660-0.953) |
|           |                |                     |                      |                      |                     |
| Combo 5   | 5 genes (1)    | 0.704 (0.591-0.841) | 0.289 (0.108-0.489)  | 0.383 (0.050-0.533)  | 0.646 (0.539-0.697) |
| Combo 5   | 5 genes (2)    | 0.797 (0.750-0.884) | 0.164 (0.072-0.237)  | 0.400 (0.200-0.600)  | 0.702 (0.609-0.847) |
| Combo 5   | 10 genes (1)   | 0.805 (0.718-0.848) | 0.164 (0.090-0.277)  | 0.392 (0.250-0.733)  | 0.702 (0.493-0.791) |
| Combo 5   | 10 genes (2)   | 0.864 (0.838-0.902) | 0.102 (0.072-0.129)  | 0.333 (0.200-0.467)  | 0.772 (0.700-0.843) |
| Combo 5   | 15 genes (1)   | 0.900 (0.864-       | 0.095 (0.027-        | 0.150 (0.000-        | 0.874 (0.805-       |

|         |              |                            |                            |                            |                             |
|---------|--------------|----------------------------|----------------------------|----------------------------|-----------------------------|
|         |              | 0.937)                     | 0.167)                     | 0.333)                     | 0.914)                      |
| Combo 5 | 15 genes (2) | <b>0.867</b> (0.829-0.929) | <b>0.104</b> (0.045-0.144) | <b>0.292</b> (0.200-0.467) | <b>0.794</b> (0.684-0.8420) |
| Combo 5 | All 25 genes | <b>0.896</b> (0.829-0.929) | <b>0.073</b> (0.044-0.122) | <b>0.269</b> (0.200-0.467) | <b>0.821</b> (0.684-0.870)  |
|         |              |                            |                            |                            |                             |
| Combo 4 | 5 genes (1)  | <b>0.807</b> (0.680-0.873) | <b>0.167</b> (0.082-0.325) | <b>0.361</b> (0.200-0.467) | <b>0.724</b> (0.686-0.777)  |
| Combo 4 | 5 genes (2)  | <b>0.710</b> (0.648-0.764) | <b>0.290</b> (0.189-0.356) | <b>0.333</b> (0.050-0.800) | <b>0.669</b> (0.403-0.801)  |
| Combo 4 | 10 genes (1) | <b>0.807</b> (0.705-0.884) | <b>0.138</b> (0.062-0.256) | <b>0.522</b> (0.350-0.867) | <b>0.626</b> (0.350-0.751)  |
| Combo 4 | 10 genes (2) | <b>0.809</b> (0.741-0.839) | <b>0.166</b> (0.103-0.229) | <b>0.367</b> (0.000-0.533) | <b>0.716</b> (0.605-0.878)  |
| Combo 4 | 15 genes (1) | <b>0.843</b> (0.800-0.911) | <b>0.122</b> (0.021-0.217) | <b>0.403</b> (0.000-0.600) | <b>0.706</b> (0.601-0.885)  |
| Combo 4 | 15 genes (2) | <b>0.854</b> (0.800-0.920) | <b>0.114</b> (0.021-0.181) | <b>0.356</b> (0.050-0.600) | <b>0.744</b> (0.589-0.8820) |
| Combo 4 | All 23 genes | <b>0.882</b> (0.829-0.929) | <b>0.087</b> (0.010-0.145) | <b>0.325</b> (0.000-0.467) | <b>0.776</b> (0.700-0.925)  |

\* Randomly selected sets of genes derived from the Combo sets.

\* Prediction measures are given as means and range of values (in parentheses) for six training/test sets using 24 hour array data and random subsets of genes. Unit of prediction was the animal and the predictive classification was for kidney tubular necrosis observed at 72 hours after treatment.

\*\* Standard prediction measures were used as defined in Materials and Methods. As described in Materials and Methods in cases where no prediction was made because the p-value ratio exceeded the cutoff-value (generally 0.5) the non-call was considered to be incorrect.

Table 18 Comparison of Predictivity for True Kidney Toxicity Classification and Random Classification Using Combo Gene Sets and Random Subsets and 24h data

| Gene List* | Gene Subset* | Accuracy                 |         |           | Accuracy                |         |           |
|------------|--------------|--------------------------|---------|-----------|-------------------------|---------|-----------|
|            |              | Correct Classification** |         |           | Random Classification** |         |           |
|            |              | Mean                     | Min     | Max       | Mean                    | Min.    | Max.      |
| Combo All  | All Genes    | 0.911                    | ( 0.861 | - 0.945 ) | 0.173                   | ( 0.024 | - 0.304 ) |
|            | 5 genes (1)  | 0.581                    | ( 0.324 | - 0.778 ) | 0.265                   | ( 0.076 | - 0.381 ) |
|            | 5 genes (2)  | 0.651                    | ( 0.476 | - 0.813 ) | 0.240                   | ( 0.093 | - 0.429 ) |
|            | 10 genes (1) | 0.740                    | ( 0.593 | - 0.875 ) | 0.237                   | ( 0.157 | - 0.384 ) |
|            | 10 genes (2) | 0.836                    | ( 0.786 | - 0.929 ) | 0.225                   | ( 0.065 | - 0.304 ) |
|            | 15 genes (1) | 0.823                    | ( 0.718 | - 0.884 ) | 0.252                   | ( 0.074 | - 0.384 ) |
|            | 15 genes (2) | 0.790                    | ( 0.713 | - 0.911 ) | 0.228                   | ( 0.102 | - 0.397 ) |
|            |              |                          |         |           |                         |         |           |
| Combo 6    | All Genes    | 0.921                    | ( 0.867 | - 0.955 ) | 0.203                   | ( 0.102 | - 0.393 ) |
|            | 5 genes (1)  | 0.799                    | ( 0.713 | - 0.845 ) | 0.238                   | ( 0.076 | - 0.429 ) |
|            | 5 genes (2)  | 0.757                    | ( 0.629 | - 0.902 ) | 0.223                   | ( 0.093 | - 0.446 ) |
|            | 10 genes (1) | 0.893                    | ( 0.861 | - 0.944 ) | 0.225                   | ( 0.037 | - 0.473 ) |
|            | 10 genes (2) | 0.872                    | ( 0.808 | - 0.929 ) | 0.207                   | ( 0.074 | - 0.473 ) |
|            | 15 genes (1) | 0.910                    | ( 0.886 | - 0.955 ) | 0.224                   | ( 0.086 | - 0.545 ) |
|            | 15 genes (2) | 0.914                    | ( 0.883 | - 0.964 ) | 0.229                   | ( 0.056 | - 0.429 ) |
|            |              |                          |         |           |                         |         |           |
| Combo 5    | All Genes    | 0.896                    | ( 0.829 | - 0.929 ) | 0.258                   | ( 0.157 | - 0.348 ) |
|            | 5 genes (1)  | 0.704                    | ( 0.591 | - 0.841 ) | 0.263                   | ( 0.176 | - 0.357 ) |
|            | 5 genes (2)  | 0.797                    | ( 0.750 | - 0.884 ) | 0.279                   | ( 0.074 | - 0.446 ) |
|            | 10 genes (1) | 0.805                    | ( 0.718 | - 0.848 ) | 0.227                   | ( 0.105 | - 0.381 ) |
|            | 10 genes (2) | 0.864                    | ( 0.838 | - 0.902 ) | 0.254                   | ( 0.046 | - 0.460 ) |
|            | 15 genes (1) | 0.900                    | ( 0.864 | - 0.937 ) | 0.264                   | ( 0.148 | - 0.336 ) |
|            | 15 genes (2) | 0.867                    | ( 0.829 | - 0.929 ) | 0.223                   | ( 0.093 | - 0.339 ) |
|            |              |                          |         |           |                         |         |           |
| Combo 4    | All Genes    | 0.882                    | ( 0.829 | - 0.929 ) | 0.235                   | ( 0.074 | - 0.348 ) |
|            | 5 genes (1)  | 0.807                    | ( 0.680 | - 0.873 ) | 0.199                   | ( 0.130 | - 0.321 ) |
|            | 5 genes (2)  | 0.710                    | ( 0.648 | - 0.764 ) | 0.253                   | ( 0.165 | - 0.393 ) |
|            | 10 genes (1) | 0.807                    | ( 0.705 | - 0.884 ) | 0.246                   | ( 0.111 | - 0.393 ) |
|            | 10 genes (2) | 0.809                    | ( 0.741 | - 0.839 ) | 0.239                   | ( 0.139 | - 0.411 ) |
|            | 15 genes (1) | 0.843                    | ( 0.800 | - 0.911 ) | 0.203                   | ( 0.056 | - 0.366 ) |
|            | 15 genes (2) | 0.855                    | ( 0.800 | - 0.920 ) | 0.191                   | ( 0.037 | - 0.402 ) |
|            |              |                          |         |           |                         |         |           |
| Combo 3    | All Genes    | 0.839                    | ( 0.778 | - 0.911 ) | 0.242                   | ( 0.148 | - 0.295 ) |
|            |              |                          |         |           |                         |         |           |
| Combo 2    | All Genes    | 0.733                    | ( 0.641 | - 0.821 ) | 0.240                   | ( 0.056 | - 0.349 ) |
|            |              |                          |         |           |                         |         |           |
| Combo 1    | All Genes    | 0.787                    | ( 0.667 | - 0.884 ) | 0.220                   | ( 0.083 | - 0.321 ) |
|            |              |                          |         |           |                         |         |           |
| All-Pred   | 5 genes (1)  | 0.372                    | ( 0.229 | - 0.500 ) | 0.234                   | ( 0.220 | - 0.242 ) |
|            | 5 genes (2)  | 0.355                    | ( 0.194 | - 0.518 ) | 0.258                   | ( 0.102 | - 0.429 ) |
|            | 10 genes (1) | 0.565                    | ( 0.448 | - 0.661 ) | 0.208                   | ( 0.130 | - 0.268 ) |
|            | 10 genes (2) | 0.541                    | ( 0.380 | - 0.696 ) | 0.246                   | ( 0.171 | - 0.375 ) |
|            | 15 genes (1) | 0.502                    | ( 0.287 | - 0.661 ) | 0.233                   | ( 0.208 | - 0.258 ) |

- \* For Combo lists all genes were used or random subsets. All-Pred used genes randomly selected from genes that were present on the array but not in the predictive list.
- \*\* Accuracy = proportion of the total number of predictions that are correct. Non-calls are counted as incorrect predictions. Accuracy was calculated for correct classifications of kidney toxicity assigned to the samples and for randomized classifications in the same proportions as the correct classifications. Values presented are the mean accuracy values for 6 training/test sets with minimum and maximum accuracy values.

Table 19 Distribution of Compounds\* in Individual Training and Test Sets  
for 6 Hour Kidney Data

Training and Test Set A

| Set A Train<br>Negative** | Set A Train<br>Positive | Set A Test<br>Negative | Set A Test<br>Positive |
|---------------------------|-------------------------|------------------------|------------------------|
| AMPB                      | CAD                     | ANIT                   | CHCL3                  |
| AZA                       | CIS                     | 5-FU                   | CPHOS                  |
| CHLOR                     | HYD                     | APAP                   | GAN                    |
| CLO                       | LPS                     | BEN                    |                        |
| CYCA                      | TET                     | BAP                    |                        |
| DEX                       |                         | BRB                    |                        |
| DIF                       |                         | BUS                    |                        |
| DOX                       |                         | CCL4                   |                        |
| ERY                       |                         | CAR                    |                        |
| EST                       |                         | CLOZ                   |                        |
| ETH                       |                         | CMC                    |                        |
| GEN                       |                         | CHEX                   |                        |
| MET                       |                         | DMN                    |                        |
| PHEN                      |                         | ISON                   |                        |
| PUR                       |                         | KETO                   |                        |
| TAM                       |                         | NAL                    |                        |
| TET                       |                         | PBARB                  |                        |
|                           |                         | PEG                    |                        |
|                           |                         | QUIN                   |                        |
|                           |                         | STRZ                   |                        |

Random Training and Test Set 1 (Randomly assigned)

| Training Set 1 Negative | Training Set 1<br>Positive | Test Set 1 Negative | Test Set 1 Positive |
|-------------------------|----------------------------|---------------------|---------------------|
| ANIT                    | CAD                        | 5-FU                | CHCL3               |
| APAP                    | CIS                        | AMPB                | CPHOS               |
| AZA                     | GAN                        | BRB                 | LPS                 |
| BAP                     | HYD                        | BUS                 |                     |
| BEN                     | TET                        | CCL4                |                     |
| CAR                     |                            | CHLOR               |                     |
| CHEX                    |                            | CYCA                |                     |
| CLO                     |                            | ERY                 |                     |
| CLOZ                    |                            | EST                 |                     |
| CMC                     |                            | ETH                 |                     |
| DEX                     |                            | ISON                |                     |
| DIF                     |                            | MET                 |                     |
| DMN                     |                            | STRZ                |                     |

|       |  |  |  |
|-------|--|--|--|
| DOX   |  |  |  |
| GEN   |  |  |  |
| KETO  |  |  |  |
| NAL   |  |  |  |
| PBARB |  |  |  |
| PEG   |  |  |  |
| PHEN  |  |  |  |
| PUR   |  |  |  |
| QUIN  |  |  |  |
| TAM   |  |  |  |

Random Training and Test Set 2 (Randomly assigned)

| Training Set 2<br>Negative | Training Set 2<br>Positive | Test Set 2<br>Negative | Test Set 2 Positive |
|----------------------------|----------------------------|------------------------|---------------------|
| APAP                       | CHCL3                      | 5-FU                   | CAD                 |
| AZA                        | CPHOS                      | AMPB                   | CIS                 |
| BUS                        | HYD                        | ANIT                   | GAN                 |
| CAR                        | LPS                        | BAP                    |                     |
| CCL4                       | TET                        | BEN                    |                     |
| CHLOR                      |                            | BRB                    |                     |
| CLO                        |                            | CHEX                   |                     |
| CLOZ                       |                            | CMC                    |                     |
| DEX                        |                            | CYCA                   |                     |
| DOX                        |                            | DIF                    |                     |
| EST                        |                            | DMN                    |                     |
| ETH                        |                            | ERY                    |                     |
| GEN                        |                            | ISON                   |                     |
| KETO                       |                            |                        |                     |
| MET                        |                            |                        |                     |
| NAL                        |                            |                        |                     |
| PBARB                      |                            |                        |                     |
| PEG                        |                            |                        |                     |
| PHEN                       |                            |                        |                     |
| PUR                        |                            |                        |                     |
| QUIN                       |                            |                        |                     |
| STRZ                       |                            |                        |                     |
| TAM                        |                            |                        |                     |

Random Training and Test Set 3 (Randomly assigned)

| Training Set 3 | Training Set 3 | Test Set 3 | Test Set 3 Positive |
|----------------|----------------|------------|---------------------|
|----------------|----------------|------------|---------------------|

| Negative | Positive | Negative |     |
|----------|----------|----------|-----|
| AMPB     | CAD      | 5-FU     | HYD |
| ANIT     | CHCL3    | APAP     | LPS |
| AZA      | CIS      | BAP      | TET |
| BEN      | CPHOS    | BRB      |     |
| BUS      | GAN      | CAR      |     |
| CCL4     |          | CLOZ     |     |
| CHEX     |          | DEX      |     |
| CHLOR    |          | DIF      |     |
| CLO      |          | DMN      |     |
| CMC      |          | ERY      |     |
| CYCA     |          | KETO     |     |
| DOX      |          | MET      |     |
| EST      |          | PEG      |     |
| ETH      |          |          |     |
| GEN      |          |          |     |
| ISON     |          |          |     |
| NAL      |          |          |     |
| PBARB    |          |          |     |
| PHEN     |          |          |     |
| PUR      |          |          |     |
| QUIN     |          |          |     |
| STRZ     |          |          |     |
| TAM      |          |          |     |

Random Training and Test Set 4 (Randomly assigned)

| Training Set 4<br>Negative | Training Set 4<br>Positive | Test Set 4<br>Negative | Test Set 4 Positive |
|----------------------------|----------------------------|------------------------|---------------------|
| ANIT                       | CAD                        | 5-FU                   | CIS                 |
| APAP                       | CHCL3                      | AMPB                   | CPHOS               |
| AZA                        | GAN                        | CAR                    | TET                 |
| BAP                        | HYD                        | CHEX                   |                     |
| BEN                        | LPS                        | CHLOR                  |                     |
| BRB                        |                            | CLO                    |                     |
| BUS                        |                            | CMC                    |                     |
| CCL4                       |                            | DEX                    |                     |
| CLOZ                       |                            | GEN                    |                     |
| CYCA                       |                            | ISON                   |                     |
| DIF                        |                            | QUIN                   |                     |
| DMN                        |                            | STRZ                   |                     |
| DOX                        |                            | TAM                    |                     |
| ERY                        |                            |                        |                     |
| EST                        |                            |                        |                     |



|       |  |  |  |
|-------|--|--|--|
| ETH   |  |  |  |
| KETO  |  |  |  |
| MET   |  |  |  |
| NAL   |  |  |  |
| PBARB |  |  |  |
| PEG   |  |  |  |
| PHEN  |  |  |  |
| PUR   |  |  |  |

Random Training and Test Set 5 (Randomly assigned)

| Training Set 5 Neg | Training Set 5 Pos | Test Set 5 Neg | Test Set 5 Pos |
|--------------------|--------------------|----------------|----------------|
| 5-FU               | CAD                | AMPB           | HYD            |
| APAP               | CHCL3              | ANIT           | LPS            |
| AZA                | CIS                | CCL4           | TET            |
| BAP                | CPHOS              | CHEX           |                |
| BEN                | GAN                | CHLOR          |                |
| BRB                |                    | CLO            |                |
| BUS                |                    | CLOZ           |                |
| CAR                |                    | DIF            |                |
| CMC                |                    | DMN            |                |
| CYCA               |                    | GEN            |                |
| DEX                |                    | ISON           |                |
| DOX                |                    | NAL            |                |
| ERY                |                    | PHEN           |                |
| EST                |                    |                |                |
| ETH                |                    |                |                |
| KETO               |                    |                |                |
| MET                |                    |                |                |
| PBARB              |                    |                |                |
| PEG                |                    |                |                |
| PUR                |                    |                |                |
| QUIN               |                    |                |                |
| STRZ               |                    |                |                |
| TAM                |                    |                |                |

\* For abbreviations please see Table 1 (Compound, Dose, Abbreviation, etc.)

\*\* Negative= Compounds that did not elicit histopathology (score=1)

Positive= Compounds that did elicit histopathology (score of 2 or greater)

Table 20 List of Genes, Whose Expression at 6 h Directly Correlates with Kidney Tubular Necrosis at 72h, Ranked by Pearson Correlation Coefficient

| Gene   | Combination<br>(No. of<br>Occurrences) |
|--|--|
| Alpha-tubulin  | 6                                      |
| Calreticulin   | 6                                      |
| Cathepsin L  | 6                                      |
| c-H-ras  | 6                                      |
| Cyclin E   | 6                                      |
| Gadd153  | 6                                      |
| Gadd45   | 6                                      |
| Glyceraldehyde 3-phosphate dehydrogenase               | 6                                      |
| ID-1   | 6                                      |
| Insulin-like growth factor binding protein 1           | 6                                      |
| Multidrug resistant protein-3                          | 6                                      |
| RCT-111  | 6                                      |
| RCT-12   | 6                                      |
| 14-3-3 zeta  | 5                                      |
| ADP-ribosylation factor-like protein ARL184            | 5                                      |
| Aldehyde dehydrogenase 2                               | 5                                      |
| Beta-tubulin, class I                                  | 5                                      |
| Decorin  | 5                                      |
| Epidermal growth factor                                | 5                                      |
| Gamma-glutamyl transpeptidase                          | 5                                      |
| Heme binding protein 23                                | 5                                      |
| Na/K ATPase alpha-1                                    | 5                                      |
| RCT-103  | 5                                      |
| RCT-221  | 5                                      |
| RCT-50   | 5                                      |
| Pyruvate kinase, muscle                                | 5                                      |
| Ribosomal protein L13A                                 | 5                                      |
| Superoxide dismutase Mn                                | 5                                      |
| Thymosin beta-10                                       | 5                                      |
| Tryptophan hydroxylase                                 | 5                                      |
| Zinc finger protein                                    | 5                                      |
| alpha-1,2-fucosyltransferase                           | 4                                      |
| Aquaporin-3 (AQP3)                                     | 4                                      |
| Cathepsin L, sequence 2                                | 4                                      |
| Endogenous retroviral sequence, 5' and 3' LTR          | 4                                      |
| Hypoxanthine-guanine phosphoribosyltransferase         | 4                                      |
| Interferon related developmental regulator IFRD1 (PC4) | 4                                      |

|   |   |
|---|---|
| Interleukin-1 beta  | 4 |
| Macrophage inflammatory protein-2 alpha                               | 4 |
| Peroxisomal 3-ketoacyl-CoA thiolase 2                                 | 4 |
| RCT-102   | 4 |
| RCT-109   | 4 |
| RCT-144   | 4 |
| RCT-24  | 4 |
| Inositol polyphosphate multikinase (lpmk)                             | 4 |
| RCT-49  | 4 |
| Protein tyrosine phosphatase alpha                                    | 4 |
| Thiol-specific antioxidant (natural killer cell-enhancing factor B)   | 4 |
| Uncoupling protein 2  | 4 |
| RCT-139   | 3 |
| Bcl-2   | 3 |
| Calpactin I heavy chain   | 3 |
| c-fos   | 3 |
| Connexin-32   | 3 |
| Cytochrome P450 1A1   | 3 |
| Ecto-ATPase   | 3 |
| Heme oxygenase  | 3 |
| Hepatocyte growth factor receptor                                     | 3 |
| Integrin beta1  | 3 |
| N-cadherin  | 3 |
| N-hydroxy-2-acetylaminofluorene sulfotransferase (ST1C1)              | 3 |
| Ornithine decarboxylase   | 3 |
| RCT-147   | 3 |
| RCT-182   | 3 |
| RCT-228   | 3 |
| RCT-240   | 3 |
| RCT-245   | 3 |
| RCT-277   | 3 |
| RCT-43  | 3 |
| RCT-83  | 3 |
| Stathmin  | 3 |
| Alpha-1 microglobulin/bikunin precursor (Ambp)                        | 2 |
| Aspartoacylase  | 2 |
| Colony-stimulating factor-1   | 2 |
| Equilibrative nitrobenzylthioinosine-sensitive nucleoside transporter | 2 |
| Ferritin H-chain  | 2 |
| Glutathione S-transferase Yb2 subunit                                 | 2 |
| IgE binding protein   | 2 |
| Macrophage metalloelastase  | 2 |

|   |   |
|---|---|
| Malate dehydrogenase, cytosolic                                     | 2 |
| Matrix metalloproteinase-1  | 2 |
| MHC class I antigen RT1.A1(f) alpha-chain                           | 2 |
| Monoamine oxidase A   | 2 |
| NADPH cytochrome P450 reductase                                     | 2 |
| RCT-108   | 2 |
| RCT-127   | 2 |
| Apoptosis-regulating basic protein                                  | 2 |
| RCT-14  | 2 |
| RCT-146   | 2 |
| RCT-151   | 2 |
| RCT-166   | 2 |
| RCT-179   | 2 |
| RCT-180   | 2 |
| Calgranulin B   | 2 |
| RCT-211   | 2 |
| RCT-251   | 2 |
| RCT-274   | 2 |
| RCT-281   | 2 |
| Voltage-dependent anion channel 2 (Vdac2)                           | 2 |
| RCT-60  | 2 |
| RCT-76  | 2 |
| RCT-80  | 2 |
| Phosphatidylethanolamine-binding protein                            | 2 |
| PTEN/MMAC1  | 2 |
| Sterol carrier protein 2  | 2 |
| Thioredoxin-1 (Trx1)  | 2 |
| Thioredoxin-2 (Trx2)  | 2 |
| Tissue inhibitor of metalloproteinases-1                            | 2 |
| Transferrin   | 2 |
| Hemoglobin alpha 1 chain (alternate clone)                          | 1 |
| 60S ribosomal protein L6 (alternate clone 1)                        | 1 |
| Acetylcholine receptor epsilon                                      | 1 |
| Aldehyde dehydrogenase 1  | 1 |
| Alpha-1 acid glycoprotein   | 1 |
| Alpha-fibrinogen  | 1 |
| Apolipoprotein CIII   | 1 |
| Argininosuccinate lyase   | 1 |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk) | 1 |
| Calbindin-D (9K)  | 1 |
| Carbamyl phosphate synthetase I                                     | 1 |
| Caspase 7   | 1 |
| CD44 metastasis suppressor gene                                     | 1 |
| Cholesterol 7-alpha-hydroxylase (P450 VII)                          | 1 |

|  |   |
|--|---|
| c-jun  | 1 |
| c-myc  | 1 |
| Cyclin dependent kinase 4  | 1 |
| Cytochrome c oxidase subunit IV                                  | 1 |
| Cytochrome P450 2C11   | 1 |
| DNA topoisomerase I  | 1 |
| Dynein light chain 1   | 1 |
| Focal adhesion kinase (pp125FAK)                                 | 1 |
| Gamma-actin, cytoplasmic   | 1 |
| Hemoglobin alpha 1 chain   | 1 |
| Hepatocyte nuclear factor 4                                      | 1 |
| Hypoxia-inducible factor 1 alpha                                 | 1 |
| Intracellular calcium-binding protein (MRP8)                     | 1 |
| Jagged 1   | 1 |
| Major basic protein 1  | 1 |
| Methylacyl-CoA racemase alpha                                    | 1 |
| Multidrug resistant protein-2                                    | 1 |
| Na/H antiporter (APNH1)  | 1 |
| NADP-dependent isocitrate dehydrogenase, cytosolic               | 1 |
| NGF-inducible anti-proliferative putative secreted protein (PC3) | 1 |
| Ornithine aminotransferase                                       | 1 |
| PAR interacting protein  | 1 |
| Peroxisome assembly factor 2                                     | 1 |
| RCT-142  | 1 |
| RCT-148  | 1 |
| RCT-153  | 1 |
| RCT-177  | 1 |
| RCT-194  | 1 |
| RCT-198  | 1 |
| RCT-205  | 1 |
| RCT-214  | 1 |
| RCT-246  | 1 |
| RCT-268  | 1 |
| RCT-28   | 1 |
| RCT-280  | 1 |
| RCT-40   | 1 |
| RCT-53   | 1 |
| RCT-59   | 1 |
| RCT-61   | 1 |
| RCT-64   | 1 |
| RCT-66   | 1 |
| RCT-68   | 1 |
| RCT-74   | 1 |

|   |   |
|---|---|
| RCT-94                                    | 1 |
| Phosphoglycerate kinase                   | 1 |
| Retinoid X receptor alpha                 | 1 |
| Sarcoplasmic reticulum calcium ATPase     | 1 |
| Serotonin transporter (SERT)              | 1 |
| Superoxide dismutase Cu/Zn                | 1 |
| Thymidylate synthase                      | 1 |
| Transitional endoplasmic reticulum ATPase | 1 |
| Very long-chain acyl-CoA synthetase       | 1 |
| VL30 element                              | 1 |

Table 21 List of Genes, Whose Expression at 6 h Inversely Correlates with Kidney Tubular Necrosis at 72h, Ranked by Spearman Correlation Coefficient

| Gene   | Correlation Coefficient |
|--|-------------------------|
| RCT-229  | -0.35021                |
| T-cell cyclophilin                                 | -0.35156                |
| Phosphoglycerate kinase                            | -0.35228                |
| NADP-dependent isocitrate dehydrogenase, cytosolic | -0.35233                |
| Senescence marker protein-30                       | -0.35299                |
| RCT-102  | -0.35413                |
| Alpha-1 acid glycoprotein                          | -0.35452                |
| RCT-41   | -0.35839                |
| Protein tyrosine phosphatase alpha                 | -0.36371                |
| Cytochrome P450 2B1/2B2                            | -0.36443                |
| CCR-5  | -0.36576                |
| RCT-218  | -0.37234                |
| RCT-30   | -0.37235                |
| RCT-245  | -0.37273                |
| Thymidylate synthase                               | -0.37344                |
| Cytochrome c oxidase subunit I (alternate clone)   | -0.37359                |
| Malate dehydrogenase, cytosolic                    | -0.37368                |
| RCT-260  | -0.37504                |
| RCT-128  | -0.37762                |
| RCT-55   | -0.37788                |
| Cytochrome P450 2A3                                | -0.38623                |
| RCT-29   | -0.38647                |
| Transforming growth factor-beta3                   | -0.38899                |
| Vesicular monoamine transporter (VMAT)             | -0.3894                 |
| Adrenomedullin                                     | -0.38953                |
| RCT-28   | -0.39362                |
| RCT-83   | -0.39619                |
| RCT-155  | -0.39701                |
| RCT-98   | -0.39733                |
| Iron-responsive element-binding protein            | -0.4082                 |
| Mullerian inhibiting substance                     | -0.40974                |
| Inositol polyphosphate multikinase (lpmk)          | -0.41105                |
| Sarcoplasmic reticulum calcium ATPase              | -0.41428                |
| Na/H antiporter (APNH1)                            | -0.41496                |
| Maspin   | -0.41712                |
| Osteoactivin                                       | -0.42233                |
| Empty  | -0.4236                 |
| Cytochrome P450 1A1                                | -0.42401                |
| RCT-246  | -0.42616                |

|                                     |          |
|-------------------------------------|----------|
| Protein kinase C alpha              | -0.43582 |
| Cyclin D1                           | -0.43742 |
| Caveolin-3                          | -0.44097 |
| RCT-3                               | -0.44517 |
| RCT-69                              | -0.4463  |
| RCT-80                              | -0.44717 |
| RCT-194                             | -0.4479  |
| Carbamyl phosphate synthetase I     | -0.44845 |
| RCT-119                             | -0.45514 |
| Selenoprotein P                     | -0.45557 |
| RCT-112                             | -0.46143 |
| Hepatocyte nuclear factor 4         | -0.46336 |
| Macrophage metalloelastase          | -0.46368 |
| RCT-74                              | -0.46524 |
| Decorin                             | -0.46894 |
| RCT-139                             | -0.47817 |
| Very long-chain acyl-CoA synthetase | -0.48218 |
| Hepatocyte growth factor receptor   | -0.48369 |
| RCT-270                             | -0.48392 |
| RCT-182                             | -0.48529 |
| Histone 2A                          | -0.51079 |
| Phospholipase D                     | -0.51088 |
| Fatty acyl-CoA oxidase              | -0.5219  |
| RCT-268                             | -0.52288 |
| Gamma-actin, cytoplasmic            | -0.54554 |
| Aquaporin-3 (AQP3)                  | -0.5821  |
| Epidermal growth factor             | -0.62877 |



Table 22 List of genes whose expression at 6 hours is predictive of kidney toxicity at 72 hours

| Gene   | Combination (No. of Occurrences) |
|--|----------------------------------|
| Alpha-tubulin  | 6                                |
| Calreticulin   | 6                                |
| Cathepsin L  | 6                                |
| c-H-ras  | 6                                |
| Cyclin E   | 6                                |
| Gadd153  | 6                                |
| Gadd45   | 6                                |
| Glyceraldehyde 3-phosphate dehydrogenase               | 6                                |
| ID-1   | 6                                |
| Insulin-like growth factor binding protein 1           | 6                                |
| Multidrug resistant protein-3                          | 6                                |
| RCT-111  | 6                                |
| RCT-12   | 6                                |
| 14-3-3 zeta  | 5                                |
| ADP-ribosylation factor-like protein ARL184            | 5                                |
| Aldehyde dehydrogenase 2                               | 5                                |
| Beta-tubulin, class I                                  | 5                                |
| Decorin  | 5                                |
| Epidermal growth factor                                | 5                                |
| Gamma-glutamyl transpeptidase                          | 5                                |
| Heme binding protein 23                                | 5                                |
| Na/K ATPase alpha-1                                    | 5                                |
| RCT-103  | 5                                |
| RCT-221  | 5                                |
| RCT-50   | 5                                |
| Pyruvate kinase, muscle                                | 5                                |
| Ribosomal protein L13A                                 | 5                                |
| Superoxide dismutase Mn                                | 5                                |
| Thymosin beta-10                                       | 5                                |
| Tryptophan hydroxylase                                 | 5                                |
| Zinc finger protein                                    | 5                                |
| alpha-1,2-fucosyltransferase                           | 4                                |
| Aquaporin-3 (AQP3)                                     | 4                                |
| Cathepsin L, sequence 2                                | 4                                |
| Endogenous retroviral sequence, 5' and 3' LTR          | 4                                |
| Hypoxanthine-guanine phosphoribosyltransferase         | 4                                |
| Interferon related developmental regulator IFRD1 (PC4) | 4                                |
| Interleukin-1 beta                                     | 4                                |

|   |   |
|---|---|
| Macrophage inflammatory protein-2 alpha                               | 4 |
| Peroxisomal 3-ketoacyl-CoA thiolase 2                                 | 4 |
| RCT-102   | 4 |
| RCT-109   | 4 |
| RCT-144   | 4 |
| RCT-24  | 4 |
| Inositol polyphosphate multikinase (Ipmk)                             | 4 |
| RCT-49  | 4 |
| Protein tyrosine phosphatase alpha                                    | 4 |
| Thiol-specific antioxidant (natural killer cell-enhancing factor B)   | 4 |
| Uncoupling protein 2  | 4 |
| RCT-139   | 3 |
| Bcl-2   | 3 |
| Calpactin I heavy chain   | 3 |
| c-fos   | 3 |
| Connexin-32   | 3 |
| Cytochrome P450 1A1   | 3 |
| Ecto-ATPase   | 3 |
| Heme oxygenase  | 3 |
| Hepatocyte growth factor receptor                                     | 3 |
| Integrin beta1  | 3 |
| N-cadherin  | 3 |
| N-hydroxy-2-acetylaminofluorene sulfotransferase (ST1C1)              | 3 |
| Ornithine decarboxylase   | 3 |
| RCT-147   | 3 |
| RCT-182   | 3 |
| RCT-228   | 3 |
| RCT-240   | 3 |
| RCT-245   | 3 |
| RCT-277   | 3 |
| RCT-43  | 3 |
| RCT-83  | 3 |
| Stathmin  | 3 |
| Alpha-1 microglobulin/bikunin precursor (Ambp)                        | 2 |
| Aspartoacylase  | 2 |
| Colony-stimulating factor-1   | 2 |
| Equilibrative nitrobenzylthioinosine-sensitive nucleoside transporter | 2 |
| Ferritin H-chain  | 2 |
| Glutathione S-transferase Yb2 subunit                                 | 2 |
| IgE binding protein   | 2 |
| Macrophage metalloelastase  | 2 |

|   |   |
|---|---|
| Malate dehydrogenase, cytosolic                                     | 2 |
| Matrix metalloproteinase-1  | 2 |
| MHC class I antigen RT1.A1(f) alpha-chain                           | 2 |
| Monoamine oxidase A   | 2 |
| NADPH cytochrome P450 reductase                                     | 2 |
| RCT-108   | 2 |
| RCT-127   | 2 |
| Apoptosis-regulating basic protein                                  | 2 |
| RCT-14  | 2 |
| RCT-146   | 2 |
| RCT-151   | 2 |
| RCT-166   | 2 |
| RCT-179   | 2 |
| RCT-180   | 2 |
| Calgranulin B   | 2 |
| RCT-211   | 2 |
| RCT-251   | 2 |
| RCT-274   | 2 |
| RCT-281   | 2 |
| Voltage-dependent anion channel 2 (Vdac2)                           | 2 |
| RCT-60  | 2 |
| RCT-76  | 2 |
| RCT-80  | 2 |
| Phosphatidylethanolamine-binding protein                            | 2 |
| PTEN/MMAC1  | 2 |
| Sterol carrier protein 2  | 2 |
| Thioredoxin-1 (Trx1)  | 2 |
| Thioredoxin-2 (Trx2)  | 2 |
| Tissue inhibitor of metalloproteinases-1                            | 2 |
| Transferrin   | 2 |
| Hemoglobin alpha 1 chain (alternate clone)                          | 1 |
| 60S ribosomal protein L6 (alternate clone 1)                        | 1 |
| Acetylcholine receptor epsilon                                      | 1 |
| Aldehyde dehydrogenase 1  | 1 |
| Alpha-1 acid glycoprotein   | 1 |
| Alpha-fibrinogen  | 1 |
| Apolipoprotein CIII   | 1 |
| Argininosuccinate lyase   | 1 |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk) | 1 |
| Calbindin-D (9K)  | 1 |
| Carbamyl phosphate synthetase I                                     | 1 |
| Caspase 7   | 1 |
| CD44 metastasis suppressor gene                                     | 1 |
| Cholesterol 7-alpha-hydroxylase (P450 VII)                          | 1 |

|  |   |
|--|---|
| c-jun  | 1 |
| c-myc  | 1 |
| Cyclin dependent kinase 4  | 1 |
| Cytochrome c oxidase subunit IV                                  | 1 |
| Cytochrome P450 2C11   | 1 |
| DNA topoisomerase I  | 1 |
| Dynein light chain 1   | 1 |
| Focal adhesion kinase (pp125FAK)                                 | 1 |
| Gamma-actin, cytoplasmic   | 1 |
| Hemoglobin alpha 1 chain   | 1 |
| Hepatocyte nuclear factor 4                                      | 1 |
| Hypoxia-inducible factor 1 alpha                                 | 1 |
| Intracellular calcium-binding protein (MRP8)                     | 1 |
| Jagged 1   | 1 |
| Major basic protein 1  | 1 |
| Methylacyl-CoA racemase alpha                                    | 1 |
| Multidrug resistant protein-2                                    | 1 |
| Na/H antiporter (APNH1)  | 1 |
| NADP-dependent isocitrate dehydrogenase, cytosolic               | 1 |
| NGF-inducible anti-proliferative putative secreted protein (PC3) | 1 |
| Ornithine aminotransferase                                       | 1 |
| PAR interacting protein  | 1 |
| Peroxisome assembly factor 2                                     | 1 |
| RCT-142  | 1 |
| RCT-148  | 1 |
| RCT-153  | 1 |
| RCT-177  | 1 |
| RCT-194  | 1 |
| RCT-198  | 1 |
| RCT-205  | 1 |
| RCT-214  | 1 |
| RCT-246  | 1 |
| RCT-268  | 1 |
| RCT-28   | 1 |
| RCT-280  | 1 |
| RCT-40   | 1 |
| RCT-53   | 1 |
| RCT-59   | 1 |
| RCT-61   | 1 |
| RCT-64   | 1 |
| RCT-66   | 1 |
| RCT-68   | 1 |
| RCT-74   | 1 |

|   |   |
|---|---|
| RCT-94                                    | 1 |
| Phosphoglycerate kinase                   | 1 |
| Retinoid X receptor alpha                 | 1 |
| Sarcoplasmic reticulum calcium ATPase     | 1 |
| Serotonin transporter (SERT)              | 1 |
| Superoxide dismutase Cu/Zn                | 1 |
| Thymidylate synthase                      | 1 |
| Transitional endoplasmic reticulum ATPase | 1 |
| Very long-chain acyl-CoA synthetase       | 1 |
| VL30 element                              | 1 |

\* Combination category is the number of training/test set gene list occurrences.

**Table 23 Kidney Toxicity Compound-Dose Prediction Values for 6 Hour Data Predictive Genes (Combined List and Subsets)**

| Gene Set  | Number of Genes | Prediction Measure*        |                          |                          |                          |
|-----------|-----------------|----------------------------|--------------------------|--------------------------|--------------------------|
|           |                 | Accuracy**                 | False Positive**         | False Negative**         | Geometric Mean**         |
| Combo All | 176             | <b>0.719</b> (0.571-0.793) | <b>0.258</b> (0.12-0.45) | <b>0.442</b> (0.167-0.8) | <b>0.61</b> (0.42-0.75)  |
| Combo 6   | 15              | <b>0.747</b> (0.567-0.8)   | <b>0.217</b> (0.08-0.48) | <b>0.489</b> (0.167-1.0) | <b>0.542</b> (0-0.8)     |
| Combo 5   | 16              | <b>0.536</b> (0.33-0.7)    | <b>0.473</b> (0.2-0.76)  | <b>0.469</b> (0.2-0.8)   | <b>0.48</b> (0.4-0.65)   |
| Combo 4   | 19              | <b>0.731</b> (0.607-0.875) | <b>0.224</b> (0.05-0.4)  | <b>0.525</b> (0.2-0.8)   | <b>0.584</b> (0.4-0.74)  |
| Combo 3   | 21              | <b>0.635</b> (0.33-0.83)   | <b>0.348</b> (0.04-0.68) | <b>0.514</b> (0.17-0.8)  | <b>0.514</b> (0.35-0.63) |
| Combo 2   | 38              | <b>0.607</b> (0.35-0.83)   | <b>0.358</b> (0.04-0.68) | <b>0.63</b> (0.4-1.0)    | <b>0.402</b> (0-0.6)     |
| Combo 1   | 67              | <b>0.588</b> (0.42-0.82)   | <b>0.406</b> (0.11-0.64) | <b>0.497</b> (0.2-0.8)   | <b>0.509</b> (0.39-0.63) |

Table 24 Distribution of Compounds\* in Individual Training  
and Test Sets for 72 Hour Kidney Data

Training and Test Set A

| Training Set A<br>Negative** | Training Set A<br>Positive | Test Set A<br>Negative | Test Set A<br>Positive |
|------------------------------|----------------------------|------------------------|------------------------|
| AMPB                         | CIS                        | ANIT                   | CHCL3                  |
| AZA                          | HYD                        | 5-FU                   | CPHOS                  |
| CAD                          | LPS                        | APAP                   | GAN                    |
| CHLOR                        | TET                        | BEN                    |                        |
| CLO                          |                            | BAP                    |                        |
| CYCA                         |                            | BRB                    |                        |
| DEX                          |                            | BUS                    |                        |
| DIF                          |                            | CCL4                   |                        |
| DOX                          |                            | CAR                    |                        |
| ERY                          |                            | CLOZ                   |                        |
| EST                          |                            | CMC                    |                        |
| ETH                          |                            | CHEX                   |                        |
| GEN                          |                            | DMN                    |                        |
| MET                          |                            | ISON                   |                        |
| PHEN                         |                            | KETO                   |                        |
| PUR                          |                            | NAL                    |                        |
| TAM                          |                            | PBARB                  |                        |
| TET                          |                            | PEG                    |                        |
|                              |                            | QUIN                   |                        |
|                              |                            | STRZ                   |                        |
|                              |                            | THEO                   |                        |

Training and Test Set 1

| Training Set 1 Negative | Training Set 1<br>Positive | Test Set 1 Negative | Test Set 1 Positive |
|-------------------------|----------------------------|---------------------|---------------------|
| AMPB                    | CPHOS                      | 5-FU                | CHCL3               |
| ANIT                    | GAN                        | APAP                | CIS                 |
| AZA                     | LPS                        | BEN                 | HYD                 |
| BAP                     | TET                        | BRB                 |                     |
| CAD                     |                            | BUS                 |                     |
| CAR                     |                            | CLOZ                |                     |
| CCL4                    |                            | CMC                 |                     |
| CHEX                    |                            | DIF                 |                     |
| CHLOR                   |                            | DMN                 |                     |
| CLO                     |                            | DOX                 |                     |
| CYCA                    |                            | ERY                 |                     |
| DEX                     |                            | ETH                 |                     |

|       |  |      |  |
|-------|--|------|--|
| EST   |  | NAL  |  |
| GEN   |  | PEG  |  |
| ISON  |  | PUR  |  |
| KETO  |  | STRZ |  |
| MET   |  | TAM  |  |
| PBARB |  |      |  |
| PHEN  |  |      |  |
| QUIN  |  |      |  |
| THEO  |  |      |  |

Training and Test Set 2

| Training Set 2<br>Negative | Training Set 2<br>Positive | Test Set 2<br>Negative | Test Set 2 Positive |
|----------------------------|----------------------------|------------------------|---------------------|
| AMPB                       | CHCL3                      | 5-FU                   | CPHOS               |
| APAP                       | CIS                        | ANIT                   | LPS                 |
| AZA                        | GAN                        | BRB                    | TET                 |
| BAP                        | HYD                        | CAD                    |                     |
| BEN                        |                            | CHEX                   |                     |
| BUS                        |                            | CHLOR                  |                     |
| CAR                        |                            | CLOZ                   |                     |
| CCL4                       |                            | CMC                    |                     |
| CLO                        |                            | DEX                    |                     |
| CYCA                       |                            | DMN                    |                     |
| DIF                        |                            | GEN                    |                     |
| DOX                        |                            | NAL                    |                     |
| ERY                        |                            | PUR                    |                     |
| EST                        |                            | QUIN                   |                     |
| ETH                        |                            | STRZ                   |                     |
| ISON                       |                            | TAM                    |                     |
| KETO                       |                            | THEO                   |                     |
| MET                        |                            |                        |                     |
| PBARB                      |                            |                        |                     |
| PEG                        |                            |                        |                     |
| PHEN                       |                            |                        |                     |

Training and Test Set 3

| Training Set 3<br>Negative | Training Set 3<br>Positive | Test Set 3<br>Negative | Test Set 3 Positive |
|----------------------------|----------------------------|------------------------|---------------------|
| ANIT                       | CHCL3                      | 5-FU                   | CPHOS               |
| APAP                       | CIS                        | AMPB                   | LPS                 |
| BEN                        | GAN                        | AZA                    | TET                 |
| BUS                        | HYD                        | BAP                    |                     |
| CAD                        |                            | BRB                    |                     |



|       |  |       |  |
|-------|--|-------|--|
| CAR   |  | CCL4  |  |
| CHLOR |  | CHEX  |  |
| CLO   |  | CYCA  |  |
| CLOZ  |  | DIF   |  |
| CMC   |  | DOX   |  |
| DEX   |  | ERY   |  |
| DMN   |  | GEN   |  |
| EST   |  | ISON  |  |
| ETH   |  | PBARB |  |
| KETO  |  | PHEN  |  |
| MET   |  | PUR   |  |
| NAL   |  | STRZ  |  |
| PEG   |  |       |  |
| QUIN  |  |       |  |
| TAM   |  |       |  |
| THEO  |  |       |  |

Training and Test Set 4

| Training Set 4<br>Negative | Training Set 4<br>Positive | Test Set 4<br>Negative | Test Set 4 Positive |
|----------------------------|----------------------------|------------------------|---------------------|
| 5-FU                       | CHCL3                      | AMPB                   | CPHOS               |
| APAP                       | CIS                        | ANIT                   | HYD                 |
| BEN                        | GAN                        | AZA                    | LPS                 |
| CAR                        | TET                        | BAP                    |                     |
| CHEX                       |                            | BRB                    |                     |
| CHLOR                      |                            | BUS                    |                     |
| CLO                        |                            | CAD                    |                     |
| CLOZ                       |                            | CCL4                   |                     |
| CMC                        |                            | DEX                    |                     |
| CYCA                       |                            | ERY                    |                     |
| DIF                        |                            | EST                    |                     |
| DMN                        |                            | ETH                    |                     |
| DOX                        |                            | KETO                   |                     |
| GEN                        |                            | PBARB                  |                     |
| ISON                       |                            | QUIN                   |                     |
| MET                        |                            | TAM                    |                     |
| NAL                        |                            | THEO                   |                     |
| PEG                        |                            |                        |                     |
| PHEN                       |                            |                        |                     |
| PUR                        |                            |                        |                     |
| STRZ                       |                            |                        |                     |

Training and Test Set 5

| Training Set 5<br>Negative | Training Set 5<br>Positive | Test Set 5<br>Negative | Test Set 5 Positive |
|----------------------------|----------------------------|------------------------|---------------------|
| AZA                        | CPHOS                      | 5-FU                   | CHCL3               |
| BAP                        | GAN                        | AMPB                   | CIS                 |
| BRB                        | HYD                        | ANIT                   | TET                 |
| BUS                        | LPS                        | APAP                   |                     |
| CAR                        |                            | BEN                    |                     |
| CHEX                       |                            | CAD                    |                     |
| CHLOR                      |                            | CCL4                   |                     |
| CLO                        |                            | CMC                    |                     |
| CLOZ                       |                            | DEX                    |                     |
| CYCA                       |                            | ERY                    |                     |
| DIF                        |                            | EST                    |                     |
| DMN                        |                            | ETH                    |                     |
| DOX                        |                            | GEN                    |                     |
| KETO                       |                            | ISON                   |                     |
| NAL                        |                            | MET                    |                     |
| PBARB                      |                            | QUIN                   |                     |
| PEG                        |                            | THEO                   |                     |
| PHEN                       |                            |                        |                     |
| PUR                        |                            |                        |                     |
| STRZ                       |                            |                        |                     |
| TAM                        |                            |                        |                     |

\* For abbreviations please see Table 1 (Compound, Dose, Abbreviation, etc.)

\*\* Negative= Compounds that did not elicit histopathology (score=1)

Positive= Compounds that did elicit histopathology (score of 2 or greater)

Table 25 List of Genes, Whose Expression at 72 h Directly Correlates with  
Kidney Tubular Necrosis at 72h, Ranked by Pearson Correlation Coefficient

| Gene   | Correlation Coefficient |
|--|-------------------------|
| Clusterin                                      | 0.6981305               |
| RCT-274  | 0.665856                |
| Gadd153  | 0.6007961               |
| Multidrug resistant protein-1                  | 0.5731272               |
| Alpha-tubulin                                  | 0.5714773               |
| Dynein light chain 1                           | 0.5593824               |
| Multidrug resistant protein-3                  | 0.5498183               |
| Beta-tubulin, class I                          | 0.5419734               |
| Tissue inhibitor of metalloproteinases-1       | 0.5197937               |
| CD44 metastasis suppressor gene                | 0.511474                |
| Thymosin beta-10                               | 0.5042843               |
| Calpactin I heavy chain                        | 0.4974941               |
| Alpha-fibrinogen                               | 0.4904063               |
| RCT-207  | 0.4767162               |
| RCT-127  | 0.4754919               |
| Uncoupling protein 2                           | 0.461348                |
| Beta-actin, sequence 2                         | 0.4559092               |
| MHC class I antigen RT1.A1(f) alpha-chain      | 0.4462703               |
| IgE binding protein                            | 0.444906                |
| Ceruloplasmin                                  | 0.4436448               |
| c-myc  | 0.442725                |
| RCT-24   | 0.4374066               |
| Insulin-like growth factor binding protein 1   | 0.4345538               |
| RCT-50   | 0.4314294               |
| Cyclin G                                       | 0.4260349               |
| RCT-12   | 0.419707                |
| RCT-59   | 0.4164921               |
| Zinc finger protein                            | 0.4164407               |
| Alpha-1 microglobulin/bikunin precursor (Ambp) | 0.4004037               |
| Complement component C3                        | 0.3995206               |
| RCT-49   | 0.3986999               |
| Liver fatty acid binding protein               | 0.3981068               |
| Monocyte chemotactic protein receptor (CCR2)   | 0.3974403               |
| RCT-240  | 0.3924163               |
| RCT-126  | 0.3918833               |

|  |           |
|--|-----------|
| RCT-241  | 0.3856618 |
| Integrin beta-4                                | 0.3792303 |
| RCT-267  | 0.3748433 |
| Emerin   | 0.3741759 |
| Glyceraldehyde 3-phosphate dehydrogenase       | 0.3684493 |
| Vascular cell adhesion molecule 1 (VCAM-1)     | 0.3678838 |
| Ribosomal protein L13A                         | 0.3664144 |
| Hypoxanthine-guanine phosphoribosyltransferase | 0.3659874 |
| Suppressor of cytokine signaling 3             | 0.3630873 |
| Activating transcription factor 3              | 0.3625623 |
| Major acute phase protein alpha-1              | 0.3620322 |
| Major basic protein 1                          | 0.3614528 |
| RCT-258  | 0.3607649 |
| RCT-293  | 0.3592598 |
| RCT-138  | 0.3578431 |
| Alanine aminotransferase                       | 0.3506821 |

Table 26 List of Genes, Whose Expression at 72 h Inversely Correlates with Kidney Tubular Necrosis at 72h, Ranked by Spearman Correlation Coefficient

| Gene                                     | Correlation Coefficient |
|--|-------------------------|
| RCT-42                                   | -0.25083                |
| Membrane bound cytochrome b5             | -0.25275                |
| RCT-132                                  | -0.25352                |
| RCT-99                                   | -0.25374                |
| Four repeat ion channel                  | -0.25412                |
| RCT-62                                   | -0.25524                |
| RCT-137                                  | -0.25548                |
| AT-1                                     | -0.25881                |
| UDP-glucuronosyltransferase 2B           | -0.26029                |
| RCT-214                                  | -0.26618                |
| Methylacyl-CoA racemase alpha            | -0.26791                |
| Cyclin D1                                | -0.27006                |
| Organic anion transporting polypeptide 1 | -0.27038                |
| Cystatin C                               | -0.27304                |
| Matrin F/G                               | -0.27305                |
| RCT-181                                  | -0.27455                |
| RCT-25                                   | -0.27625                |
| RCT-143                                  | -0.27626                |
| RCT-93                                   | -0.28389                |
| Protein tyrosine phosphatase alpha       | -0.28421                |
| RCT-79                                   | -0.28485                |
| Caspase 2                                | -0.28686                |
| Vascular endothelial growth factor       | -0.28716                |
| Glutathione S-transferase Ya             | -0.28785                |
| Senescence marker protein-30             | -0.29192                |
| RCT-178                                  | -0.29272                |
| Organic anion transporter K1             | -0.29329                |
| RCT-256                                  | -0.2943                 |
| 25-DX                                    | -0.29444                |
| RCT-22                                   | -0.29564                |
| Sarcoplasmic reticulum calcium ATPase    | -0.2974                 |
| RCT-280                                  | -0.29749                |
| RCT-148                                  | -0.30758                |
| Arginosuccinate synthetase 1             | -0.30894                |
| RCT-142                                  | -0.31028                |
| RCT-260                                  | -0.31039                |
| Apoptosis-regulating basic protein       | -0.31798                |
| Organic anion transporter 3              | -0.32302                |

|  |          |
|--|----------|
| Ornithine aminotransferase   | -0.32748 |
| Hemoglobin alpha 1 chain (alternate clone)                                 | -0.33449 |
| Cytochrome P450 2A3  | -0.33951 |
| Hemoglobin alpha 1 chain   | -0.34347 |
| Selenoprotein P  | -0.34685 |
| Cytochrome P450 2C23   | -0.34696 |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II)                   | -0.34712 |
| RCT-38   | -0.34982 |
| Iron-responsive element-binding protein                                    | -0.3572  |
| RCT-10   | -0.36278 |
| Epidermal growth factor  | -0.36487 |
| Sodium/glucose cotransporter 1   | -0.36594 |
| RCT-212  | -0.36604 |
| Cytochrome c oxidase subunit II  | -0.36678 |
| RCT-89   | -0.37036 |
| Acyl-CoA dehydrogenase, medium chain                                       | -0.37526 |
| RCT-39   | -0.37793 |
| RCT-34   | -0.37992 |
| Malate dehydrogenase, cytosolic  | -0.38206 |
| D-dopachrome tautomerase   | -0.38497 |
| RCT-87   | -0.3857  |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II) (alternate clone) | -0.40004 |
| RCT-101  | -0.40144 |
| RCT-69   | -0.40543 |
| Thiopurine methyltransferase   | -0.41035 |
| Very long-chain acyl-CoA synthetase  | -0.41248 |
| Fatty acyl-CoA oxidase   | -0.42391 |
| RCT-287  | -0.4351  |
| Dimethylarginine dimethylaminohydrolase                                    | -0.4413  |
| RCT-182  | -0.44238 |
| RCT-291  | -0.4606  |
| 3-hydroxyisobutyrate dehydrogenase   | -0.48712 |

Table 27 List of genes whose expression at 72 hours is predictive of kidney toxicity at 72 hours

| Gene   | Combinations<br>(No of<br>Occurrences) |
|--|--|
| Alanine aminotransferase                       | 6                                      |
| Alpha-tubulin                                  | 6                                      |
| Beta-actin, sequence 2                         | 6                                      |
| Beta-tubulin, class I                          | 6                                      |
| Gadd153  | 6                                      |
| Glyceraldehyde 3-phosphate dehydrogenase       | 6                                      |
| Insulin-like growth factor binding protein 1   | 6                                      |
| Integrin beta-4                                | 6                                      |
| Major basic protein 1                          | 6                                      |
| MHC class I antigen RT1.A1(f) alpha-chain      | 6                                      |
| Monocyte chemotactic protein receptor (CCR2)   | 6                                      |
| Multidrug resistant protein-3                  | 6                                      |
| RCT-211  | 6                                      |
| RCT-24   | 6                                      |
| RCT-240  | 6                                      |
| RCT-274  | 6                                      |
| Alpha-fibrinogen                               | 5                                      |
| Calpactin I heavy chain                        | 5                                      |
| CD44 metastasis suppressor gene                | 5                                      |
| Ceruloplasmin                                  | 5                                      |
| c-myc  | 5                                      |
| Dynein light chain 1                           | 5                                      |
| Emerin   | 5                                      |
| Hypoxanthine-guanine phosphoribosyltransferase | 5                                      |
| IgE binding protein                            | 5                                      |
| Liver fatty acid binding protein               | 5                                      |
| Major acute phase protein alpha-1              | 5                                      |
| Multidrug resistant protein-1                  | 5                                      |
| RCT-12   | 5                                      |
| RCT-127  | 5                                      |
| RCT-182  | 5                                      |
| RCT-293  | 5                                      |
| RCT-49   | 5                                      |
| RCT-50   | 5                                      |
| RCT-59   | 5                                      |
| Ribosomal protein L13A                         | 5                                      |
| Suppressor of cytokine signaling 3             | 5                                      |
| Thymosin beta-10                               | 5                                      |

|  |   |
|--|---|
| Tissue inhibitor of metalloproteinases-1                                   | 5 |
| Uncoupling protein 2   | 5 |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II) (alternate clone) | 4 |
| 14-3-3 zeta  | 4 |
| Activating transcription factor 3  | 4 |
| Alpha-1 microglobulin/bikunin precursor (Ambp)                             | 4 |
| Clusterin  | 4 |
| Complement component C3  | 4 |
| Cyclin dependent kinase 4  | 4 |
| Fatty acyl-CoA oxidase   | 4 |
| Gadd45   | 4 |
| Na/K ATPase alpha-1  | 4 |
| Notch 1  | 4 |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II)                   | 4 |
| RCT-126  | 4 |
| RCT-138  | 4 |
| RCT-207  | 4 |
| RCT-241  | 4 |
| RCT-267  | 4 |
| RCT-68   | 4 |
| Stathmin   | 4 |
| Superoxide dismutase Mn  | 4 |
| Thrombomodulin   | 4 |
| Vascular cell adhesion molecule 1 (VCAM-1)                                 | 4 |
| Zinc finger protein  | 4 |
| 25-hydroxyvitamin D3-1 alpha-hydroxylase                                   | 3 |
| 3-hydroxyisobutyrate dehydrogenase   | 3 |
| 3-methyladenine DNA glycosylase  | 3 |
| Annexin V  | 3 |
| Bax (alpha)  | 3 |
| Carbonyl reductase   | 3 |
| Caspase 2  | 3 |
| c-jun  | 3 |
| Cyclin G   | 3 |
| Cytochrome P450 2C23   | 3 |
| D-dopachrome tautomerase   | 3 |
| Dimethylarginine dimethylaminohydrolase                                    | 3 |
| DNA binding protein inhibitor ID2  | 3 |
| Ecto-ATPase  | 3 |
| Epidermal growth factor  | 3 |
| Interleukin-10   | 3 |
| Macrophage inflammatory protein-2 alpha                                    | 3 |
| NADPH cytochrome P450 oxidoreductase                                       | 3 |



|                                     |   |
|-------------------------------------|---|
| RCT-101                             | 3 |
| RCT-109                             | 3 |
| RCT-146                             | 3 |
| RCT-155                             | 3 |
| RCT-192                             | 3 |
| RCT-212                             | 3 |
| RCT-258                             | 3 |
| RCT-287                             | 3 |
| RCT-291                             | 3 |
| RCT-296                             | 3 |
| RCT-87                              | 3 |
| Preproalbumin                       | 3 |
| RAD                                 | 3 |
| Thioredoxin-2 (Trx2)                | 3 |
| Very long-chain acyl-CoA synthetase | 3 |
| 25-DX                               | 2 |
| Activin receptor type II            | 2 |
| Aldehyde dehydrogenase, microsomal  | 2 |
| Cathepsin L, sequence 2             | 2 |
| Cathepsin S                         | 2 |
| CCR-5                               | 2 |
| CXCR4                               | 2 |
| Cyclin D1                           | 2 |
| Cyclin dependent kinase 2           | 2 |
| Cyclooxygenase 2                    | 2 |
| Cytochrome c oxidase subunit II     | 2 |
| Cytochrome P450 1A1                 | 2 |
| Diacylglycerol kinase zeta          | 2 |
| E-selectin                          | 2 |
| Glucose-6-phosphate dehydrogenase   | 2 |
| ID-1                                | 2 |
| Malate dehydrogenase, cytosolic     | 2 |
| Monoamine oxidase B                 | 2 |
| Myelin basic protein                | 2 |
| Organic anion transporter K1        | 2 |
| RCT-10                              | 2 |
| RCT-141                             | 2 |
| RCT-145                             | 2 |
| RCT-215                             | 2 |
| RCT-237                             | 2 |
| RCT-271                             | 2 |
| RCT-34                              | 2 |
| RCT-39                              | 2 |
| RCT-6                               | 2 |
| RCT-66                              | 2 |

|   |   |
|---|---|
| RCT-69  | 2 |
| RCT-89  | 2 |
| RCT-92  | 2 |
| Phosphatidylethanolamine-binding protein                            | 2 |
| Prostaglandin H synthase  | 2 |
| Selenoprotein P   | 2 |
| Senescence marker protein-30  | 2 |
| Sodium/glucose cotransporter 1                                      | 2 |
| Thiol-specific antioxidant (natural killer cell-enhancing factor B) | 2 |
| Thiopurine methyltransferase  | 2 |
| Tissue factor   | 2 |
| RCT-171   | 1 |
| Hemoglobin alpha 1 chain (alternate clone)                          | 1 |
| 3-beta-hydroxysteroid dehydrogenase (HSD3B1)                        | 1 |
| 60S ribosomal protein L6  | 1 |
| Acyl-CoA dehydrogenase, medium chain                                | 1 |
| ADP-ribosylation factor-like protein ARL184                         | 1 |
| Aldehyde dehydrogenase 2  | 1 |
| Aryl hydrocarbon receptor   | 1 |
| Aspartoacylase  | 1 |
| Calcineurin-B   | 1 |
| Calreticulin  | 1 |
| Carbonic anhydrase III, sequence 2                                  | 1 |
| Cathepsin L   | 1 |
| Cellular nucleic acid binding protein (CNBP)                        | 1 |
| c-H-ras   | 1 |
| Connexin-32   | 1 |
| Cystatin C  | 1 |
| Cytochrome P450 1B1   | 1 |
| Cytochrome P450 2B1/2B2   | 1 |
| Cytochrome P450 2C11  | 1 |
| DNA topoisomerase I   | 1 |
| Ferritin H-chain  | 1 |
| Gamma-glutamyl transpeptidase                                       | 1 |
| Glutathione S-transferase mu-2                                      | 1 |
| Glycine methyltransferase   | 1 |
| Heme oxygenase  | 1 |
| Hemoglobin alpha 1 chain  | 1 |
| Hepatocyte nuclear factor 4   | 1 |
| Interferon related developmental regulator IFRD1 (PC4)              | 1 |
| Interleukin-1 beta  | 1 |
| Interleukin-18  | 1 |
| Iron-responsive element-binding protein                             | 1 |

|  |   |
|--|---|
| Matrix metalloproteinase-1                               | 1 |
| Methylacyl-CoA racemase alpha                            | 1 |
| Monoamine oxidase A                                      | 1 |
| Mxl protein  | 1 |
| Na/H antiporter (APNH1)                                  | 1 |
| N-cadherin   | 1 |
| N-hydroxy-2-acetylaminofluorene sulfotransferase (ST1C1) | 1 |
| Organic anion transporter 3                              | 1 |
| Organic anion transporting polypeptide 1                 | 1 |
| Ornithine aminotransferase                               | 1 |
| Osteopontin  | 1 |
| RCT-165  | 1 |
| RCT-128  | 1 |
| Apoptosis-regulating basic protein                       | 1 |
| RCT-137  | 1 |
| RCT-143  | 1 |
| RCT-148  | 1 |
| RCT-149  | 1 |
| RCT-161  | 1 |
| RCT-166  | 1 |
| RCT-179  | 1 |
| RCT-180  | 1 |
| RCT-181  | 1 |
| RCT-193  | 1 |
| RCT-197  | 1 |
| Vacuole membrane protein 1                               | 1 |
| RCT-22   | 1 |
| RCT-228  | 1 |
| RCT-242  | 1 |
| RCT-244  | 1 |
| RCT-26   | 1 |
| RCT-260  | 1 |
| RCT-264  | 1 |
| RCT-280  | 1 |
| RCT-284  | 1 |
| RCT-288  | 1 |
| RCT-295  | 1 |
| RCT-38   | 1 |
| RCT-45   | 1 |
| RCT-62   | 1 |
| RCT-64   | 1 |
| RCT-99   | 1 |
| Poly(ADP-ribose) polymerase                              | 1 |
| Protein tyrosine phosphatase alpha                       | 1 |

|  |   |
|--|---|
| Pyruvate kinase, muscle                  | 1 |
| Ribosomal protein S8                     | 1 |
| Ribosomal protein S9                     | 1 |
| Sarcoplasmic reticulum calcium ATPase    | 1 |
| Thioredoxin-1 (Trx1)                     | 1 |
| Tryptophan hydroxylase                   | 1 |
| UDP-glucuronosyltransferase              | 1 |
| Urokinase plasminogen activator receptor | 1 |
| Vascular endothelial growth factor       | 1 |

\* Combination category is the number of training/test set gene list occurrences.

Table 28 Kidney Toxicity Compound-Dose Prediction Values for 72 Hour Data  
Predictive Genes (Combined List and Subsets)

| Gene Set  | Number of Genes | Accuracy**          | Prediction Measure* |                    | Geometric Mean**      |
|-----------|-----------------|---------------------|---------------------|--------------------|-----------------------|
|           |                 |                     | False Positive**    | False Negative**   |                       |
| Combo All | 225             | 0.882 (0.643-0.974) | 0.086 (0-0.364)     | 0.361 (0.167-0.75) | 0.747 (0.500 - 0.913) |
| Combo 6   | 16              | 0.808 (0.607-0.902) | 0.166 (0-0.455)     | 0.444 (0.167-1.0)  | 0.601 (0-0.869)       |
| Combo 5   | 27              | 0.742 (0.429-0.921) | 0.228 (0.026-0.591) | 0.486 (0.333-0.75) | 0.616 (0.452-0.803)   |
| Combo 4   | 23              | 0.828 (0.5-0.917)   | 0.138 (0-0.545)     | 0.486 (0.25-1.0)   | 0.607 (0-0.839)       |
| Combo 3   | 33              | 0.705 (0.357-0.902) | 0.226 (0.027-0.591) | 0.722 (0.5-1.0)    | 0.414 (0-0.649)       |
| Combo 2   | 41              | 0.661 (0.357-0.868) | 0.288 (0.031-0.591) | 0.681 (0.333-1.0)  | 0.412 (0-0.690)       |
| Combo 1   | 90              | 0.783 (0.536-0.941) | 0.179 (0.027-0.455) | 0.500 (0.167-1.0)  | 0.572 (0-0.896)       |

\* Prediction measures are given as means and range of values (in parentheses) for six training/test sets using 72 hour array data and gene lists. Unit of prediction was the animal and the predictive classification was for kidney tubular necrosis observed at 72 hours after treatment.

\*\* Standard prediction measures were used as defined in Materials and Methods. As described in Materials and Methods In these analyses cases where no prediction was made because the p-value ratio exceeded the cutoff-value (generally 0.5) the non-call was considered to be incorrect.

Table 29 Predictive Performance of Various Models

|   | Model Performance using 6 Sets |              |          |          |          |          |          |
|---|--------------------------------|--------------|----------|----------|----------|----------|----------|
|   |                                |              |          |          |          |          |          |
| Models  |                                | Testing Sets |          |          |          |          |          |
|   | Set 1                          | Set A        | Set 3    | Set 2    | Set 5    | Set 4    | Mean     |
| KNN (Log Trans)   | 0.92489                        | 0.878164     | 0.86155  | 0.850047 | 0.952774 | 0.739369 | 0.867799 |
| Logistic  | 0.828702                       | 0.60604      | 0.851969 | 0.803219 | 0.74162  | 0.802773 | 0.772387 |
| Centroid  | 0.863092                       | 0.892898     | 0.61051  | 0.596941 | 0.849274 | 0.762296 | 0.762502 |
| Nnet (Log Trans)  | 0.831605                       | 0.83795      | 0.676123 | 0.722401 | 0.703167 | 0.663883 | 0.739188 |
| Logistic (Log Trans)  | 0.826518                       | 0.603062     | 0.847566 | 0.753487 | 0.625389 | 0.551093 | 0.701186 |
| Tree  | 0.537733                       | 0.879581     | 0.921401 | 0.794245 | 0.544671 | 0.516398 | 0.699005 |
| Nnet  | 0.769916                       | 0.83395      | 0.565445 | 0.714419 | 0.667083 | 0.607362 | 0.693029 |
| Mean  | 0.797494                       | 0.790235     | 0.76208  | 0.747823 | 0.726283 | 0.663311 |          |
| Performance Measure = Geometric Mean of the True Positives and True Negatives |                                |              |          |          |          |          |          |
| Best Performance in Bold  |                                |              |          |          |          |          |          |
| Centroid values are averaged over 5 runs                                      |                                |              |          |          |          |          |          |

Table 30 Logistic Discrimination Coefficients

|                         | Absolute Value of Coefficient | Coefficient |
|-------------------------|-------------------------------|-------------|
| PAR interacting protein | 3948.7722                     | 3948.7722   |
| RCT-145                 | 1756.2178                     | -1756.2178  |
| Gadd153                 | 1502.4772                     | 1502.4772   |
| Ribosomal protein L13A  | 1497.8289                     | -1497.8289  |
| Alpha tubulin           | 1060.1632                     | 1060.1632   |
| Cathepsin L sequence 2  | 821.1935                      | 821.1935    |
| RCT 271                 | 564.5671                      | -564.5671   |
| c-myc                   | 514.0376                      | -514.0376   |
| Uncoupling protein 2    | 483.928                       | 483.928     |

Table 31 Prediction of Kidney Toxicity for Samples External to Database

| Predicting Gene Set* | Treatment                          | Animal | Prediction | P-Value Ratio | Prediction Values**<br>No Votes | No P-Value | Yes Votes | Yes P Value |
|----------------------|------------------------------------|--------|------------|---------------|---------------------------------|------------|-----------|-------------|
| Combo 6              | Cephaloridine 1500 mg/kg i.p. 24 h | 501    | yes        | 0.000         | 0                               | 1          | 10        | 0           |
| Combo 6              | Cephaloridine 1500 mg/kg i.p. 24 h | 506    | yes        | 0.000         | 0                               | 1          | 10        | 0           |
| Combo 6              | Cephaloridine 1500 mg/kg i.p. 24 h | 508    | yes        | 0.000         | 0                               | 1          | 10        | 0           |
| Combo 6              | Cisplatin 20 mg/kg i.p. 24 h       | 602    | yes        | 0.000         | 2                               | 1          | 8         | 0           |
| Combo 6              | Cisplatin 20 mg/kg i.p. 24 h       | 603    | yes        | 0.000         | 0                               | 1          | 10        | 0           |
| Combo 6              | Cisplatin 20 mg/kg i.p. 24 h       | 604    | yes        | 0.000         | 0                               | 1          | 10        | 0           |
| Combo 5              | Cephaloridine 1500 mg/kg i.p. 24 h | 501    | yes        | 0.001         | 4                               | 1          | 6         | 0.001       |
| Combo 5              | Cephaloridine 1500 mg/kg i.p. 24 h | 506    | yes        | 0.000         | 1                               | 1          | 9         | 0           |
| Combo 5              | Cephaloridine 1500 mg/kg i.p. 24 h | 508    | yes        | 0.000         | 2                               | 1          | 8         | 0           |
| Combo 5              | Cisplatin 20 mg/kg i.p. 24 h       | 602    | yes        | 0.208         | 7                               | 0.945      | 3         | 0.197       |
| Combo 5              | Cisplatin 20 mg/kg i.p. 24 h       | 603    | yes        | 0.208         | 7                               | 0.945      | 3         | 0.197       |
| Combo 5              | Cisplatin 20 mg/kg i.p. 24 h       | 604    | yes        | 0.001         | 4                               | 1          | 6         | 0.001       |
| Combo 4              | Cephaloridine 1500 mg/kg i.p. 24 h | 501    | yes        | 0.000         | 1                               | 1          | 9         | 0           |
| Combo 4              | Cephaloridine 1500 mg/kg i.p. 24 h | 506    | yes        | 0.000         | 2                               | 1          | 8         | 0           |
| Combo 4              | Cephaloridine 1500 mg/kg i.p. 24 h | 508    | yes        | 0.000         | 0                               | 1          | 10        | 0           |
| Combo 4              | Cisplatin 20 mg/kg i.p. 24 h       | 602    | yes        | 0.010         | 5                               | 0.999      | 5         | 0.01        |
| Combo 4              | Cisplatin 20 mg/kg i.p. 24 h       | 603    | yes        | 0.000         | 1                               | 1          | 9         | 0           |
| Combo 4              | Cisplatin 20 mg/kg i.p. 24 h       | 604    | yes        | 0.000         | 1                               | 1          | 9         | 0           |
| Combo 3              | Cephaloridine 1500 mg/kg i.p. 24 h | 501    | yes        | 0.001         | 4                               | 1          | 6         | 0.001       |
| Combo 3              | Cephaloridine 1500 mg/kg i.p. 24 h | 506    | yes        | 0.208         | 7                               | 0.945      | 3         | 0.197       |
| Combo 3              | Cephaloridine 1500 mg/kg i.p. 24 h | 508    |            | 0.606         | 8                               | 0.803      | 2         | 0.487       |
| Combo 3              | Cisplatin 20 mg/kg i.p. 24 h       | 602    | yes        | 0.208         | 7                               | 0.945      | 3         | 0.197       |
| Combo 3              | Cisplatin 20 mg/kg i.p. 24 h       | 603    | yes        | 0.001         | 4                               | 1          | 6         | 0.001       |
| Combo 3              | Cisplatin 20 mg/kg i.p. 24 h       | 604    | yes        | 0.055         | 6                               | 0.99       | 4         | 0.055       |
| Combo 2              | Cephaloridine 1500 mg/kg i.p.      | 501    | yes        | 0.000         | 3                               | 1          | 7         | 0           |



|         |                                       |     |     |       |   |       |   |       |
|---------|---------------------------------------|-----|-----|-------|---|-------|---|-------|
|         | 24 h                                  |     |     |       |   |       |   |       |
| Combo 2 | Cephaloridine 1500 mg/kg i.p.<br>24 h | 506 | yes | 0.000 | 3 | 1     | 7 | 0     |
| Combo 2 | Cephaloridine 1500 mg/kg i.p.<br>24 h | 508 | yes | 0.000 | 3 | 1     | 7 | 0     |
| Combo 2 | Cisplatin 20 mg/kg i.p. 24 h          | 602 | yes | 0.010 | 5 | 0.999 | 5 | 0.01  |
| Combo 2 | Cisplatin 20 mg/kg i.p. 24 h          | 603 | yes | 0.000 | 3 | 1     | 7 | 0     |
| Combo 2 | Cisplatin 20 mg/kg i.p. 24 h          | 604 | yes | 0.000 | 2 | 1     | 8 | 0     |
|         |                                       |     |     |       |   |       |   |       |
| Combo 1 | Cephaloridine 1500 mg/kg i.p.<br>24 h | 501 | yes | 0.000 | 1 | 1     | 9 | 0     |
| Combo 1 | Cephaloridine 1500 mg/kg i.p.<br>24 h | 506 | yes | 0.000 | 1 | 1     | 9 | 0     |
| Combo 1 | Cephaloridine 1500 mg/kg i.p.<br>24 h | 508 | yes | 0.000 | 3 | 1     | 7 | 0     |
| Combo 1 | Cisplatin 20 mg/kg i.p. 24 h          | 602 | yes | 0.001 | 4 | 1     | 6 | 0.001 |
| Combo 1 | Cisplatin 20 mg/kg i.p. 24 h          | 603 | yes | 0.000 | 3 | 1     | 7 | 0     |
| Combo 1 | Cisplatin 20 mg/kg i.p. 24 h          | 604 | yes | 0.000 | 3 | 1     | 7 | 0     |

\* All genes used for Combo Gene Lists.

\*\* Prediction values are output from prediction program. Values include prediction (yes=kidney toxicity predicted, no=no kidney toxicity predicted), numbers of yes and no votes from 10 nearest neighbors, the p-value for the no and yes votes and the p-value ratio for the predicted class over the not predicted class. A p-value ratio cutoff of 0.5 was used

Table 33 Kidney Predictive Genes (376 genes)  
Organized by Time Point and Combo Category\*

| Gene   | 6h        | 24h       | 72h       |
|--|-----------|-----------|-----------|
| 60S ribosomal protein L6 (alternate clone 1)                               | Combo 1   | Combo 6   | Not Found |
| RCT-171  | Not Found | Not Found | Combo 1   |
| Preproalbumin, sequence 2 (alternate clone 1)                              | Not Found | Combo 4   | Not Found |
| Hemoglobin alpha 1 chain (alternate clone)                                 | Combo 1   | Not Found | Combo 1   |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II) (alternate clone) | Not Found | Combo 3   | Combo 4   |
| I4-3-3 zeta  | Combo 5   | Combo 1   | Combo 4   |
| RCT-139  | Combo 3   | Not Found | Not Found |
| 25-DX  | Not Found | Not Found | Combo 2   |
| 25-hydroxyvitamin D3-1 alpha-hydroxylase                                   | Not Found | Not Found | Combo 3   |
| 3-beta-hydroxysteroid dehydrogenase (HSD3B1)                               | Not Found | Not Found | Combo 1   |
| 3-hydroxyisobutyrate dehydrogenase   | Not Found | Not Found | Combo 3   |
| 3-methyladenine DNA glycosylase  | Not Found | Not Found | Combo 3   |
| 60S ribosomal protein L6   | Not Found | Combo 5   | Combo 1   |
| Acetylcholine receptor epsilon   | Combo 1   | Not Found | Not Found |
| Activating transcription factor 3  | Not Found | Not Found | Combo 4   |
| Activin receptor type II   | Not Found | Combo 2   | Combo 2   |
| Acyl-CoA dehydrogenase, medium chain                                       | Not Found | Combo 1   | Combo 1   |
| ADP-ribosylation factor-like protein ARL184                                | Combo 5   | Not Found | Combo 1   |
| Adrenodoxin reductase  | Not Found | Combo 1   | Not Found |
| Alanine aminotransferase   | Not Found | Not Found | Combo 6   |
| Alcohol dehydrogenase 1  | Not Found | Combo 1   | Not Found |
| Aldehyde dehydrogenase 1   | Combo 1   | Not Found | Not Found |
| Aldehyde dehydrogenase 2   | Combo 5   | Not Found | Combo 1   |
| Aldehyde dehydrogenase, microsomal   | Not Found | Not Found | Combo 2   |
| Alpha-1 acid glycoprotein  | Combo 1   | Not Found | Not Found |
| Alpha-1 microglobulin/bikunin precursor (Ambp)                             | Combo 2   | Not Found | Combo 4   |
| alpha-1,2-fucosyltransferase   | Combo 4   | Not Found | Not Found |
| Alpha-2-macroglobulin  | Not Found | Combo 1   | Not Found |
| Alpha-fibrinogen   | Combo 1   | Combo 5   | Combo 5   |
| Alpha-tubulin  | Combo 6   | Combo 6   | Combo 6   |
| Annexin V  | Not Found | Combo 3   | Combo 3   |
| Apolipoprotein CIII  | Combo 1   | Not Found | Not Found |
| Aquaporin-3 (AQP3)   | Combo 4   | Not Found | Not Found |
| Argininosuccinate lyase  | Combo 1   | Not Found | Not Found |
| Argininosuccinate synthetase 1   | Not Found | Combo 1   | Not Found |
| Aryl hydrocarbon receptor  | Not Found | Not Found | Combo 1   |
| Aspartoacylase   | Combo 2   | Combo 3   | Combo 1   |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk)        | Combo 1   | Combo 4   | Not Found |
| Bax (alpha)  | Not Found | Not Found | Combo 3   |
| Bcl-2  | Combo 3   | Combo 1   | Not Found |
| Beta-actin, sequence 2   | Not Found | Combo 5   | Combo 6   |
| Beta-tubulin, class I  | Combo 5   | Combo 5   | Combo 6   |

|   |           |           |           |
|---|-----------|-----------|-----------|
| Calbindin-D (9K)                                    | Combo 1   | Not Found | Not Found |
| Calcineurin-B                                       | Not Found | Not Found | Combo 1   |
| Calnexin  | Not Found | Combo 1   | Not Found |
| Calpactin I heavy chain                             | Combo 3   | Combo 6   | Combo 5   |
| Calreticulin  | Combo 6   | Combo 3   | Combo 1   |
| Canalicular multispecific organic anion transporter | Not Found | Combo 5   | Not Found |
| Carbamyl phosphate synthetase I                     | Combo 1   | Not Found | Not Found |
| Carbonic anhydrase III, sequence 2                  | Not Found | Combo 5   | Combo 1   |
| Carbonyl reductase                                  | Not Found | Combo 1   | Combo 3   |
| Casein-alpha  | Not Found | Combo 2   | Not Found |
| Caspase 2   | Not Found | Not Found | Combo 3   |
| Caspase 7   | Combo 1   | Not Found | Not Found |
| Cathepsin L   | Combo 6   | Combo 6   | Combo 1   |
| Cathepsin L, sequence 2                             | Combo 4   | Combo 6   | Combo 2   |
| Cathepsin S   | Not Found | Combo 3   | Combo 2   |
| CCR-5   | Not Found | Not Found | Combo 2   |
| CD44 metastasis suppressor gene                     | Combo 1   | Combo 4   | Combo 5   |
| CDK102  | Not Found | Combo 2   | Not Found |
| CDK108  | Not Found | Combo 6   | Not Found |
| Cellular nucleic acid binding protein (CNBP)        | Not Found | Combo 2   | Combo 1   |
| Ceruloplasmin                                       | Not Found | Combo 4   | Combo 5   |
| c-fos   | Combo 3   | Not Found | Not Found |
| Cholesterol 7-alpha-hydroxylase (P450 VII)          | Combo 1   | Not Found | Not Found |
| Cholesterol esterase                                | Not Found | Combo 1   | Not Found |
| c-H-ras   | Combo 6   | Not Found | Combo 1   |
| c-jun   | Combo 1   | Not Found | Combo 3   |
| Clusterin   | Not Found | Combo 6   | Combo 4   |
| c-myc   | Combo 1   | Combo 6   | Combo 5   |
| Colony-stimulating factor-1                         | Combo 2   | Not Found | Not Found |
| Complement component C3                             | Not Found | Combo 2   | Combo 4   |
| Connexin-32   | Combo 3   | Combo 4   | Combo 1   |
| CXCR4   | Not Found | Not Found | Combo 2   |
| Cyclin D1   | Not Found | Not Found | Combo 2   |
| Cyclin dependent kinase 2                           | Not Found | Not Found | Combo 2   |
| Cyclin dependent kinase 4                           | Combo 1   | Not Found | Combo 4   |
| Cyclin E  | Combo 6   | Not Found | Not Found |
| Cyclin G  | Not Found | Not Found | Combo 3   |
| Cyclooxygenase 2                                    | Not Found | Not Found | Combo 2   |
| Cystatin C  | Not Found | Not Found | Combo 1   |
| Cytochrome c oxidase subunit II                     | Not Found | Not Found | Combo 2   |
| Cytochrome c oxidase subunit IV                     | Combo 1   | Not Found | Not Found |
| Cytochrome P450 14DM                                | Not Found | Combo 1   | Not Found |
| Cytochrome P450 1A1                                 | Combo 3   | Not Found | Combo 2   |
| Cytochrome P450 1B1                                 | Not Found | Not Found | Combo 1   |
| Cytochrome P450 2A3                                 | Not Found | Combo 1   | Not Found |
| Cytochrome P450 2B1/2B2                             | Not Found | Not Found | Combo 1   |
| Cytochrome P450 2C11                                | Combo 1   | Combo 1   | Combo 1   |
| Cytochrome P450 2C23                                | Not Found | Combo 1   | Combo 3   |

|   |           |           |           |
|---|-----------|-----------|-----------|
| D-dopachrome tautomerase  | Not Found | Not Found | Combo 3   |
| Decorin   | Combo 5   | Not Found | Not Found |
| Defender against cell death-1   | Not Found | Combo 2   | Not Found |
| Diacylglycerol kinase zeta  | Not Found | Not Found | Combo 2   |
| Dimethylarginine dimethylaminohydrolase                               | Not Found | Combo 3   | Combo 3   |
| DNA binding protein inhibitor ID2                                     | Not Found | Combo 1   | Combo 3   |
| DNA topoisomerase I   | Combo 1   | Combo 2   | Combo 1   |
| Dynein light chain 1  | Combo 1   | Combo 6   | Combo 5   |
| Ecto-ATPase   | Combo 3   | Combo 3   | Combo 3   |
| eIF-4E  | Not Found | Combo 1   | Not Found |
| Elongation factor-1 alpha   | Not Found | Combo 2   | Not Found |
| Emerin  | Not Found | Not Found | Combo 5   |
| Endogenous retroviral sequence, 5' and 3' LTR                         | Combo 4   | Not Found | Not Found |
| Epidermal growth factor   | Combo 5   | Combo 4   | Combo 3   |
| Equilibrative nitrobenzylthioinosine-sensitive nucleoside transporter | Combo 2   | Combo 1   | Not Found |
| E-selectin  | Not Found | Not Found | Combo 2   |
| Fatty acyl-CoA oxidase  | Not Found | Combo 2   | Combo 4   |
| Ferritin H-chain  | Combo 2   | Combo 4   | Combo 1   |
| Fetuin beta (Fetub)   | Not Found | Combo 2   | Not Found |
| Fibrinogen gamma chain  | Not Found | Combo 1   | Not Found |
| Focal adhesion kinase (pp125FAK)                                      | Combo 1   | Not Found | Not Found |
| Gadd153   | Combo 6   | Combo 6   | Combo 6   |
| Gadd45  | Combo 6   | Combo 6   | Combo 4   |
| Gamma-actin, cytoplasmic  | Combo 1   | Not Found | Not Found |
| Gamma-glutamyl transpeptidase   | Combo 5   | Combo 1   | Combo 1   |
| Glucose transporter 1   | Not Found | Combo 2   | Not Found |
| Glucose-Combo 6-phosphate dehydrogenase                               | Not Found | Combo 1   | Combo 2   |
| Glucose-regulated protein 78  | Not Found | Combo 1   | Not Found |
| Glutathione S-transferase Yb2 subunit                                 | Combo 2   | Not Found | Combo 1   |
| Glyceraldehyde 3-phosphate dehydrogenase                              | Combo 6   | Not Found | Combo 6   |
| Glycine methyltransferase   | Not Found | Combo 2   | Combo 1   |
| Heme binding protein 23   | Combo 5   | Combo 5   | Not Found |
| Heme oxygenase  | Combo 3   | Combo 1   | Combo 1   |
| Hemoglobin alpha 1 chain  | Combo 1   | Not Found | Combo 1   |
| Hepatocyte growth factor receptor                                     | Combo 3   | Not Found | Not Found |
| Hepatocyte nuclear factor 4   | Combo 1   | Not Found | Combo 1   |
| Histidine-rich glycoprotein   | Not Found | Combo 2   | Not Found |
| HMG CoA reductase   | Not Found | Combo 1   | Not Found |
| Hypoxanthine-guanine phosphoribosyltransferase                        | Combo 4   | Combo 4   | Combo 5   |
| Hypoxia-inducible factor 1 alpha                                      | Combo 1   | Combo 2   | Not Found |
| ID-1  | Combo 6   | Not Found | Combo 2   |
| IgE binding protein   | Combo 2   | Combo 5   | Combo 5   |
| Insulin-like growth factor binding protein 1                          | Combo 6   | Combo 6   | Combo 6   |
| Insulin-like growth factor binding protein 3                          | Not Found | Combo 2   | Not Found |
| Integrin beta1  | Combo 3   | Not Found | Not Found |
| Integrin beta-4   | Not Found | Not Found | Combo 6   |
| Interferon related developmental regulator IFRD1 (PC4)                | Combo 4   | Not Found | Combo 1   |
| Interleukin-1 beta  | Combo 4   | Combo 4   | Combo 1   |

|  |           |           |           |
|--|-----------|-----------|-----------|
| Interleukin-10   | Not Found | Not Found | Combo 3   |
| Interleukin-18   | Not Found | Not Found | Combo 1   |
| Intracellular calcium-binding protein (MRP8)                     | Combo 1   | Not Found | Not Found |
| Iron-responsive element-binding protein                          | Not Found | Combo 1   | Combo 1   |
| Jagged 1   | Combo 1   | Not Found | Not Found |
| Keratinocyte growth factor                                       | Not Found | Combo 5   | Not Found |
| Liver fatty acid binding protein                                 | Not Found | Not Found | Combo 5   |
| Low density lipoprotein receptor                                 | Not Found | Combo 1   | Not Found |
| Macrophage inflammatory protein-1 alpha                          | Not Found | Combo 1   | Not Found |
| Macrophage inflammatory protein-2 alpha                          | Combo 4   | Not Found | Combo 3   |
| Macrophage metalloelastase                                       | Combo 2   | Combo 1   | Not Found |
| Major acute phase protein alpha-1                                | Not Found | Not Found | Combo 5   |
| Major basic protein 1  | Combo 1   | Not Found | Combo 6   |
| Malate dehydrogenase, cytosolic                                  | Combo 2   | Combo 2   | Combo 2   |
| Matrix metalloproteinase-1                                       | Combo 2   | Combo 4   | Combo 1   |
| Methylacyl-CoA racemase alpha                                    | Combo 1   | Combo 3   | Combo 1   |
| MHC class I antigen RT1.A1(f) alpha-chain                        | Combo 2   | Combo 5   | Combo 6   |
| Mitogen activated protein kinase (P38)                           | Not Found | Combo 1   | Not Found |
| Monoamine oxidase A  | Combo 2   | Not Found | Combo 1   |
| Monoamine oxidase B  | Not Found | Not Found | Combo 2   |
| Monocyte chemotactic protein receptor (CCR2)                     | Not Found | Combo 1   | Combo 6   |
| Mullerian inhibiting substance                                   | Not Found | Combo 1   | Not Found |
| Multidrug resistant protein-1                                    | Not Found | Combo 4   | Combo 5   |
| Multidrug resistant protein-2                                    | Combo 1   | Not Found | Not Found |
| Multidrug resistant protein-3                                    | Combo 6   | Combo 5   | Combo 6   |
| Mx1 protein  | Not Found | Not Found | Combo 1   |
| Myelin basic protein   | Not Found | Not Found | Combo 2   |
| Na/H antiporter (APNH1)  | Combo 1   | Not Found | Combo 1   |
| Na/K ATPase alpha-1  | Combo 5   | Combo 1   | Combo 4   |
| NADP-dependent isocitrate dehydrogenase, cytosolic               | Combo 1   | Not Found | Not Found |
| NADPH cytochrome P450 oxidoreductase                             | Not Found | Not Found | Combo 3   |
| NADPH cytochrome P450 reductase                                  | Combo 2   | Not Found | Not Found |
| N-cadherin   | Combo 3   | Combo 1   | Combo 1   |
| Nerve growth factor receptor                                     | Not Found | Combo 1   | Not Found |
| NGF-inducible anti-proliferative putative secreted protein (PC3) | Combo 1   | Not Found | Not Found |
| N-hydroxy-2-acetylaminofluorene sulfotransferase (ST1C1)         | Combo 3   | Combo 2   | Combo 1   |
| Notch 1  | Not Found | Not Found | Combo 4   |
| Organic anion transporter 3                                      | Not Found | Combo 2   | Combo 1   |
| Organic anion transporter K1                                     | Not Found | Combo 1   | Combo 2   |
| Organic anion transporting polypeptide 1                         | Not Found | Combo 2   | Combo 1   |
| Organic cation transporter 2                                     | Not Found | Combo 1   | Not Found |
| Organic cation transporter 3                                     | Not Found | Combo 4   | Not Found |
| Ornithine aminotransferase                                       | Combo 1   | Combo 2   | Combo 1   |
| Ornithine decarboxylase  | Combo 3   | Not Found | Not Found |
| Osteopontin  | Not Found | Combo 5   | Combo 1   |
| p53  | Not Found | Combo 3   | Not Found |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II)         | Not Found | Combo 4   | Combo 4   |

|  |           |           |           |
|--|-----------|-----------|-----------|
| PAR interacting protein                          | Combo 1   | Combo 6   | Not Found |
| Peroxisomal 3-ketoacyl-CoA thiolase 2            | Combo 4   | Not Found | Not Found |
| Peroxisomal multifunctional enzyme type II       | Not Found | Combo 1   | Not Found |
| Peroxisome assembly factor 2                     | Combo 1   | Not Found | Not Found |
| Peroxisome proliferator activated receptor alpha | Not Found | Combo 1   | Not Found |
| RCT-165  | Not Found | Combo 1   | Combo 1   |
| RCT-252  | Not Found | Combo 1   | Not Found |
| RCT-10   | Not Found | Combo 3   | Combo 2   |
| RCT-101  | Not Found | Combo 1   | Combo 3   |
| RCT-102  | Combo 4   | Not Found | Not Found |
| RCT-103  | Combo 5   | Not Found | Not Found |
| RCT-108  | Combo 2   | Not Found | Not Found |
| RCT-109  | Combo 4   | Combo 6   | Combo 3   |
| RCT-111  | Combo 6   | Combo 1   | Not Found |
| Protein O-mannosyltransferase 1 (Pomt1)          | Not Found | Combo 1   | Not Found |
| RCT-12   | Combo 6   | Not Found | Combo 5   |
| RCT-126  | Not Found | Combo 5   | Combo 4   |
| RCT-127  | Combo 2   | Combo 2   | Combo 5   |
| RCT-128  | Not Found | Not Found | Combo 1   |
| RCT-129  | Not Found | Combo 1   | Not Found |
| Apoptosis-regulating basic protein               | Combo 2   | Combo 1   | Combo 1   |
| RCT-137  | Not Found | Not Found | Combo 1   |
| RCT-138  | Not Found | Combo 4   | Combo 4   |
| RCT-14   | Combo 2   | Not Found | Not Found |
| RCT-140  | Not Found | Combo 1   | Not Found |
| RCT-141  | Not Found | Not Found | Combo 2   |
| RCT-142  | Combo 1   | Not Found | Not Found |
| RCT-143  | Not Found | Not Found | Combo 1   |
| RCT-144  | Combo 4   | Combo 6   | Not Found |
| RCT-145  | Not Found | Combo 6   | Combo 2   |
| RCT-146  | Combo 2   | Not Found | Combo 3   |
| RCT-147  | Combo 3   | Combo 1   | Not Found |
| RCT-148  | Combo 1   | Not Found | Combo 1   |
| RCT-149  | Not Found | Combo 3   | Combo 1   |
| RCT-151  | Combo 2   | Not Found | Not Found |
| RCT-152  | Not Found | Combo 6   | Not Found |
| RCT-153  | Combo 1   | Combo 1   | Not Found |
| RCT-155  | Not Found | Combo 2   | Combo 3   |
| RCT-158  | Not Found | Combo 6   | Not Found |
| RCT-161  | Not Found | Not Found | Combo 1   |
| RCT-162  | Not Found | Combo 2   | Not Found |
| RCT-164  | Not Found | Combo 1   | Not Found |
| RCT-166  | Combo 2   | Combo 1   | Combo 1   |
| RCT-177  | Combo 1   | Not Found | Not Found |
| RCT-179  | Combo 2   | Combo 5   | Combo 1   |
| RCT-18   | Not Found | Combo 1   | Not Found |
| RCT-180  | Combo 2   | Combo 4   | Combo 1   |
| RCT-181  | Not Found | Combo 1   | Combo 1   |

|   |           |           |           |
|---|-----------|-----------|-----------|
| RCT-182                                   | Combo 3   | Combo 5   | Combo 5   |
| RCT-185                                   | Not Found | Combo 1   | Not Found |
| RCT-192                                   | Not Found | Combo 3   | Combo 3   |
| RCT-193                                   | Not Found | Not Found | Combo 1   |
| RCT-194                                   | Combo 1   | Not Found | Not Found |
| RCT-196                                   | Not Found | Combo 3   | Not Found |
| RCT-197                                   | Not Found | Not Found | Combo 1   |
| RCT-198                                   | Combo 1   | Combo 6   | Not Found |
| Vacuole membrane protein 1                | Not Found | Combo 6   | Combo 1   |
| RCT-205                                   | Combo 1   | Not Found | Not Found |
| RCT-206                                   | Not Found | Combo 1   | Not Found |
| RCT-207                                   | Not Found | Not Found | Combo 4   |
| Calgranulin B                             | Combo 2   | Not Found | Not Found |
| RCT-211                                   | Combo 2   | Combo 5   | Combo 6   |
| RCT-212                                   | Not Found | Not Found | Combo 3   |
| RCT-214                                   | Combo 1   | Combo 2   | Not Found |
| RCT-215                                   | Not Found | Combo 2   | Combo 2   |
| RCT-22                                    | Not Found | Combo 3   | Combo 1   |
| RCT-220                                   | Not Found | Combo 1   | Not Found |
| RCT-221                                   | Combo 5   | Combo 1   | Not Found |
| RCT-228                                   | Combo 3   | Not Found | Combo 1   |
| RCT-237                                   | Not Found | Not Found | Combo 2   |
| RCT-24                                    | Combo 4   | Combo 6   | Combo 6   |
| RCT-240                                   | Combo 3   | Combo 4   | Combo 6   |
| RCT-241                                   | Not Found | Combo 6   | Combo 4   |
| RCT-242                                   | Not Found | Combo 2   | Combo 1   |
| RCT-244                                   | Not Found | Combo 2   | Combo 1   |
| RCT-245                                   | Combo 3   | Not Found | Not Found |
| RCT-246                                   | Combo 1   | Combo 2   | Not Found |
| RCT-251                                   | Combo 2   | Not Found | Not Found |
| RCT-256                                   | Not Found | Combo 3   | Not Found |
| RCT-258                                   | Not Found | Combo 5   | Combo 3   |
| Inositol polyphosphate multikinase (lpmk) | Combo 4   | Combo 1   | Combo 1   |
| RCT-260                                   | Not Found | Combo 2   | Combo 1   |
| RCT-264                                   | Not Found | Not Found | Combo 1   |
| Ubiquitin D (Ubd)                         | Not Found | Combo 3   | Combo 4   |
| RCT-268                                   | Combo 1   | Combo 1   | Not Found |
| RCT-271                                   | Not Found | Combo 6   | Combo 2   |
| RCT-274                                   | Combo 2   | Combo 5   | Combo 6   |
| RCT-276                                   | Not Found | Combo 1   | Not Found |
| RCT-277                                   | Combo 3   | Not Found | Not Found |
| RCT-279                                   | Not Found | Combo 1   | Not Found |
| RCT-28                                    | Combo 1   | Not Found | Not Found |
| RCT-280                                   | Combo 1   | Combo 2   | Combo 1   |
| RCT-281                                   | Combo 2   | Not Found | Not Found |
| RCT-284                                   | Not Found | Not Found | Combo 1   |
| RCT-287                                   | Not Found | Combo 4   | Combo 3   |
| RCT-288                                   | Not Found | Not Found | Combo 1   |

|   |           |           |           |
|---|-----------|-----------|-----------|
| RCT-291                                   | Not Found | Combo 2   | Combo 3   |
| RCT-292                                   | Not Found | Combo 2   | Not Found |
| RCT-293                                   | Not Found | Combo 4   | Combo 5   |
| Voltage-dependent anion channel 2 (Vdac2) | Combo 2   | Not Found | Combo 1   |
| RCT-296                                   | Not Found | Not Found | Combo 3   |
| RCT-31                                    | Not Found | Combo 1   | Not Found |
| RCT-34                                    | Not Found | Combo 3   | Combo 2   |
| RCT-36                                    | Not Found | Combo 1   | Not Found |
| RCT-38                                    | Not Found | Combo 4   | Combo 1   |
| RCT-39                                    | Not Found | Not Found | Combo 2   |
| RCT-40                                    | Combo 1   | Not Found | Not Found |
| RCT-42                                    | Not Found | Combo 2   | Not Found |
| RCT-43                                    | Combo 3   | Combo 1   | Not Found |
| RCT-45                                    | Not Found | Not Found | Combo 1   |
| RCT-49                                    | Combo 4   | Combo 5   | Combo 5   |
| RCT-50                                    | Combo 5   | Combo 5   | Combo 5   |
| RCT-53                                    | Combo 1   | Not Found | Not Found |
| RCT-59                                    | Combo 1   | Not Found | Combo 5   |
| RCT-6                                     | Not Found | Not Found | Combo 2   |
| RCT-60                                    | Combo 2   | Combo 5   | Not Found |
| RCT-61                                    | Combo 1   | Combo 1   | Not Found |
| RCT-62                                    | Not Found | Not Found | Combo 1   |
| RCT-64                                    | Combo 1   | Not Found | Combo 1   |
| RCT-66                                    | Combo 1   | Not Found | Combo 2   |
| RCT-68                                    | Combo 1   | Combo 6   | Combo 4   |
| RCT-69                                    | Not Found | Not Found | Combo 2   |
| RCT-72                                    | Not Found | Combo 1   | Not Found |
| RCT-74                                    | Combo 1   | Not Found | Not Found |
| RCT-76                                    | Combo 2   | Combo 1   | Not Found |
| RCT-8                                     | Not Found | Combo 3   | Not Found |
| RCT-80                                    | Combo 2   | Not Found | Not Found |
| RCT-83                                    | Combo 3   | Not Found | Not Found |
| RCT-84                                    | Not Found | Combo 2   | Not Found |
| RCT-87                                    | Not Found | Not Found | Combo 3   |
| RCT-88                                    | Not Found | Combo 2   | Not Found |
| RCT-89                                    | Not Found | Combo 3   | Combo 2   |
| RCT-91                                    | Not Found | Combo 2   | Not Found |
| RCT-92                                    | Not Found | Combo 2   | Combo 2   |
| RCT-94                                    | Combo 1   | Not Found | Not Found |
| RCT-99                                    | Not Found | Not Found | Combo 1   |
| Phosphatidylethanolamine-binding protein  | Combo 2   | Not Found | Combo 2   |
| Phosphoglycerate kinase                   | Combo 1   | Not Found | Not Found |
| Poly(ADP-ribose) polymerase               | Not Found | Not Found | Combo 1   |
| Preproalbumin                             | Not Found | Not Found | Combo 3   |
| Proliferating cell nuclear antigen gene   | Not Found | Combo 5   | Not Found |
| Prostaglandin H synthase                  | Not Found | Not Found | Combo 2   |
| Proteasome activator 28 alpha             | Not Found | Combo 2   | Not Found |
| Protein tyrosine phosphatase alpha        | Combo 4   | Not Found | Combo 1   |



|   |           |           |           |
|---|-----------|-----------|-----------|
| PTEN/MMAC1  | Combo 2   | Not Found | Not Found |
| Pyruvate kinase, muscle   | Combo 5   | Combo 4   | Combo 1   |
| RAD   | Not Found | Not Found | Combo 3   |
| Ref-1   | Not Found | Combo 4   | Not Found |
| Renal organic anion transporter                                     | Not Found | Combo 1   | Not Found |
| Retinoid X receptor alpha   | Combo 1   | Combo 1   | Not Found |
| Retinol dehydrogenase type III                                      | Not Found | Combo 1   | Not Found |
| Retinol-binding protein (RBP)                                       | Not Found | Combo 1   | Not Found |
| Ribosomal protein L13A  | Combo 5   | Combo 6   | Combo 5   |
| Ribosomal protein L27   | Not Found | Combo 2   | Not Found |
| Ribosomal protein S8  | Not Found | Combo 6   | Combo 1   |
| Ribosomal protein S9  | Not Found | Combo 5   | Combo 1   |
| Sarcoplasmic reticulum calcium ATPase                               | Combo 1   | Combo 1   | Combo 1   |
| Selenoprotein P   | Not Found | Combo 2   | Combo 2   |
| Senescence marker protein-30  | Not Found | Combo 2   | Combo 2   |
| Serotonin transporter (SERT)  | Combo 1   | Not Found | Not Found |
| Sodium/glucose cotransporter 1                                      | Not Found | Not Found | Combo 2   |
| Stathmin  | Combo 3   | Combo 2   | Combo 4   |
| Sterol carrier protein 2  | Combo 2   | Not Found | Not Found |
| Sulfotransferase K2   | Not Found | Combo 1   | Not Found |
| Superoxide dismutase Cu/Zn  | Combo 1   | Combo 1   | Not Found |
| Superoxide dismutase Mn   | Combo 5   | Combo 4   | Combo 4   |
| Suppressor of cytokine signaling 3                                  | Not Found | Not Found | Combo 5   |
| T-cell cyclophilin  | Not Found | Combo 1   | Not Found |
| Thiol-specific antioxidant (natural killer cell-enhancing factor B) | Combo 4   | Combo 1   | Combo 2   |
| Thiopurine methyltransferase  | Not Found | Combo 1   | Combo 2   |
| Thioredoxin-1 (Trx1)  | Combo 2   | Combo 2   | Combo 1   |
| Thioredoxin-2 (Trx2)  | Combo 2   | Not Found | Combo 3   |
| Thrombin receptor (PAR-1)   | Not Found | Combo 1   | Not Found |
| Thrombomodulin  | Not Found | Not Found | Combo 4   |
| Thymidylate synthase  | Combo 1   | Not Found | Not Found |
| Thymosin beta-10  | Combo 5   | Combo 5   | Combo 5   |
| Tissue factor   | Not Found | Not Found | Combo 2   |
| Tissue inhibitor of metalloproteinases-1                            | Combo 2   | Combo 6   | Combo 5   |
| Transferrin   | Combo 2   | Not Found | Not Found |
| Transitional endoplasmic reticulum ATPase                           | Combo 1   | Not Found | Not Found |
| Tryptophan hydroxylase  | Combo 5   | Not Found | Combo 1   |
| Ubiquitin conjugating enzyme (RAD 6 homologue)                      | Not Found | Combo 4   | Not Found |
| UDP-glucuronosyltransferase   | Not Found | Not Found | Combo 1   |
| Uncoupling protein 2  | Combo 4   | Combo 6   | Combo 5   |
| Urokinase plasminogen activator receptor                            | Not Found | Not Found | Combo 1   |
| Vascular cell adhesion molecule 1 (VCAM-1)                          | Not Found | Combo 2   | Combo 4   |
| Vascular endothelial growth factor                                  | Not Found | Not Found | Combo 1   |
| Very long-chain acyl-CoA synthetase                                 | Combo 1   | Not Found | Combo 3   |
| Vesicular monoamine transporter (VMAT)                              | Not Found | Combo 2   | Not Found |
| VL30 element  | Combo 1   | Not Found | Not Found |
| Zinc finger protein   | Combo 5   | Combo 5   | Combo 4   |

\* A Combo entry number indicates that the gene was on the predictive list for that time point and the number of occurrences of that gene on optimal combined training/test set lists. "Not Found" indicates that the gene was not on the optimal combined list for that time point.

Table 34 RCT genes (ESTs) Predictive for Kidney Tubular  
Necrosis: Best Homology Matches

| Gene Name | Homology   |
|-----------|--|
| RCT-10    | Rattus norvegicus methylmalonate semialdehyde dehydrogenase gene (Mmsdh)   |
| RCT-101   | no significant homology found  |
| RCT-102   | Mouse pentylenetetrazol-related mRNA PTZ-17 (3'UTR of E3.1)  |
| RCT-103   | no significant homology found  |
| RCT-108   | no significant homology found  |
| RCT-109   | Rattus norvegicus nesprin-1 mRNA   |
| RCT-111   | Mus musculus B lymphoid kinase (Blk)   |
| RCT-12    | no significant homology found  |
| RCT-126   | Homo sapiens, clone MGC:9483 IMAGE:3919901, mRNA   |
| RCT-127   | no significant homology found  |
| RCT-128   | Mus musculus angiopoietin-related protein 3 (Angptl3)  |
| RCT-129   | Mus musculus Nedd4 WW binding protein 4 (N4wbp4-pending), mRNA   |
| RCT-137   | Mus musculus adult male tongue cDNA  |
| RCT-138   | Mus musculus DAP10 (Dap10) gene  |
| RCT-139   | no significant homology found  |
| RCT-14    | Rat brain nicotinic receptor alpha 7 subunit   |
| RCT-140   | Mouse 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3100001I08                                   |
| RCT-141   | Mus musculus proteoglycan 3 (megakaryocyte stimulating factor, articular superficial zone protein) (Prg4)              |
| RCT-142   | Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1190008J14                                 |
| RCT-143   | Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase) (NDUFS8)                |
| RCT-144   | Mus musculus, similar to nucleolar protein (KKE/D repeat), clone IMAGE:3491448, mRNA, partial cds.                     |
| RCT-145   | Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810014B19, full insert sequence |
| RCT-146   | Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730458E20                                  |
| RCT-147   | Rattus norvegicus clone RP31-188L2   |
| RCT-148   | Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610010B16                              |
| RCT-149   | Mouse mRNA fragment for serum amyloid A (SAA) 3 protein  |
| RCT-151   | Mus musculus, Similar to sphingomyelin phosphodiesterase 1, acid lysosomal, clone MGC:11522 IMAGE:3964394              |

|         |  |
|---------|--|
| RCT-152 | Mus musculus, eukaryotic translation elongation factor 1 beta 2, clone MGC:6763 IMAGE:3600850, mRNA, complete cds. |
| RCT-153 | Mouse adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500015I13                             |
| RCT-155 | Mus musculus type XV collagen mRNA   |
| RCT-158 | Rattus norvegicus cyclin-dependent kinase inhibitor 1B   |
| RCT-161 | Mus musculus adult male spleen cDNA, RIKEN full-length enriched library, clone:0910001D19                          |
| RCT-162 | Mus musculus, clone IMAGE:3501507  |
| RCT-164 | Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932443D16                          |
| RCT-165 | Mus musculus adiponutrin (Adpn-pending), mRNA  |
| RCT-166 | Mus musculus, Similar to glutathione S-transferase theta 1, clone MGC:6769 IMAGE:3601446                           |
| RCT-171 | no significant homology found  |
| RCT-177 | Mus musculus, Similar to peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase, clone MGC:5644 IMAGE:3591615       |
| RCT-179 | Rat nucleolar protein B23.2 mRNA   |
| RCT-18  | no significant homology found  |
| RCT-180 | Mus musculus B-cell receptor-associated protein 37 (Bcap37   |
| RCT-181 | Mus musculus adult male testis cDNA  |
| RCT-182 | Rattus norvegicus glb mRNA for diacetyl/L-xylulose reductase   |
| RCT-185 | no significant homology found  |
| RCT-192 | Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110033J19                             |
| RCT-193 | no significant homology found  |
| RCT-194 | Mus musculus ectodermal-neural cortex 1 (Enc1)   |
| RCT-196 | Homolous to Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3010001M15            |
| RCT-197 | Rattus norvegicus Protein kinase, interferon-inducible double stranded RNA dependent (Prkr), mRNA                  |
| RCT-198 | Mus musculus adult male kidney cDNA  |
| RCT-205 | no significant homology found  |
| RCT-206 | Homo sapiens, clone IMAGE:3867552  |
| RCT-207 | Mus musculus Ran binding protein 5 mRNA, partial cds   |
| RCT-211 | Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610009C22                          |
| RCT-212 | Mus musculus nuclear localization signal protein absent in velo-cardio-facial patients (Nlvcf)                     |

|         |  |
|---------|--|
| RCT-214 | Mus musculus putative NAD(P)H steroid dehydrogenase mRNA   |
| RCT-215 | Mus musculus RAB/Rip protein mRNA  |
| RCT-22  | Mus musculus, clone MGC:19042 IMAGE:4188988, mRNA  |
| RCT-220 | no significant homology found  |
| RCT-221 | no significant homology found  |
| RCT-228 | no significant homology found  |
| RCT-237 | M.musculus mRNA for low density lipoprotein receptor   |
| RCT-24  | Mus musculus, tubulin alpha 8, clone MGC:28850 IMAGE:4507364, mRNA,                              |
| RCT-240 | Mus musculus, clone MGC:7041   |
| RCT-241 | Mus musculus oncostatin receptor (Osmr), mRNA  |
| RCT-242 | Rattus norvegicus B-cell translocation gene 2, anti-proliferative(Btg2),                         |
| RCT-244 | Mus musculus RIKEN cDNA 2810408B13 gene  |
| RCT-245 | no significant homology found  |
| RCT-246 | no significant homology found  |
| RCT-251 | no significant homology found  |
| RCT-252 | Mus musculus EH-domain containing 3 (Ehd3),  |
| RCT-256 | Mus musculus, Similar to betaine-homocysteine methyltransferase 2, clone MGC:19186 IMAGE:4235455 |
| RCT-258 | Mus musculus, clone MGC:6139 IMAGE:3487295, mRNA   |
| RCT-260 | Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900024P20   |
| RCT-264 | Mus musculus sodium-sulfate cotransporter (Nas1) gene  |
| RCT-268 | Mouse adult male liver cDNA, RIKEN full-length enriched library, clone:1300017J02                |
| RCT-271 | Homologous to Mus musculus, clone MGC:27581 IMAGE:4489072, mRNA                                  |
| RCT-274 | Rattus norvegicus Clusterin (Clu)  |
| RCT-276 | Homo sapiens KIAA1224 protein  |
| RCT-277 | no significant homology found  |
| RCT-279 | no significant homology found  |
| RCT-28  | no significant homology found  |
| RCT-280 | Mus musculus carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (Chst1)                     |
| RCT-281 | Mus musculus, Similar to TNF-induced protein, clone MGC:11714                                    |
| RCT-284 | Homo sapiens complement component C1q receptor (C1QR), mRNA                                      |
| RCT-287 | Mus musculus adult male kidney cDNA clone:0610010I20   |
| RCT-288 | no significant homology found  |
| RCT-291 | no significant homology found  |
| RCT-292 | Rattus norvegicus 2'5' oligoadenylate synthetase-2   |
| RCT-293 | Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1110021C22           |
| RCT-296 | Mus musculus corticosteroid binding globulin (Cbg)   |

|        |   |
|--------|---|
| RCT-31 | Mouse 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810437P06 |
| RCT-34 | no significant homology found   |
| RCT-36 | no significant homology found   |
| RCT-38 | Mus musculus betaine-homocysteine methyltransferase 2 (Bhmt2) mRNA,                 |
| RCT-39 | no significant homology found   |
| RCT-40 | Rattus norvegicus Cathepsin C (dipeptidyl peptidase I) (Ctsc)                       |
| RCT-42 | Mus musculus STAT5B (Stat5b)  |
| RCT-43 | no significant homology found   |
| RCT-45 | Mus musculus Nedd4-binding brain specific protein BEAN mRNA, partial cds            |
| RCT-49 | No match with score above 200   |
| RCT-50 | Mus musculus fibroblast growth factor regulated protein 2                           |
| RCT-53 | no significant homology found   |
| RCT-59 | no significant homology found   |
| RCT-6  | sdpr=serum deprivation response [mice, NIH3T3 cells, mRNA, 2909 nt]                 |
| RCT-60 | Mouse, Similar to tyrosyl-tRNA synthetase, clone MGC:19350                          |
| RCT-61 | no significant homology found   |
| RCT-62 | no significant homology found   |
| RCT-64 | no significant homology found   |
| RCT-66 | M.musculus mRNA for low density lipoprotein receptor                                |
| RCT-68 | Rattus norvegicus nucleosome assembly protein mRNA                                  |
| RCT-69 | Mus musculus, RIKEN cDNA 0610033L19 gene, clone MGC:25463 IMAGE:4458296             |
| RCT-72 | no significant homology found   |
| RCT-74 | no significant homology found   |
| RCT-76 | no significant homology found   |
| RCT-8  | Messenger RNA for rat preproalbumin   |
| RCT-80 | no significant homology found   |
| RCT-83 | no significant homology found   |
| RCT-84 | no significant homology found   |
| RCT-87 | Mus musculus adult male tongue cDNA   |
| RCT-88 | no significant homology found   |
| RCT-89 | no significant homology found   |
| RCT-91 | no significant homology found   |
| RCT-92 | no significant homology found   |
| RCT-94 | Rattus norvegicus Glutamate receptor, metabotropic 5 (Grm5)                         |
| RCT-99 | no significant homology found   |

\* Homologies are given from BLAST searches using the Phase 1 RCT sequence as the query sequence and GenBank NR database as the target sequence database. The best BLAST homology sequence observed is given. In general, no significant homology

indicates that no BLAST match was observed with a BIT score  $>100$ . BLAST searches in this category were conducted as recently as February, 2002.

Table 35 Fifty-three Genes that are Predictive at all Three Time Points

| Gene   | 6h      | 24h     | 72h     |
|--|---------|---------|---------|
| Alpha-tubulin  | Combo 6 | Combo 6 | Combo 6 |
| Aspartoacylase   | Combo 2 | Combo 3 | Combo 1 |
| Beta-tubulin, class I                                    | Combo 5 | Combo 5 | Combo 6 |
| Calpactin I heavy chain                                  | Combo 3 | Combo 6 | Combo 5 |
| Calreticulin   | Combo 6 | Combo 3 | Combo 1 |
| Cathepsin L  | Combo 6 | Combo 6 | Combo 1 |
| Cathepsin L, sequence 2                                  | Combo 4 | Combo 6 | Combo 2 |
| CD44 metastasis suppressor gene                          | Combo 1 | Combo 4 | Combo 5 |
| c-myc  | Combo 1 | Combo 6 | Combo 5 |
| Connexin-32  | Combo 3 | Combo 4 | Combo 1 |
| Cytochrome P450 2C11                                     | Combo 1 | Combo 1 | Combo 1 |
| DNA topoisomerase I                                      | Combo 1 | Combo 2 | Combo 1 |
| Dynein light chain 1                                     | Combo 1 | Combo 6 | Combo 5 |
| Ecto-ATPase  | Combo 3 | Combo 3 | Combo 3 |
| Epidermal growth factor                                  | Combo 5 | Combo 4 | Combo 3 |
| Ferritin H-chain   | Combo 2 | Combo 4 | Combo 1 |
| Gamma-glutamyl transpeptidase                            | Combo 5 | Combo 1 | Combo 1 |
| Heme oxygenase   | Combo 3 | Combo 1 | Combo 1 |
| Hypoxanthine-guanine phosphoribosyltransferase           | Combo 4 | Combo 4 | Combo 5 |
| IgE binding protein                                      | Combo 2 | Combo 5 | Combo 5 |
| Insulin-like growth factor binding protein 1             | Combo 6 | Combo 6 | Combo 6 |
| Interleukin-1 beta                                       | Combo 4 | Combo 4 | Combo 1 |
| Malate dehydrogenase, cytosolic                          | Combo 2 | Combo 2 | Combo 2 |
| Matrix metalloproteinase-1                               | Combo 2 | Combo 4 | Combo 1 |
| Methylacyl-CoA racemase alpha                            | Combo 1 | Combo 3 | Combo 1 |
| MHC class I antigen RT1.A1(f) alpha-chain                | Combo 2 | Combo 5 | Combo 6 |
| Multidrug resistant protein-3                            | Combo 6 | Combo 5 | Combo 6 |
| Na/K ATPase alpha-1                                      | Combo 5 | Combo 1 | Combo 4 |
| N-cadherin   | Combo 3 | Combo 1 | Combo 1 |
| N-hydroxy-2-acetylaminofluorene sulfotransferase (ST1C1) | Combo 3 | Combo 2 | Combo 1 |
| Ornithine aminotransferase                               | Combo 1 | Combo 2 | Combo 1 |
| RCT-109  | Combo 4 | Combo 6 | Combo 3 |
| RCT-127  | Combo 2 | Combo 2 | Combo 5 |
| Apoptosis-regulating basic protein                       | Combo 2 | Combo 1 | Combo 1 |
| RCT-166  | Combo 2 | Combo 1 | Combo 1 |
| RCT-179  | Combo 2 | Combo 5 | Combo 1 |
| RCT-180  | Combo 2 | Combo 4 | Combo 1 |
| RCT-182  | Combo 3 | Combo 5 | Combo 5 |
| RCT-211  | Combo 2 | Combo 5 | Combo 6 |
| RCT-24   | Combo 4 | Combo 6 | Combo 6 |
| RCT-240  | Combo 3 | Combo 4 | Combo 6 |



|  |         |         |         |
|--|---------|---------|---------|
| RCT-280                                  | Combo 1 | Combo 2 | Combo 1 |
| RCT-49                                   | Combo 4 | Combo 5 | Combo 5 |
| RCT-50                                   | Combo 5 | Combo 5 | Combo 5 |
| RCT-68                                   | Combo 1 | Combo 6 | Combo 4 |
| Ribosomal protein L13A                   | Combo 5 | Combo 6 | Combo 5 |
| Sarcoplasmic reticulum calcium ATPase    | Combo 1 | Combo 1 | Combo 1 |
| Stathmin                                 | Combo 3 | Combo 2 | Combo 4 |
| Superoxide dismutase Mn                  | Combo 5 | Combo 4 | Combo 4 |
| Thymosin beta-10                         | Combo 5 | Combo 5 | Combo 5 |
| Tissue inhibitor of metalloproteinases-1 | Combo 2 | Combo 6 | Combo 5 |
| Uncoupling protein 2                     | Combo 4 | Combo 6 | Combo 5 |
| Zinc finger protein                      | Combo 5 | Combo 5 | Combo 4 |

Table 36 Twenty-three Genes that are the most predictive across the time points

| Gene  | 6h      | 24h     | 72h     |
|---|---------|---------|---------|
| Alpha-tubulin                                     | Combo 6 | Combo 6 | Combo 6 |
| Beta-tubulin, class I                             | Combo 5 | Combo 5 | Combo 6 |
| Cathepsin L                                       | Combo 6 | Combo 6 | Combo 1 |
| Cathepsin L, sequence 2                           | Combo 4 | Combo 6 | Combo 2 |
| c-myc   | Combo 1 | Combo 6 | Combo 5 |
| Epidermal growth factor                           | Combo 5 | Combo 4 | Combo 3 |
| Hypoxanthine-guanine<br>phosphoribosyltransferase | Combo 4 | Combo 4 | Combo 5 |
| IgE binding protein                               | Combo 2 | Combo 5 | Combo 5 |
| Insulin-like growth factor binding protein 1      | Combo 6 | Combo 6 | Combo 6 |
| Interleukin-1 beta                                | Combo 4 | Combo 4 | Combo 1 |
| Multidrug resistant protein-3                     | Combo 6 | Combo 5 | Combo 6 |
| RCT-211   | Combo 2 | Combo 5 | Combo 6 |
| RCT-24  | Combo 4 | Combo 6 | Combo 6 |
| RCT-240   | Combo 3 | Combo 4 | Combo 6 |
| RCT-49  | Combo 4 | Combo 5 | Combo 5 |
| RCT-50  | Combo 5 | Combo 5 | Combo 5 |
| RCT-68  | Combo 1 | Combo 6 | Combo 4 |
| Ribosomal protein L13A                            | Combo 5 | Combo 6 | Combo 5 |
| Superoxide dismutase Mn                           | Combo 5 | Combo 4 | Combo 4 |
| Thymosin beta-10                                  | Combo 5 | Combo 5 | Combo 5 |
| Tissue inhibitor of metalloproteinases-1          | Combo 2 | Combo 6 | Combo 5 |
| Uncoupling protein 2                              | Combo 4 | Combo 6 | Combo 5 |
| Zinc finger protein                               | Combo 5 | Combo 5 | Combo 4 |

| Table 37 Kidney Toxicity Predictive Genes Whose Protein Products Are Known to be Secreted |  |
|---|--|
| Ceruloplasmin   |  |
| Colony-stimulating factor-1   |  |
| Complement component C3   |  |
| Cystatin C  |  |
| Epidermal growth factor   |  |
| Ferritin H-chain  |  |
| Fibrinogen gamma chain  |  |
| Interleukin-1 beta  |  |
| Interleukin-10  |  |
| Interleukin-18  |  |
| Keratinocyte growth factor  |  |
| Macrophage inflammatory protein-1 alpha   |  |
| Macrophage inflammatory protein-2 alpha   |  |
| Major acute phase protein alpha-1   |  |
| Mullerian inhibiting substance  |  |
| NGF-inducible anti-proliferative putative secreted protein (PC3)                          |  |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II)                                  |  |
| T-cell cyclophilin  |  |
| Thioredoxin-1 (Trx1)  |  |
| Tissue factor   |  |
| Tissue inhibitor of metalloproteinases-1  |  |
| Transferrin   |  |
| Vascular endothelial growth factor  |  |

| Table 42 Summary Output of Predictive Computer Software Product |              |            |          |      |                         |           |
|---|--------------|------------|----------|------|-------------------------|-----------|
| Sample  | Slide Number | Tissue     | Dose     | Time | Prediction              | Certitude |
| paraquat  | 16477        | Rat Kidney | 25 mg/kg | 24h  | Kidney Tubular Necrosis | 0.472     |
| paraquat  | 16478        | Rat Kidney | 25 mg/kg | 24h  | Negative                | 0.999     |
| paraquat  | 16479        | Rat Kidney | 25 mg/kg | 24h  | Kidney Tubular          | 0.796     |

|               |       |            |          |     |          |       |
|---------------|-------|------------|----------|-----|----------|-------|
|               |       |            |          |     | Necrosis |       |
| phenobarbital | 11494 | Rat Kidney | 80 mg/kg | 24h | Negative | 0.999 |
| phenobarbital | 11495 | Rat Kidney | 80 mg/kg | 24h | Negative | 0.999 |
| phenobarbital | 11496 | Rat Kidney | 80 mg/kg | 24h | Negative | 0.999 |

Table 43 Detailed Output of Predictive Computer Software Product

| Sample paraquat 16477 RatKidney 25mg/kg 24h 503r#3132    |  |             |                |
|--|--|-------------|----------------|
| Predictagen  |  | Performance | Kidney Tubular |
| Necrosis   |  | Negative    |                |
| 24hKidneyCombo1.txt                                      |  | 1.000       | 0.752          |
| 24hKidneyCombo2.txt                                      |  | 1.000       |                |
| 24hKidneyCombo3.txt                                      |  | 1.000       | 0.752          |
| 24hKidneyCombo4.txt                                      |  | 1.000       | 0.584          |
| 24hKidneyCombo5.txt                                      |  | 1.000       | 0.997          |
| 24hKidneyCombo6.txt                                      |  | 1.000       | 0.977          |
| Prediction: Kidney Tubular Necrosis with certitude 0.472 |  |             |                |

| Sample paraquat 16478 RatKidney 25mg/kg 24h 503r#3133 |             |                |
|---|-------------|----------------|
| Predictagen   | Performance | Kidney Tubular |
| Necrosis  | Negative    |                |
| 24hKidneyCombo1.txt                                   | 1.000       | 0.752          |
| 24hKidneyCombo2.txt                                   | 1.000       | 0.752          |
| 24hKidneyCombo3.txt                                   | 1.000       | 0.752          |
| 24hKidneyCombo4.txt                                   | 1.000       | 0.752          |
| 24hKidneyCombo5.txt                                   | 1.000       | 0.752          |
| 24hKidneyCombo6.txt                                   | 1.000       | 0.752          |
| Prediction: Negative with certitude 0.999             |             |                |

| Sample paraquat 16479 RatKidney 25mg/kg 24h 503r#3134    |             |                |
|--|-------------|----------------|
| Predictagen  | Performance | Kidney Tubular |
| Necrosis   | Negative    |                |
| 24hKidneyCombo1.txt                                      | 1.000       | 0.752          |
| 24hKidneyCombo2.txt                                      | 1.000       |                |
| 24hKidneyCombo3.txt                                      | 1.000       |                |
| 24hKidneyCombo4.txt                                      | 1.000       | 0.882          |
| 24hKidneyCombo5.txt                                      | 1.000       | 0.997          |
| 24hKidneyCombo6.txt                                      | 1.000       | 0.999          |
| Prediction: Kidney Tubular Necrosis with certitude 0.796 |             |                |

|  |             |                |
|--|-------------|----------------|
| Sample phenobarbital 11494 RatKidney 80mg/kg 24h H375#2634 |             |                |
| Predictagen  | Performance | Kidney Tubular |
| Necrosis   | Negative    |                |
| 24hKidneyComb01.txt  | 1.000       | 0.752          |

|  |       |       |
|--|-------|-------|
| 24hKidneyCombo2.txt                              | 1.000 | 0.752 |
| 24hKidneyCombo3.txt                              | 1.000 | 0.752 |
| 24hKidneyCombo4.txt                              | 1.000 | 0.752 |
| 24hKidneyCombo5.txt                              | 1.000 | 0.752 |
| 24hKidneyCombo6.txt                              | 1.000 | 0.752 |
| <b>Prediction: Negative with certitude 0.999</b> |       |       |

|   |             |                |
|---|-------------|----------------|
| <b>Sample phenobarbital 11495 RatKidney 80mg/kg 24h H375#2635</b> |             |                |
| Predictagen   | Performance | Kidney Tubular |
| Necrosis  | Negative    |                |
| 24hKidneyCombo1.txt   | 1.000       | 0.752          |
| 24hKidneyCombo2.txt   | 1.000       | 0.752          |
| 24hKidneyCombo3.txt   | 1.000       | 0.752          |
| 24hKidneyCombo4.txt   | 1.000       | 0.752          |
| 24hKidneyCombo5.txt   | 1.000       | 0.752          |
| 24hKidneyCombo6.txt   | 1.000       | 0.752          |
| <b>Prediction: Negative with certitude 0.999</b>                  |             |                |

|   |             |                |
|---|-------------|----------------|
| <b>Sample phenobarbital 11496 RatKidney 80mg/kg 24h H375#2636</b> |             |                |
| Predictagen   | Performance | Kidney Tubular |
| Necrosis  | Negative    |                |
| 24hKidneyCombo1.txt   | 1.000       | 0.752          |
| 24hKidneyCombo2.txt   | 1.000       | 0.752          |
| 24hKidneyCombo3.txt   | 1.000       | 0.752          |
| 24hKidneyCombo4.txt   | 1.000       | 0.752          |
| 24hKidneyCombo5.txt   | 1.000       | 0.752          |
| 24hKidneyCombo6.txt   | 1.000       | 0.752          |
| <b>Prediction: Negative with certitude 0.999</b>                  |             |                |

Table 44. Protein Marker Candidate Identification

| Gene Name                | Mean<br>Overall<br>Correct<br>Calls* | Codes<br>for<br>Protein | Avg<br>Neg<br>FI** | Avg<br>Pos<br>FI** | Secreted |
|--------------------------|--------------------------------------|-------------------------|--------------------|--------------------|----------|
|                          | Mean                                 |                         |                    |                    |          |
| Phase-1 RCT-241          | 79.9%                                | yes?                    | -0.02              | 0.85               |          |
| Cathepsin L, sequence 2  | 76.7%                                | yes                     | 0.08               | 1.19               |          |
| Phase-1 RCT-145          | 76.2%                                | yes?                    | -0.01              | 0.41               |          |
| Cathepsin L              | 76.0%                                | yes                     | 0.10               | 1.40               |          |
| 60S ribosomal protein L6 | 75.6%                                | yes                     | -0.06              | 0.75               |          |
| Clusterin                | 75.3%                                | yes                     | -0.02              | 0.48               |          |

|  |       |      |       |       |     |
|--|-------|------|-------|-------|-----|
| Osteopontin                                  | 75.3% | yes  | -0.08 | 0.04  |     |
| Dynein light chain 1                         | 74.6% | yes  | -0.06 | 0.23  |     |
| Tissue inhibitor of metalloproteinases-1     | 74.0% | yes  | 0.08  | 2.98  | yes |
| Uncoupling protein 2                         | 73.7% | yes  | -0.07 | 0.95  |     |
| Ribosomal protein S9                         | 72.9% | yes  | -0.03 | 0.57  |     |
| Phase-1 RCT-258                              | 72.5% | yes? | -0.02 | 0.30  |     |
| (Ribosomal protein L6)                       | 71.4% | yes  | 0.00  | 0.58  |     |
| Gadd153                                      | 70.8% | yes  | 0.08  | 0.85  |     |
| Proliferating cell nuclear antigen gene      | 70.5% | yes  | -0.06 | 0.12  |     |
| Gadd45                                       | 69.9% | yes  | 0.03  | 0.45  |     |
| Phase-1 RCT-274                              | 69.8% | ?    | 0.03  | 0.78  |     |
| Phase-1 RCT-109                              | 69.8% | ?    | 0.00  | 0.46  |     |
| Thymosin beta-10                             | 67.8% | yes  | -0.02 | 0.49  |     |
| c-myc  | 67.7% | yes  | 0.14  | 0.59  |     |
| Phase-1 RCT-158                              | 67.6% | yes? | 0.01  | 0.27  |     |
| Insulin-like growth factor binding protein 1 | 67.4% | yes  | 0.11  | 1.87  | yes |
| Phase-1 RCT-179                              | 67.2% | yes? | 0.06  | 0.62  |     |
| Multidrug resistant protein-3                | 66.8% | yes  | 0.03  | -0.02 |     |
| PAR interacting protein                      | 66.4% | yes  | 0.01  | 0.37  |     |
| Phase-1 RCT-198                              | 66.1% | ?    | 0.05  | 0.28  |     |
| Beta-actin, sequence 2                       | 65.8% | yes  | 0.01  | 0.05  |     |
| Phase-1 RCT-24                               | 65.4% | ?    | 0.12  | 0.03  |     |
| Alpha-tubulin                                | 65.2% | yes  | 0.00  | 0.05  |     |
| Phase-1 RCT-152                              | 64.9% | yes? | -0.05 | 0.73  |     |
| Phase-1 RCT-60                               | 64.7% | ?    | 0.05  | 0.23  |     |
| Phase-1 RCT-68                               | 64.5% | ?    | 0.06  | 0.32  |     |
| Keratinocyte growth factor                   | 63.2% | yes  | 0.07  | 0.99  | yes |
| Calpactin I heavy chain                      | 62.5% | yes  | 0.06  | 0.62  |     |
| Alpha-fibrinogen                             | 62.2% | yes  | 0.09  | 2.29  |     |
| Phase-1 RCT-49                               | 61.2% | ?    | -0.02 | 0.37  |     |
| Phase-1 RCT-199                              | 60.8% | yes? | -0.03 | 0.08  |     |
| IgE binding protein                          | 60.0% | yes  | -0.07 | 0.75  |     |

\*Mean Percent Accuracy for six training/test sets for individual gene predictive performance.

\*\*Mean fold induction relative to 0= no induction for expression in kidney samples treated with nontoxic treatments (Neg FI) or treatments producing kidney toxicity (Pos FI)

Table 45. Input data used for predictive computer program product

| Gene  | paraquat, 16477, Rat<br>Kidney, 25 mg/kg, 24 h,<br>603r #3132 | paraquat, 16478, Rat<br>Kidney, 25 mg/kg, 24 h,<br>603r #3133 | paraquat, 16479, Rat<br>Kidney, 25 mg/kg, 24 h,<br>h, 503r #3134 | phenobarbital, 11494, Rat<br>Kidney, 80 mg/kg, 24 h,<br>H375 #2635 | phenobarbital, 11495, Rat<br>Kidney, 80 mg/kg, 24 h,<br>H375 #2638 |
|---|---|---|--|--|--|
| 14-3-3 zeta                                   | 1.06  | 1.08  | 1.26   | 1.11   | 1.04   |
| 17 beta hydroxysteroid dehydrogenase, type 2  | 1.66  | 1.3   | 1.57   | -1.1   | -1.15  |
| 22kDa integral peroxisomal membrane protein   | 1.05  | -1.04   | -1.08  | -1.21  | -1.24  |
| 25-DX   | 1.01  | 1.24  | 1.14   | -1.19  | 1.01   |
| 25-hydroxyvitamin D3-1 alpha-hydroxylase      | 1.17  | 1.19  | 1.19   | 1.07   | -1   |
| 3-beta-hydroxysteroid dehydrogenase (HSD3B1)  | -1.27   | -1.13   | -1.03  | 1.05   | -1.01  |
| 3-hydroxyisobutyrate dehydrogenase            | -1.37   | -1.22   | -1.23  | 1.02   | 1.13   |
| 3-methyladenine DNA glycosylase               | 1.13  | 1.26  | 1.19   | 1.22   | 1.17   |
| 6S ribosomal protein L5                       | 1.03  | -1.04   | 1.16   | -1.12  | 1.22   |
| 8-oxoguanine DNA glycosylase                  | -1.01   | -1.04   | -1.02  | 1.06   | 1.01   |
| Acetyl-CoA carboxylase                        | -1.6  | -1.54   | -1.48  | -1.02  | -1.4   |
| Acetylcholine receptor epsilon                | -1.42   | -1.13   | -1.48  | -1.07  | -1.09  |
| Activating transcription factor 3             | -1.02   | -1  | -1.03  | -1   | 1.13   |
| Activin receptor type II                      | 1.1   | 1.03  | -1.02  | -1.08  | -1.19  |
| Acyl-CoA dehydrogenase, medium chain          | -1.13   | 1.02  | -1.07  | 1.12   | 1.01   |
| Adenine nucleotide translocator 1             | -1.4  | -1.26   | -1.06  | -1.08  | 1  |
| ADP-ribosylation factor-like protein ARL184   | 1.15  | 1.1   | 1.17   | -1.05  | -1.11  |
| Adrenomedullin                                | 1.01  | -1.04   | -1.09  | -1.07  | -1.01  |
| Adrenomedullin                                | -1.02   | -1  | -1.03  | 1.03   | -1.03  |
| Albustin B1 aldehyde reductase                | -1.35   | -1.21   | 1.05   | -1.26  | 1.02   |
| Alanine aminotransferase                      | 1.04  | 1.06  | 1.09   | 1.11   | -1.07  |
| Alcohol dehydrogenase 1                       | 1.31  | 1.28  | 1.14   | 1.05   | 1.11   |
| Aldehyde dehydrogenase 1                      | -1.13   | -1.06   | -1.1   | -1.32  | -1.06  |
| Aldehyde dehydrogenase 2                      | -1.05   | -1  | -1.02  | 1.01   | 1.1  |
| Aldehyde dehydrogenase, microsomal            | -1.09   | -1.02   | -1.09  | 1.08   | 1.04   |
| Alpha 1 - inhibitor II                        | -1.22   | -1.09   | -1.04  | -1.11  | -1.07  |
| Alpha 1-antitrypsin                           | -1.25   | -1.13   | -1.12  | 1.05   | 1.08   |
| Alpha-1 acid glycoprotein                     | 1.07  | -1.02   | -1.11  | 1.03   | -1   |
| Alpha-1 microglobulin/filipin precursor (Amp) | 1.05  | -1.06   | -1.04  | 1.04   | -1.01  |
| alpha-1,2-fucosyltransferase                  | -1.08   | -1  | -1.04  | -1.07  | -1.12  |
| Alpha-2-macroglobulin                         | 1.03  | -1  | 1  | 1.08   | 1.11   |
| Alpha-2-macroglobulin, sequence 2             | 1.2   | 1.33  | 1.24   | -1.02  | 1.05   |
| Alpha-2-microglobulin                         | 1.17  | 1.01  | 1.07   | 1.02   | -1.01  |
| Alpha-fetoprotein                             | -1.12   | -1.09   | -1.1   | 1  | -1.06  |
| Alpha-fibrinogen                              | 4.73  | 2.36  | 4.97   | 1.21   | 1.11   |
| Alpha-prothymosin                             | 1   | 1.04  | 1.18   | 1.06   | -1.08  |
| Alpha-tubulin                                 | 1.29  | -1.02   | 1.35   | -1.03  | -1.2   |
| Annexin V                                     | -1.22   | -1.11   | -1.02  | -1.24  | -1.19  |
| Apolipoprotein AII                            | 1.2   | 1.15  | 1.11   | 1.21   | 1.38   |
| Apolipoprotein C1                             | -1.15   | -1.08   | -1.1   | -1.14  | 1.08   |
| Apolipoprotein CIII                           | 1.2   | 1.18  | 1.11   | 1.06   | 1.25   |
| Apolipoprotein E                              | -1.38   | -1.22   | -1.34  | 1.13   | -1   |
| Aquepoin-2                                    | -1.63   | -1.5  | -1.69  | 1.06   | -1.13  |
| Aquepoin-3 (AQP3)                             | -1.15   | -1.05   | -1.3   | 1.22   | 1.03   |
| Argininosuccinate lyase                       | 1.12  | 1.28  | 1.16   | 1.17   | 1.16   |
| Argininosuccinate synthetase 1                | -1.33   | -1.07   | -1.22  | 1.06   | 1.16   |
| Aryl hydrocarbon receptor                     | -1.03   | -1.05   | -1.05  | 1.1  | 1.11   |
| Aryl sulfotransferase                         | -1.14   | 1.03  | -1.05  | 1.39   | 1.13   |
| Arylsulfatase B                               | -1.04   | -1.05   | -1.05  | 1.07   | -1.05  |

Table 45

1/13

|   |       |       |       |       |       |       |
|---|-------|-------|-------|-------|-------|-------|
| Aspartate aminotransferase, mitochondrial                           | 1.04  | -1.04 | 1.14  | -1.08 | -1.04 | 1.03  |
| Asparaginase  | -1.76 | -1.58 | -1.58 | -1.19 | -1.15 | 1.08  |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gyk) | -1.44 | -1.25 | -1.26 | -1.09 | 1.11  | -1    |
| ATPase inhibitor [rat mitochondrial IF1 protein]                    | 1.09  | 1.03  | 1.11  | 1.02  | 1.02  | 1.05  |
| Aun   | -1.16 | -1.14 | -1.13 | 1.11  | 1.07  | -1.08 |
| BAK   | 1.08  | 1.09  | 1.07  | -1.3  | -1.11 | -1.14 |
| Bax (alpha)   | -1.02 | 1.03  | -1.09 | 1.06  | 1.01  | 1.06  |
| Bcl-2   | 1.08  | 1.13  | 1.02  | 1     | -1.01 | 1.12  |
| Bcl-XL  | -1.16 | -1.06 | -1.02 | 1.01  | 1     | 1     |
| Beta-actin  | 1.18  | 1.2   | 1.25  | 1.06  | 1.18  | 1.55  |
| Beta-actin, sequence 2  | -1.17 | -1.15 | -1.02 | 1.02  | 1.05  | 1.08  |
| Beta-alanine synthase   | 1.07  | 1.19  | -1.09 | 1.11  | 1.57  | 1.11  |
| Beta-tubulin, class I   | 1.38  | 1.17  | 1.53  | 1.01  | -1.09 | 1     |
| Bedaine homocysteine methyltransferase (BHMT)                       | 2.02  | 1.83  | 1.17  | 1.24  | 1.65  | 1.18  |
| Bile salt export pump (sister of P-glycoprotein)                    | 1.15  | 1.2   | 1.15  | 1.08  | 1.27  | 1.05  |
| Bilirubin UDP-glucuronosyltransferase isozyme 1                     | 1.32  | 1.35  | 1.86  | -1.03 | 1.03  | 1.13  |
| Bilirubin reductase   | 1.2   | 1.09  | 1.08  | 1.11  | -1.33 | -1.05 |
| BRCA1   | -1.05 | -1.06 | -1.13 | 1     | -1.04 | -1.04 |
| c-erb B-2   | 1.03  | 1.03  | -1.05 | 1.08  | 1.06  | 1.09  |
| c-fos   | 1     | 1.01  | -1.01 | 1.19  | 1.03  | 1.02  |
| c-Hras  | -1.01 | 1.02  | 1.09  | -1.01 | 1.08  | 1.05  |
| c-jun   | 1.31  | 1.12  | 1.13  | 1.06  | 1.03  | -1.08 |
| c-myc   | 1.39  | 1.23  | 1.32  | 1.12  | -1    | -1    |
| C-reactive protein  | 1.06  | 1.23  | 1.13  | -1.04 | -1.07 | 1.02  |
| Cal-binding protein   | -1.12 | -1.12 | -1    | -1.03 | -1.08 | -1.09 |
| Calbindin-D (9K)  | 1.16  | 1.02  | -1    | 1.02  | 1.02  | -1.01 |
| Caldesmon-B   | 1.21  | 1.14  | 1.23  | 1.14  | 1.51  | 1.14  |
| Calneon   | -1.1  | -1.02 | -1.03 | 1.29  | 1.16  | 1.50  |
| Calpastin I heavy chain   | 1.82  | 1.18  | 1.76  | 1.13  | 1.05  | 1.1   |
| Calpastin 2   | -1.07 | -1.04 | 1.01  | -1.02 | -1.08 | -1.02 |
| Calreticulin  | 1.12  | 1.18  | 1.19  | 1.2   | 1.15  | 1.29  |
| Carbamoyl multisppecific organic anion transporter                  | 1.55  | 1.29  | 1.82  | -1.01 | 1.04  | -1    |
| Carbamoyl phosphate synthetase I                                    | -1.02 | -1.11 | -1.16 | -1.03 | -1.02 | -1.1  |
| Carbonic anhydrase II   | -1.45 | -1.3  | -1.25 | 1.13  | 1.24  | 1.19  |
| Carbonic anhydrase III  | -1.59 | -1.64 | -1.93 | -1.23 | -1.12 | -1.15 |
| Carbonic anhydrase III, sequence 2                                  | -1.14 | -1.07 | -1.21 | 1.23  | 1.05  | -1.23 |
| Carbonyl reductase  | 1.03  | 1.01  | -1.01 | -1.05 | -1.09 | -1.05 |
| Carotene palmityl-CoA transferase                                   | 1.25  | 1.32  | 1.15  | 1.2   | 1.2   | 1.29  |
| Casein-alpha  | -1.07 | -1.13 | -1.16 | -1.04 | -1.07 | -1.05 |
| Caspase 1   | 1.01  | 1.06  | 1.02  | 1.22  | 1.11  | 1.23  |
| Caspase 2   | -1.34 | -1.12 | -1.28 | -1.09 | -1.11 | -1.05 |
| Caspase 3   | -1.14 | 1.01  | -1.17 | 1.08  | 1.06  | 1.07  |
| Caspase 6   | 1.11  | 1.14  | 1.1   | -1.08 | 1.05  | 1.01  |
| Caspase 7   | -1.13 | -1.06 | -1.1  | -1.02 | 1.05  | 1     |
| Catalase  | 1.29  | 1.44  | 1.17  | 1     | 1.33  | 1.48  |
| Catechol-O-methyltransferase  | 1.21  | 1.2   | 1.03  | 1.05  | 2.14  | 1.17  |
| Cathepsin B   | -1.16 | -1.03 | 1.03  | 1.19  | 1.23  | 1.48  |
| Cathepsin L   | 1.86  | 1.52  | 2.85  | -1.08 | 1.12  | 1.03  |
| Cathepsin L, sequence 2   | 1.8   | 1.43  | 2.42  | -1.16 | 1.06  | 1.01  |
| Cathepsin S   | 1.11  | -1.02 | 1.45  | 1.04  | 1.06  | 1.07  |
| Caveolin-3  | -1.03 | -1.13 | -1.16 | -1.02 | 1.01  | -1.13 |
| CCR-5   | -1.06 | -1.08 | -1.15 | -1    | -1.03 | -1.05 |
| CD44 metastasis suppressor gene                                     | 1.19  | 1.11  | 1.23  | 1.01  | 1     | -1.03 |
| CD62-related protein kinase (NCK)                                   | -1.08 | -1.07 | -1.06 | 1.11  | 1.21  | 1.16  |
| CDK102  | -1.34 | -1.13 | -1.19 | -1.17 | -1.01 | -1.1  |
| CDK108  | -1.78 | -1.55 | -1.45 | -1.06 | -1.01 | -1.02 |
| Cellular nucleic acid binding protein (CNBP)                        | -1.03 | -1.04 | 1.09  | -1.07 | -1.04 | 1.04  |

2/13

Table 45



|   |       |       |       |       |       |       |
|---|-------|-------|-------|-------|-------|-------|
| Cellular retinoic acid binding protein 2    | 1.09  | -1    | -1.04 | 1.08  | -1.32 | -1.11 |
| Ceruloplasmin                               | 1.04  | 1.32  | -1.13 | 1.23  | 1.07  | 1.24  |
| Cholesterol 7-alpha-hydroxylase (P450 VII)  | -1.01 | -1.11 | -1.13 | 1.01  | 1.04  | -1    |
| Cholesteryl esterase                        | -1.32 | -1.22 | -1.1  | 1.19  | 1.05  | -1.02 |
| Choline kinase                              | 1.1   | -1.02 | 1     | 1.05  | 1.03  | 1.08  |
| Ciliary neurotrophic factor                 | 1.01  | -1.02 | 1.05  | 1.09  | 1.02  | 1.02  |
| Clustarin                                   | 1.54  | 1.25  | 1.55  | -1.02 | -1.09 | -1.23 |
| Codrin                                      | 1.02  | -1.07 | 1.17  | -1.03 | 1.04  | 1.04  |
| Collagen type II                            | -1.31 | -1.19 | -1.27 | 1.02  | -1.07 | 1.01  |
| Colony-stimulating factor-1                 | -1.08 | -1.08 | 1.01  | -1.04 | -1.05 | -1.09 |
| Complement component C3                     | 1.23  | -1.01 | 1.08  | -1.03 | 1.02  | -1.01 |
| Complement factor I (CFI)                   | -1.09 | -1.13 | -1.17 | 1.04  | -1.03 | 1.04  |
| Connexin-32                                 | -1.06 | 1.03  | 1.05  | 1.02  | 1.05  | 1.01  |
| Contrapsin-like protease inhibitor (CPI-21) | -1.05 | 1.18  | 1.45  | 1     | -1.02 | -1.08 |
| CTP-phosphocholine cytidylyltransferase     | 1.58  | 1.03  | 1.01  | 1.01  | 1.05  | 1.1   |
| CXCR4                                       | 1.09  | -1.28 | -1.39 | 1.09  | -1.04 | 1.01  |
| Cyclin D1                                   | -1.61 | -1    | 1.01  | -1.03 | -1.04 | -1.05 |
| Cyclin D3                                   | -1.02 | 1.04  | -1.03 | 1.03  | -1.04 | -1.01 |
| Cyclin dependent kinase 2                   | -1    | 1.08  | 1.05  | 1.02  | -1.04 | 1.02  |
| Cyclin dependent kinase 4                   | -1.01 | -1.03 | -1.05 | -1    | -1.01 | -1.08 |
| Cyclin E                                    | 1.05  | 1.08  | 1.15  | -1.08 | -1.1  | -1.06 |
| Cyclin G                                    | 1     | -1.09 | -1.06 | -1.08 | -1.23 | 1.12  |
| Cyclin-dependent kinase 4 inhibitor P27kip1 | -1.09 | -1.36 | -1.62 | 1.01  | 1.01  | -1.11 |
| Cystatin C                                  | -1.54 | -1.41 | -1.09 | -1.02 | -1.06 | -1.01 |
| Cytochrome c oxidase subunit I              | -1.57 | -1.48 | -1.05 | -1.08 | -1.16 | -1.11 |
| Cytochrome c oxidase subunit II             | -1.44 | -1.34 | -1.28 | 1.03  | -1.08 | -1.14 |
| Cytochrome c oxidase subunit IV             | 1.03  | -1.11 | 1.06  | -1.06 | 1.06  | -1.02 |
| Cytochrome P-450M6                          | 1     | 1.05  | -1.05 | 1.45  | 1.17  | -1.04 |
| Cytochrome P450 11A1                        | 1     | 1.03  | 1.14  | 1.1   | 1.01  | 1.15  |
| Cytochrome P450 140M                        | 1.17  | -1.05 | 1.1   | 1.02  | -1.06 | 1.03  |
| Cytochrome P450 17A                         | -1.02 | -1.05 | -1.12 | 1.07  | 1.01  | -1.08 |
| Cytochrome P450 1A1                         | 1.2   | -1.05 | 1.34  | 1.07  | -1.01 | -1.03 |
| Cytochrome P450 1A2                         | 1.04  | -1.05 | -1.09 | 1.03  | -1.01 | -1.04 |
| Cytochrome P450 1B1                         | -1.21 | -1.17 | -1.08 | -1.31 | -1.07 | 1.07  |
| Cytochrome P450 2A3                         | 1.08  | -1.03 | -1.08 | 1.19  | 1.12  | -1.13 |
| Cytochrome P450 2B1/2B2                     | 1.37  | 1.09  | 1.44  | 1.02  | -1.01 | 1.09  |
| Cytochrome P450 2C11                        | 1.23  | 1.12  | 1.16  | 1.19  | 1.02  | -1.11 |
| Cytochrome P450 2C12                        | 1.01  | -1.05 | 1.32  | -1.28 | -1.01 | 1.02  |
| Cytochrome P450 2C23                        | 1.09  | 1.02  | 1.31  | 1     | -1.01 | -1.03 |
| Cytochrome P450 2C39                        | 1.08  | 1.13  | 1.14  | -1.01 | -1.11 | 1.08  |
| Cytochrome P450 2D18                        | 1.25  | 1.26  | 1.26  | 1.33  | 1.54  | -1.06 |
| Cytochrome P450 2E1                         | 1.11  | -1.03 | -1.04 | -1.01 | -1.06 | 1.85  |
| Cytochrome P450 3A1                         | 1.53  | 1.48  | 1.58  | 1.13  | 1.41  | -1.07 |
| Cytochrome P450 4A1                         | 1.48  | 1.53  | 1.71  | 1.02  | 1.08  | 1.29  |
| Cytochrome P450 4A1, 50-mer                 | 1.12  | 1.22  | 1.07  | -1.01 | 1.07  | 1.15  |
| D-dopachrome tautomerase                    | 1.1   | 1.34  | -1.13 | -1.08 | -1.44 | -1.04 |
| Decorin                                     | -1.13 | -1.02 | -1.02 | 1.04  | -1.08 | -1.15 |
| Defender against cell death-1               | -1.06 | -1.03 | 1.01  | -1.01 | -1.13 | -1.04 |
| Deoxyribidine kinase                        | 1.12  | 1.1   | 1.09  | 1.07  | -1.01 | 1.03  |
| Diazepam binding inhibitor                  | -1.13 | -1.1  | -1.05 | 1.07  | -1.09 | 1.09  |
| Dimethylarginine dimethylaminohydrolase     | -1.58 | -1.4  | -1.09 | -1.07 | -1.14 | 1.08  |
| Disulfide isomerase related protein (ERp72) | 1.17  | 1.02  | 1.11  | 1.1   | 1.01  | -1.15 |
| DNA binding protein inhibitor ID2           | -1.02 | 1.12  | 1.08  | 1.4   | 1.18  | 1.12  |
| DNA polymerase beta                         | -1.02 | -1.07 | 1.1   | -1.07 | -1.02 | 1.39  |
| DNA topoisomerase I                         | -1.06 | -1.17 | 1.01  | 1.02  | 1.09  | 1.06  |

3/13

Table 45

|   |       |       |       |       |       |
|---|-------|-------|-------|-------|-------|
| Dopamine receptor D2  | -1.16 | -1.06 | 1.09  | 1.11  | 1.06  |
| Dopamine transporter  | -1.06 | -1.07 | 1     | 1.02  | -1.09 |
| Dynamin-1 (D100)  | 1.06  | -1.06 | 1.05  | -1.06 | 1.08  |
| Dynamin light chain 1   | 1.2   | 1.21  | 1.05  | -1.09 | 1.04  |
| E-selectin  | 1.06  | -1.08 | 1.05  | 1.05  | -1.02 |
| Ecto-ATPase   | 1.67  | 1.43  | -1.09 | -1.07 | -1.06 |
| eIF-4E  | -1.04 | -1.07 | 1.03  | -1.04 | -1    |
| Elongation factor-1 alpha   | -1.04 | 1.1   | -1.01 | 1.08  | 1.17  |
| Emerin  | 1.19  | -1.11 | 1.03  | 1.04  | 1.1   |
| Endogenous retroviral sequences, 5' and 3' LTR                        | 1.54  | 1.81  | 1.31  | -1.03 | 1.14  |
| Endothelin converting enzyme  | 1.1   | 1.25  | 1.13  | 1.35  | 1.34  |
| Endothelin-1  | 1.04  | -1    | -1.01 | -1.02 | 1.05  |
| Enolase alpha   | -1.26 | -1.16 | 1.14  | 1.01  | 1.07  |
| Enoyl CoA hydratase (mitochondrial)                                   | 1.22  | 1.17  | 1.27  | 1.14  | 1.18  |
| Epidermal growth factor   | -3.26 | -2.55 | -1.28 | -1.3  | -1.33 |
| Epithelial sodium channel alpha subunit (alpha-ENaC)                  | 1     | 1     | -1.04 | 1.01  | 1.09  |
| Epoxide hydrolase #2  | 1.12  | 1.11  | -1.21 | -1    | 1.04  |
| Equilibrative nitrobenzylthioinosine-sensitive nucleoside transporter | -1.09 | -1.13 | -1.13 | 1.01  | -1.1  |
| ERG-2   | -2.14 | -1.06 | 1.37  | 1.13  | 1.3   |
| Estrogen receptor   | 1.09  | 1.14  | 1.08  | 1.06  | -1    |
| Extracellular-signal-regulated kinase 1                               | -1.08 | -1.03 | -1.08 | -1.39 | -1.07 |
| F1-ATPase beta subunit  | -1.5  | -1.44 | 1.1   | 1.12  | 1.13  |
| Fas antigen   | 1.21  | 1.2   | 1.06  | 1.2   | 1.16  |
| Fatty acid synthase   | 1.02  | 1.09  | 1.28  | 1.14  | 1.37  |
| Fatty acyl-CoA oxidase  | -1.98 | -1.57 | 1.04  | 1.04  | -4.65 |
| Ferritin H-chain  | 1.84  | 1.78  | 1.06  | 1.2   | 1.33  |
| Fetuin-like protein (FRL885)  | 1.11  | 1.23  | 1.25  | 1.03  | -1.17 |
| Fibrinogen gamma chain  | 1.04  | 1.01  | -1.28 | -1.04 | -1.17 |
| Focal adhesion kinase (pp125FAK)                                      | 1.91  | 1.43  | 1.02  | -1    | -1.17 |
| Four repeat ion channel   | -1.14 | -1.09 | 1.03  | 1.03  | -1.09 |
| Gad65   | 1.02  | 1.06  | 1.14  | 1.17  | 1.01  |
| Gad65T53  | 1.17  | 1.09  | 1     | -1.04 | 1.04  |
| Gad65   | 1.22  | 1.18  | 1.22  | 1.03  | 1.04  |
| Gamma-actin, cytoplasmic  | 1.27  | 1.14  | -1.08 | -1.06 | 1.07  |
| Gamma-glutamyl transpeptidase   | 1.08  | 1.12  | -1.01 | 1     | 1.2   |
| Gap junction membrane channel protein beta 1 (Gjb1)                   | -1.06 | -1.09 | -1.13 | -1.08 | -1.14 |
| Glucokinase   | -1    | 1.02  | -1.02 | 1.06  | -1.16 |
| Glucose transporter 1   | -1.06 | -1.06 | -1.01 | 1.03  | 1.02  |
| Glucose transporter 2   | 1.35  | 1.25  | 1.07  | 1.25  | 1.01  |
| Glucose-6-phosphate dehydrogenase                                     | 1.48  | 1.38  | -1.01 | -1.07 | 1.05  |
| Glucose-regulated protein 78  | 1.26  | 1.21  | 1.1   | 1.03  | 1.28  |
| Glucosylceramide synthase   | 1     | 1.1   | 1.1   | 1.03  | 1     |
| Glutamine synthetase  | -1.18 | -1.04 | 1.07  | 1.01  | 1.14  |
| Glutathione peroxidase  | 1.11  | 1.28  | 1.12  | 1.28  | 1.29  |
| Glutathione reductase   | 1.1   | 1.12  | 1.03  | 1.07  | 1.14  |
| Glutathione S-transferase alpha subunit                               | -1.19 | 1.08  | 1.48  | 1.12  | 1.29  |
| Glutathione S-transferase mu-2  | 1.27  | 2.55  | 1.25  | 1.12  | 1.14  |
| Glutathione S-transferase P1  | 1.37  | 1.43  | -1.13 | 1.08  | 1.05  |
| Glutathione S-transferase theta-1                                     | -1.23 | -1.11 | -1.15 | -1.08 | -1.16 |
| Glutathione S-transferase Ya  | -1.18 | 1.03  | 1.58  | -1.04 | -1.16 |
| Glutathione synthetase  | 1.14  | 1.34  | 1.11  | 1.28  | 1.29  |
| Glyceraldehyde 3-phosphate dehydrogenase                              | 1.25  | 1.12  | 1.11  | 1.41  | 1.55  |
| Glycine methyltransferase   | -1.06 | 1.3   | -1.04 | 1.1   | 1.07  |
| H-rev107  | -1.07 | -1.12 | 1.02  | 1.13  | 1.05  |
| Heme binding protein 23   | 1.25  | -1.07 | -1.04 | -1.08 | -1.16 |
| Heme oxygenase  | -1.43 | 1.15  | -1.26 | -1.01 | 1.07  |
| Hemoglobin alpha 1 chain  | -1.02 | 1.03  | -1.14 | 1.04  | -1.09 |
|   |       |       |       | -1.9  | -1.33 |

|  |       |       |       |       |       |       |
|--|-------|-------|-------|-------|-------|-------|
| Hemopexin  | 1.11  | -1.06 | -1.03 | -1.02 | -1.01 | 1.08  |
| Hepatic lipase   | -1.35 | -1.28 | -1.32 | -1.03 | 1.08  | -3    |
| Hepatocyte growth factor receptor                      | -1.04 | -1.11 | -1.12 | -1.03 | -1.05 | -1.16 |
| Hepatocyte nuclear factor 4                            | -1.63 | -1.44 | -1.36 | -1.22 | -1.24 | -1.18 |
| High affinity IgE receptor gamma chain (FCER1gamma)    | -1.41 | -1.25 | -1.21 | -1.06 | 1.02  | -1.14 |
| Histidine-rich glycoprotein                            | 1.53  | 1.57  | 1.34  | 1.23  | 1.18  | 1.02  |
| Histone 2A   | -1.23 | -1.2  | -1.23 | -1.11 | -1.11 | -1.22 |
| HMG CoA reductase                                      | 1.08  | 1.03  | 1.06  | 1.11  | 1.08  | 1.34  |
| HMG-CoA synthase, cytosolic                            | -1.17 | -1.21 | -1.21 | -1.11 | -1.06 | -1.07 |
| HMG-CoA synthase, mitochondrial                        | 4.6   | 2.96  | 1.96  | 1.09  | 1.05  | -1.08 |
| Hydroxysteroid sulfotransferase a                      | 1.04  | 1.11  | -1.1  | 1.05  | -1.03 | -1.05 |
| Hypoxanthine-quanine phosphoribosyltransferase         | 1.06  | 1.1   | 1.08  | -1.02 | 1.06  | 1.05  |
| Hypoxia-inducible factor 1 alpha                       | 1.16  | 1.06  | 1.12  | 1.11  | 1.08  | 1.16  |
| ID-1   | 1.08  | 1.14  | 1.09  | 1.03  | 1     | 1.08  |
| IgE binding protein                                    | 1.05  | -1.05 | -1.03 | 1.06  | -1.03 | -1.07 |
| IKB-a  | -1.07 | 1.03  | 1.03  | 1.06  | -1.06 | -1.05 |
| Insulin-like growth factor binding protein 1           | 2.2   | 2.02  | 1.83  | -1.14 | 1.08  | -1.05 |
| Insulin-like growth factor binding protein 3           | -1.37 | -1.03 | -1.37 | -1.18 | -1.18 | 1.01  |
| Insulin-like growth factor binding protein 5           | 1.02  | 1.05  | -1.04 | 1.18  | -1.05 | 1.09  |
| Insulin-like growth factor binding protein 6           | -1.05 | -1.22 | -1.29 | -1.19 | -1.37 | -1.22 |
| Insulin-like growth factor 1                           | -1.26 | -1.28 | -1.26 | 1.05  | -1.18 | -1.12 |
| Insulin-like growth factor 1, exon 6                   | -1.06 | 1.06  | -1.15 | -1.04 | -1.27 | -1.11 |
| Integrin beta-4  | 1.03  | 1.02  | 1.09  | -1.08 | -1.06 | -1.04 |
| Integrin beta1   | 1.67  | 1.61  | 1.8   | 1.07  | 1.2   | 1.2   |
| Inter-alpha-inhibitor H4 heavy chain (Ilt4)            | -1.08 | -1.13 | -1.08 | -1.01 | -1.04 | -1.02 |
| Interferon gamma                                       | -1.06 | -1.04 | -1.04 | -1.26 | -1.05 | -1.07 |
| Interferon inducible protein 10                        | 1.04  | -1.07 | -1.09 | 1.22  | 1.08  | -1.08 |
| Interferon related developmental regulator IFRD1 (PC4) | 1.33  | 1.09  | 1.17  | -1.09 | 1.03  | -1.07 |
| Interleukin-1 beta                                     | 1.01  | 1.02  | -1.04 | -1.1  | 1.03  | -1.04 |
| Interleukin-10   | -1.03 | -1.01 | 1.02  | -1.26 | -1.15 | -1.1  |
| Interleukin-18   | 1.08  | 1.02  | 1.05  | -1.07 | -1.05 | -1.06 |
| Interleukin-6  | 1.05  | 1     | 1.08  | 1.07  | -1.01 | 1.1   |
| Intracellular calcium-binding protein (MRP14)          | 1.03  | -1.03 | 1.07  | 1.02  | -1.02 | -1.1  |
| Intracellular calcium-binding protein (MRP6)           | 1.06  | -1.03 | -1.01 | -1.1  | -1.02 | -1.1  |
| Iron-responsive element-binding protein                | 1.94  | 2.29  | 1.55  | -1    | 1.3   | 1     |
| Jagged 1   | -1.16 | -1.13 | -1.17 | -1.01 | -1.01 | 1.04  |
| JNK1 stress activated protein kinase                   | 1.22  | 1.4   | 1.01  | 1.47  | 1.25  | 1.1   |
| K-cadherin   | 1.29  | 1.18  | 1.5   | -1.08 | -1.01 | 1.03  |
| KAI1 metastasis suppressor gene (CD82)                 | -1.07 | -1.07 | -1.16 | 1.17  | 1.08  | 1.17  |
| Keratinocyte growth factor                             | 1.63  | 1.38  | 2.07  | -1.14 | 1.04  | -1.04 |
| L-gulon-gamma-lactone oxidase                          | -1.08 | -1.09 | -1.05 | 1.02  | 1.03  | -1.08 |
| Lactate dehydrogenase-B                                | -1.45 | -1.24 | -1.24 | 1.03  | 1.08  | 1.01  |
| Lectin:cholesterol acyltransferase                     | 1.02  | -1.1  | -1.12 | 1.02  | 1.03  | 1.04  |
| Leptin receptor (faty)                                 | 1.12  | -1.03 | -1.17 | 1.1   | 1.02  | 1.1   |
| Lipopolysaccharide binding protein                     | -1.06 | 1.05  | -1.06 | -1.4  | -1.18 | -1.34 |
| Lipoprotein lipase                                     | 1.3   | 1.32  | 1.03  | 1.18  | 1     | 1.09  |
| Liver fatty acid binding protein                       | 1.1   | -1.03 | 1.04  | 1.03  | -1.03 | 1.05  |
| Low density lipoprotein receptor                       | 1.14  | 1.04  | 1.1   | 1.07  | -1.04 | 1.08  |
| Lysyl hydroxylase                                      | -1.19 | -1.09 | 1     | 1.08  | 1.03  | -1    |
| Lysyl oxidase  | 1.07  | 1.19  | 1.14  | 1.11  | 1.11  | 1.21  |
| Macrophage inflammatory protein-1 alpha                | -1.03 | 1     | 1.06  | 1.05  | 1.11  | 1.05  |
| Macrophage inflammatory protein-2 alpha                | 1.21  | 1.11  | 1.18  | 1.02  | 1     | -1.03 |
| Macrophage metalloelastase                             | -1.07 | -1.11 | -1.22 | 1.05  | -1.02 | 1.02  |
| Major acute phase protein alpha-1                      | 2.04  | 1.41  | 1.58  | 1     | 1     | -1.01 |
| Major basic protein 1                                  | 1.02  | 1.03  | -1.03 | -1.13 | -1.11 | -1.13 |
| Malate dehydrogenase, cytosolic                        | -1.59 | -1.42 | -1.37 | 1.09  | 1.08  | 1.01  |
| Malic enzyme   | -1.51 | -1.4  | 1.01  | -1.1  | -1.34 | -1.27 |

5/13

Table 45

|  |       |       |       |       |       |       |
|--|-------|-------|-------|-------|-------|-------|
| MAP kinase kinase  | -1.06 | -1.09 | -1.07 | 1.01  | -1.03 | -1.08 |
| Maspin   | -1.06 | 1.03  | -1.05 | 1.01  | 1.03  | -1.03 |
| Matrin F/G   | -1.11 | -1.11 | -1.24 | -1.09 | -1.02 | 1.09  |
| Matrix metalloproteinase-1                                       | 1.12  | 1.28  | 1.27  | 1.25  | 1.06  | -1.14 |
| Melanoma-associated antigen ME491                                | 1.26  | 1.15  | 1.29  | -1.07 | 1.05  | 1.02  |
| Membrane bound cytochrome b5                                     | 1.15  | 1.2   | 1.11  | 1.08  | 1.06  | 1.07  |
| Metallothionein 1  | 2.79  | 2.16  | 2.75  | -1.44 | 1.25  | -1.27 |
| Methylacyl-CoA racemase alpha                                    | -1.31 | -1.13 | -1.32 | -1.2  | -1.02 | 1.09  |
| Methylglutaryl-CoA hydratase                                     | 1.06  | 1.08  | 1.01  | -1.01 | 1.02  | 1.01  |
| MHC class II antigen RT1.A1(f) alpha-chain                       | 1.09  | 1.13  | 1.15  | 1.08  | 1.11  | 1.14  |
| MHC class II antigen RT1.B-1 beta-chain                          | -1.05 | -1.34 | -1.51 | -1.17 | -1.11 | -2.19 |
| Mitogen activated protein kinase (P38)                           | 1.07  | 1.08  | 1.07  | 1.11  | -1.01 | 1.08  |
| Monoamine oxidase A  | -1.03 | -1.01 | -1.01 | 1.02  | 1.02  | -1.03 |
| Monoamine oxidase B  | 1.15  | 1.1   | -1.12 | 1.31  | 1.17  | 1.03  |
| Monocyte chemoattractant protein receptor (CCR2)                 | -1.02 | -1.03 | 1.04  | -1.06 | -1.04 | -1.02 |
| Mullerian inhibiting substance                                   | -1.14 | -1.06 | -1.21 | 1.06  | 1.04  | -1.06 |
| Multidrug resistant protein-1                                    | 1.2   | 1.08  | 1.13  | -1.01 | 1.09  | -1.01 |
| Multidrug resistant protein-2                                    | 1.1   | 1     | 1.02  | -1.09 | 1.05  | -1.08 |
| Multidrug resistant protein-3                                    | 1.23  | 1.19  | 1.25  | -1.01 | 1.05  | 1.08  |
| MutL homologue (MLH1)  | -1.04 | 1.04  | 1.08  | 1.1   | -1.03 | 1.06  |
| Mx1 protein  | -1.01 | -1.21 | -1.42 | -1.11 | -1.06 | -1.08 |
| Myelin basic protein   | -1.07 | 1.04  | -1.04 | -1.34 | -1.26 | -1.26 |
| N-cadherin   | 1.01  | 1.02  | 1.01  | -1.01 | 1.07  | 1.07  |
| N-hydroxy-2-acylamino-fluorene sulfotransferase (STIC1)          | -1.27 | -1.17 | -1.2  | -1.09 | -1    | -1.09 |
| Na/K antiporter (APNH1)  | 1.13  | 1.05  | 1.04  | 1.04  | -1    | -1.08 |
| Na/K ATPase alpha-1  | 1.18  | 1.34  | 1.26  | 1.2   | 1.18  | 1.29  |
| NADH-cytochrome b5 reductase                                     | -1.15 | -1.07 | -1.18 | -1.03 | -1.06 | -1.03 |
| NADPH-dependent isocitrate dehydrogenase, cytosolic              | -2.08 | -1.76 | -1.8  | -1.36 | -1.34 | -1.24 |
| NADPH cytochrome P450 oxidoreductase                             | 1.21  | 1.11  | 1.04  | 1.25  | 1.11  | 1.09  |
| NADPH cytochrome P450 reductase                                  | 1.14  | 1.18  | -1.03 | 1.24  | 1.18  | 1.13  |
| NADPH quinone oxidoreductase-1 (DT-diaphorase)                   | -1.06 | -1.03 | -1.01 | 1.27  | 1.25  | 1.11  |
| Nerve growth factor receptor                                     | -1.03 | 1.1   | 1.06  | -1.12 | 1.01  | 1.04  |
| Neurofibronin (NF1 tumor suppressor)                             | 1.05  | 1.03  | 1.01  | 1.08  | 1.02  | 1.02  |
| Neuronal cell adhesion molecule (NCAM)                           | -1.04 | -1.05 | -1.11 | -1    | 1.01  | -1.09 |
| Neuropeptide Y   | 1.01  | -1.12 | -1.13 | 1.04  | -1.14 | -1.07 |
| Neutral endopeptidase 24.11 (enkephalinase)                      | -1.82 | -1.53 | -1.52 | -1.16 | -1.04 | -1.09 |
| NGF-inducible anti-proliferative putative secreted protein (PC3) | 1.63  | 1.24  | 1.71  | 1.04  | -1.07 | 1.01  |
| NIPK   | 1.02  | 1.08  | -1.01 | -1.02 | -1.07 | -1.09 |
| Notch 1  | 1.05  | 1.07  | 1.06  | -1.01 | -1.06 | 1.03  |
| Nucleoside diphosphate kinase beta isoform                       | -1.12 | -1.11 | -1.04 | -1.11 | -1.13 | -1.06 |
| Nucleosome assembly protein                                      | 1.31  | 1.15  | 1.27  | -1.13 | -1.08 | -1.01 |
| Octamer binding protein 1  | 1.03  | 1.09  | -1.02 | 1.06  | -1.02 | 1.02  |
| Organic anion transporter K1                                     | -1.42 | -1.12 | -1.33 | -1    | -1.04 | 1.11  |
| Organic anion transporter K3                                     | -1.33 | -1.12 | -1.32 | 1.08  | 1.09  | 1.18  |
| Organic anion transporting polypeptide 1                         | -1.29 | -1.12 | -1.34 | 1.03  | -1.07 | 1.07  |
| Organic cation transporter 2                                     | -1.3  | -1.24 | -1.23 | 1.01  | -1.07 | 1.07  |
| Organic cation transporter 3                                     | 1.14  | 1.01  | 1.13  | -1.11 | -1.03 | -1    |
| Ornithine aminotransferase                                       | -1.45 | -1.29 | -1.02 | -1.32 | -1.06 | -1.11 |
| Osmotically sensitive protein                                    | -1.12 | -1.05 | 1.15  | 1.23  | 1.09  | 1.09  |
| Osteocalcin  | -1.03 | 1.07  | -1.05 | 1.12  | 1.11  | -1.02 |
| Osteopontin  | 1.62  | 1.48  | 1.64  | 1.16  | 1.2   | 1.2   |
| Oxygen regulated protein 150                                     | 1.26  | 1.23  | 1.57  | -1.33 | 1.01  | -1.15 |
| p53  | 1.07  | 1.02  | 1.13  | -1.01 | -1.04 | -1.04 |
| p55COC   | 1.01  | -1.03 | -1.02 | 1.04  | -1.06 | -1.04 |
| p70 ribosomal protein S6 kinase alpha-1                          | 1.42  | 1.2   | -1.2  | -1.01 | -1.03 | 1.01  |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II)         | -1.51 | -1.25 | -1.35 | -1.07 | 1.08  | -1.07 |
| PAR interacting protein  | 1.21  | 1.1   | 1.29  | -1.09 | -1.07 | -1.13 |

Table 45

|  |       |       |       |       |       |       |
|--|-------|-------|-------|-------|-------|-------|
| Paraoxonase 1                                    | -1.15 | -1.03 | -1.16 | -1.03 | -1.09 | -1.04 |
| Peroxisomal 3-ketocoyl-CoA thiolase 1            | 1.45  | 1.51  | 1.34  | 1.02  | 1.21  | 1.29  |
| Peroxisomal 3-ketocoyl-CoA thiolase 2            | 1.81  | 1.73  | 1.38  | 1.1   | 1.39  | 1.35  |
| Peroxisomal acyl-CoA oxidase                     | 1.75  | 1.83  | 1.61  | 1.16  | 1.47  | 1.64  |
| Peroxisomal multifunctional enzyme type II       | -1.07 | 1.1   | 1.24  | 1.23  | 1.26  | 1.19  |
| Peroxisome assembly factor 1                     | 1.21  | 1.18  | 1.1   | 1.09  | 1.12  | 1.05  |
| Peroxisome assembly factor 2                     | 1.25  | 1.27  | 1.23  | 1.03  | 1.1   | 1.02  |
| Peroxisome proliferator activated receptor alpha | 1.14  | 1.14  | 1.08  | 1.09  | 1.25  | 1.28  |
| Peroxisome proliferator activated receptor gamma | 1     | 1.03  | 1.02  | 1.11  | -1.05 | -1.1  |
| Phase-1 RCT 185                                  | -1.13 | -1.19 | -1.22 | 1.14  | -1.09 | 1     |
| Phase-1 RCT 252                                  | -1.04 | -1.07 | -1.1  | -1.08 | 1.02  | -1.1  |
| Phase-1 RCT-10                                   | -1.36 | -1.2  | -1.31 | 1.03  | 1.12  | 1.06  |
| Phase-1 RCT-101                                  | 1     | 1.02  | -1.04 | 1.09  | 1.16  | 1.16  |
| Phase-1 RCT-102                                  | -1.5  | -1.48 | -1.59 | 1.28  | -1    | 1.12  |
| Phase-1 RCT-103                                  | -1.03 | 1.02  | -1.07 | -1.31 | -1.69 | -1.13 |
| Phase-1 RCT-106                                  | -1.06 | -1.06 | 1.02  | -1.07 | -1.14 | -1.09 |
| Phase-1 RCT-107                                  | 1.09  | 1.14  | 1.2   | -1    | 1.13  | 1.03  |
| Phase-1 RCT-108                                  | -1.02 | 1.04  | -1.03 | -1.57 | -1.36 | -1.18 |
| Phase-1 RCT-109                                  | 1.02  | 1     | 1.15  | -1.12 | -1.11 | -1.1  |
| Phase-1 RCT-110                                  | 1     | -1.17 | -1.28 | -1.06 | -1.08 | -1.13 |
| Phase-1 RCT-111                                  | 1.04  | 1.02  | -1.06 | -1.32 | -1.54 | -1.16 |
| Phase-1 RCT-112                                  | -1    | -1.12 | -1.19 | 1.01  | -1.09 | -1.13 |
| Phase-1 RCT-113                                  | -1.05 | 1.01  | -1.09 | 1.04  | 1.02  | 1.14  |
| Phase-1 RCT-114                                  | -1.09 | -1.07 | -1.17 | -1    | -1.07 | 1.08  |
| Phase-1 RCT-115                                  | 1.01  | 1.01  | -1.03 | 1     | 1.12  | -1.05 |
| Phase-1 RCT-116                                  | 1.01  | -1.01 | -1.01 | 1.01  | -1.02 | -1.06 |
| Phase-1 RCT-117                                  | 1.08  | 1.07  | -1.05 | 1.1   | 1.46  | 1.05  |
| Phase-1 RCT-118                                  | 1     | -1.02 | -1.03 | 1.01  | -1.25 | -1.17 |
| Phase-1 RCT-119                                  | -1.06 | -1.15 | -1.26 | -1.05 | -1.04 | -1.12 |
| Phase-1 RCT-12                                   | -1.01 | 1.09  | 1.01  | -1.11 | -1.11 | -1.07 |
| Phase-1 RCT-121                                  | -1.02 | 1.03  | -1.1  | 1.08  | 1     | -1.08 |
| Phase-1 RCT-122                                  | 1.15  | 1.03  | 1     | 1.04  | 1.05  | 1.06  |
| Phase-1 RCT-123                                  | -1.06 | -1.08 | -1.19 | -1.11 | -1.53 | -1.07 |
| Phase-1 RCT-125                                  | -1.12 | -1.04 | -1.14 | -1.01 | -1.03 | -1.13 |
| Phase-1 RCT-126                                  | 1.22  | 1.2   | 1.16  | 1.23  | 1.07  | 1.01  |
| Phase-1 RCT-127                                  | 1.17  | 1     | -1.09 | -1.01 | 1.11  | -1.08 |
| Phase-1 RCT-128                                  | 1.04  | -1    | -1.07 | -1    | 1.08  | -1.06 |
| Phase-1 RCT-129                                  | 1.01  | -1.03 | 1.05  | 1.22  | -1.07 | 1.11  |
| Phase-1 RCT-13                                   | -1.04 | 1.41  | 1.21  | -1.72 | 1.15  | 1.29  |
| Phase-1 RCT-130                                  | -1.08 | -1.02 | -1.11 | -1.11 | -1.1  | -1.06 |
| Phase-1 RCT-131                                  | -2.19 | -1.93 | -1.79 | -1.1  | -1.32 | -1.16 |
| Phase-1 RCT-132                                  | 1.1   | -1.19 | -1.15 | -1.01 | -1.05 | 1.14  |
| Phase-1 RCT-133                                  | 1.04  | 1.05  | 1.21  | -1.1  | -1.03 | -1.05 |
| Phase-1 RCT-134                                  | -1.04 | -1.03 | 1.01  | 1.07  | 1.12  | 1.07  |
| Phase-1 RCT-136                                  | -1.08 | -1.06 | -1.05 | -1.06 | 1.01  | 1     |
| Phase-1 RCT-137                                  | 1.25  | 1.31  | 1.49  | -1.06 | 1.02  | -1.04 |
| Phase-1 RCT-138                                  | -1.18 | -1.17 | -1.16 | -1.08 | -1.06 | -1.14 |
| Phase-1 RCT-14                                   | 1.02  | 1.08  | -1.02 | -1.02 | -1.15 | -1.05 |
| Phase-1 RCT-140                                  | -1.02 | 1.06  | -1.02 | -1    | -1.03 | 1.09  |
| Phase-1 RCT-141                                  | 1.38  | 1.34  | 1.21  | -1.02 | 1.03  | 1.04  |
| Phase-1 RCT-142                                  | -1.43 | -1.27 | -1.27 | -1.06 | -1.11 | -1.07 |
| Phase-1 RCT-143                                  | -1.57 | -1.48 | -1.35 | 1.02  | -1.04 | 1.01  |
| Phase-1 RCT-144                                  | 1.08  | -1.06 | 1.2   | -1.14 | -1.19 | -1.15 |
| Phase-1 RCT-145                                  | 1.15  | 1.03  | 1.23  | 1.02  | -1.03 | -1.01 |
| Phase-1 RCT-146                                  | 1     | -1.07 | 1.02  | 1.01  | -1.05 | -1.01 |
| Phase-1 RCT-147                                  | -1.09 | -1.04 | -1.06 | -1.59 | -1.86 | -1.39 |
| Phase-1 RCT-148                                  | -1.03 | 1.09  | -1.07 | 1.03  | 1.15  | 1.05  |

Table 45

7/13

|                 |       |       |       |       |       |       |       |       |       |
|-----------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Phase-1 RCT-149 | 1.77  | 1.31  | 1.15  | -1.09 | -1.09 | -1.09 | -1.07 | -1.07 | -1.07 |
| Phase-1 RCT-15  | 1.06  | 1.02  | 1.03  | 1.11  | 1.11  | 1.06  | 1.06  | 1.06  | 1.1   |
| Phase-1 RCT-150 | -1.14 | -1.04 | -1.17 | 1.05  | 1.05  | 1.25  | 1.25  | 1.07  | 1.1   |
| Phase-1 RCT-151 | -1.2  | -1.1  | -1.21 | -1.21 | 1.07  | 1.02  | 1.02  | 1.08  | 1.08  |
| Phase-1 RCT-152 | -1.04 | -1.11 | 1.2   | -1.04 | -1.06 | -1.06 | -1.06 | -1.04 | -1.04 |
| Phase-1 RCT-153 | -1.44 | -1.29 | -1.31 | -1.31 | -1.06 | -1.02 | -1.02 | -1.09 | -1.09 |
| Phase-1 RCT-154 | -1.07 | -1.09 | -1.02 | -1.02 | 1.03  | -1.09 | -1.09 | 1.08  | 1.08  |
| Phase-1 RCT-155 | -1.1  | -1.04 | -1.15 | -1.15 | -1.04 | -1.04 | -1.04 | -1.07 | -1.07 |
| Phase-1 RCT-156 | 1.04  | -1.03 | -1    | -1    | -1.07 | -1.25 | -1.25 | -1.08 | -1.08 |
| Phase-1 RCT-158 | 1.86  | 1.35  | 2.56  | 2.56  | -1.04 | 1.65  | 1.65  | 1.06  | 1.06  |
| Phase-1 RCT-160 | 1.03  | -1.11 | -1.08 | 1     | 1     | 1.04  | 1.04  | 1.06  | 1.06  |
| Phase-1 RCT-161 | -1.3  | -1.39 | -1.29 | -1.29 | -1.03 | -1.07 | -1.07 | -1.08 | -1.08 |
| Phase-1 RCT-162 | -1.09 | -1.13 | -1.01 | -1.01 | 1.02  | -1.01 | -1.01 | 1.02  | 1.02  |
| Phase-1 RCT-164 | 1.15  | 1.05  | 1.01  | 1.17  | 1.17  | 1.11  | 1.11  | 1.39  | 1.39  |
| Phase-1 RCT-166 | -1.29 | -1.14 | 1     | -1.22 | -1.22 | 1.16  | 1.16  | -1    | -1    |
| Phase-1 RCT-168 | 1.21  | 1.11  | 1.26  | 1.02  | 1.02  | 1.01  | 1.01  | 1.09  | 1.09  |
| Phase-1 RCT-169 | -1.04 | -1.11 | -1.19 | -1.02 | -1.02 | -1.04 | -1.04 | -1.07 | -1.07 |
| Phase-1 RCT-17  | 1.02  | 1.19  | 1.01  | 1.08  | 1.08  | 1.04  | 1.04  | -1.02 | -1.02 |
| Phase-1 RCT-170 | -1.08 | -1.03 | -1.16 | -1.1  | -1.1  | -1.35 | -1.35 | -1.28 | -1.28 |
| Phase-1 RCT-173 | -1.37 | -1.1  | -1.38 | -1.05 | -1.05 | -1.03 | -1.03 | 1.11  | 1.11  |
| Phase-1 RCT-174 | -1.01 | -1.08 | -1.01 | 1.1   | 1.1   | 1.02  | 1.02  | -1.01 | -1.01 |
| Phase-1 RCT-175 | -1.46 | -1.3  | -1.23 | -1.05 | -1.05 | -1.02 | -1.02 | 1.13  | 1.13  |
| Phase-1 RCT-176 | -1.02 | -1.01 | 1.04  | 1.1   | 1.1   | 1.18  | 1.18  | 1.11  | 1.11  |
| Phase-1 RCT-177 | 1.06  | 1.08  | 1.15  | -1.14 | -1.14 | -1.07 | -1.07 | 1.07  | 1.07  |
| Phase-1 RCT-178 | -1.7  | -1.13 | -1.6  | -1.03 | -1.03 | -2.05 | -2.05 | 1.03  | 1.03  |
| Phase-1 RCT-179 | 1.15  | 1.1   | 1.48  | -1.11 | -1.11 | 1.01  | 1.01  | 1.03  | 1.03  |
| Phase-1 RCT-18  | -1.14 | -1.19 | -1.2  | -1.09 | -1.09 | -1.01 | -1.01 | -1.04 | -1.04 |
| Phase-1 RCT-180 | 1.09  | 1.11  | 1.23  | -1.01 | -1.01 | -1.02 | -1.02 | 1.03  | 1.03  |
| Phase-1 RCT-181 | -1.11 | -1.1  | -1.13 | -1.09 | -1.09 | 1.09  | 1.09  | -1.03 | -1.03 |
| Phase-1 RCT-182 | -2.1  | -1.79 | -1.67 | -1.18 | -1.18 | -1.1  | -1.1  | -1.2  | -1.2  |
| Phase-1 RCT-184 | 1.05  | -1.05 | -1.05 | -1.03 | -1.03 | -1.02 | -1.02 | -1.08 | -1.08 |
| Phase-1 RCT-185 | 1.39  | 1.24  | 1.06  | -1.03 | -1.03 | -1.18 | -1.18 | 1.3   | 1.3   |
| Phase-1 RCT-187 | -1.2  | -1.14 | -1.19 | 1.03  | 1.03  | -1.03 | -1.03 | 1.06  | 1.06  |
| Phase-1 RCT-188 | -1.13 | -1.11 | -1.08 | -1.03 | -1.03 | 1.04  | 1.04  | 1.07  | 1.07  |
| Phase-1 RCT-189 | 1.31  | 1.24  | 1.26  | 1.26  | 1.26  | 1.14  | 1.14  | 1.03  | 1.03  |
| Phase-1 RCT-191 | 1.25  | 1.22  | 1.12  | -1.04 | -1.04 | 1.06  | 1.06  | 1.01  | 1.01  |
| Phase-1 RCT-192 | -1.11 | -1.04 | 1.03  | 1.08  | 1.08  | 1.13  | 1.13  | 1.15  | 1.15  |
| Phase-1 RCT-193 | 1.12  | -1.04 | -1.04 | -1.04 | -1.04 | -1.03 | -1.03 | -1.05 | -1.05 |
| Phase-1 RCT-194 | -1    | -1.1  | -1.09 | 1     | 1     | 1.04  | 1.04  | -1.08 | -1.08 |
| Phase-1 RCT-195 | 1.01  | -1.05 | -1.04 | -1.04 | -1.04 | -1.04 | -1.04 | -1.02 | -1.02 |
| Phase-1 RCT-196 | 1.05  | 1.06  | 1.18  | 1.01  | 1.01  | 1.05  | 1.05  | 1.06  | 1.06  |
| Phase-1 RCT-197 | -1.1  | -1.09 | -1.07 | -1.07 | -1.07 | 1.05  | 1.05  | -1.05 | -1.05 |
| Phase-1 RCT-198 | -1    | -1.02 | 1.18  | -1.01 | -1.01 | -1.02 | -1.02 | -1.01 | -1.01 |
| Phase-1 RCT-199 | 2.1   | 1.64  | 2.01  | -1.01 | -1.01 | 1.01  | 1.01  | -1.01 | -1.01 |
| Phase-1 RCT-2   | 1.05  | -1.03 | -1.06 | -1.06 | -1.06 | 1.01  | 1.01  | -1.15 | -1.15 |
| Phase-1 RCT-20  | -1    | -1.06 | -1.03 | 1.03  | 1.03  | 1.04  | 1.04  | -1.01 | -1.01 |
| Phase-1 RCT-202 | -1.1  | -1.08 | -1.01 | 1.01  | 1.01  | 1.07  | 1.07  | 1.01  | 1.01  |
| Phase-1 RCT-204 | 1.01  | -1.07 | -1.23 | -1.22 | -1.22 | -1.09 | -1.09 | -1.08 | -1.08 |
| Phase-1 RCT-205 | -1.18 | -1.15 | -1.01 | -1.02 | -1.02 | 1.01  | 1.01  | -1.02 | -1.02 |
| Phase-1 RCT-206 | -1.03 | -1.11 | -1.1  | -1.03 | -1.03 | -1.02 | -1.02 | -1.02 | -1.02 |
| Phase-1 RCT-207 | 1.14  | 1.16  | 1.26  | -1.05 | -1.05 | 1.05  | 1.05  | -1.02 | -1.02 |
| Phase-1 RCT-208 | 1.12  | 1.05  | 1.02  | -1.02 | -1.02 | 1     | 1     | 1.13  | 1.13  |
| Phase-1 RCT-209 | 1.21  | 1.22  | 1.29  | 1.02  | 1.02  | 1     | 1     | 1.11  | 1.11  |
| Phase-1 RCT-21  | 1.04  | -1.04 | 1.04  | -1.01 | -1.01 | -1.17 | -1.17 | -1.19 | -1.19 |
| Phase-1 RCT-211 | -1.01 | 1.02  | 1.06  | -1.17 | -1.17 | -1.01 | -1.01 | -1.14 | -1.14 |
| Phase-1 RCT-212 | -1.08 | -1.01 | -1.04 | 1     | 1     | 1.04  | 1.04  | -1.05 | -1.05 |
| Phase-1 RCT-213 | -1.08 | -1.02 | 1.03  | -1.06 | -1.06 | -1.07 | -1.07 | 1.1   | 1.1   |

8/13

Table 45

|                 |       |       |       |       |       |       |       |
|-----------------|-------|-------|-------|-------|-------|-------|-------|
| Phase-1 RCT-214 | -1.02 | -1.01 | -1.1  | 1.09  | 1.05  | 1.05  | -1    |
| Phase-1 RCT-215 | 1.05  | 1     | 1.09  | 1.11  | 1.06  | 1.02  | -1.02 |
| Phase-1 RCT-216 | 1.05  | -1.04 | -1.1  | -1.02 | -1.01 | 1.06  | 1.06  |
| Phase-1 RCT-218 | -1.01 | -1.14 | -1.26 | -1.04 | -1.04 | -1.04 | -1.04 |
| Phase-1 RCT-219 | -1.02 | -1.11 | -1.13 | -1.02 | -1    | 1.02  | 1.02  |
| Phase-1 RCT-22  | -1.16 | -1.05 | -1.12 | -1.05 | -1.16 | -1.04 | -1.04 |
| Phase-1 RCT-220 | -1.06 | -1.02 | -1.05 | 1.09  | -1.29 | 1.02  | 1.02  |
| Phase-1 RCT-221 | -1.03 | 1.03  | -1.05 | 1.02  | -1.03 | -1.07 | -1.07 |
| Phase-1 RCT-222 | -1.02 | -1.03 | -1.09 | 1     | -1.03 | -1.02 | -1.02 |
| Phase-1 RCT-225 | 1     | -1.1  | -1.15 | 1.06  | 1.09  | -1.02 | -1.02 |
| Phase-1 RCT-227 | -1.06 | -1.15 | -1.2  | -1.04 | -1.06 | -1.12 | -1.12 |
| Phase-1 RCT-228 | 1.03  | 1.03  | -1.08 | -1.07 | -1.16 | -1.05 | -1.05 |
| Phase-1 RCT-229 | -1.03 | -1.14 | -1.25 | -1.02 | -1.11 | -1.05 | -1.05 |
| Phase-1 RCT-230 | -1.05 | -1.06 | -1.22 | 1.05  | -1.11 | -1.04 | -1.04 |
| Phase-1 RCT-231 | 1.11  | 1.02  | 1.03  | 1.03  | 1.05  | 1.14  | 1.14  |
| Phase-1 RCT-233 | 1.07  | 1.02  | -1.06 | 1.02  | 1.02  | -1.11 | -1.11 |
| Phase-1 RCT-235 | -1.07 | -1.09 | -1.01 | -1.18 | -1.16 | -1.18 | -1.18 |
| Phase-1 RCT-236 | -1.02 | -1.07 | -1.05 | 1.07  | 1     | 1.03  | 1.03  |
| Phase-1 RCT-237 | 1.13  | -1    | -1.1  | 1.05  | 1.05  | 1.07  | 1.07  |
| Phase-1 RCT-239 | 1.12  | 1.01  | -1.04 | -1.04 | -1.01 | -1.13 | -1.13 |
| Phase-1 RCT-24  | 1.35  | 1.14  | 1.39  | -1    | -1.02 | -1    | -1    |
| Phase-1 RCT-240 | 1.04  | 1.05  | 1     | 1.11  | 1.01  | -1.01 | -1.01 |
| Phase-1 RCT-241 | 1.52  | 1.25  | 1.57  | -1.01 | 1.05  | 1.09  | 1.09  |
| Phase-1 RCT-242 | 1.82  | 1.31  | 1.88  | 1.04  | 1.06  | -1.12 | -1.12 |
| Phase-1 RCT-243 | -1.05 | -1    | -1.01 | -1.02 | -1.03 | -1.08 | -1.08 |
| Phase-1 RCT-244 | -1.14 | 1.04  | -1.04 | 1.08  | -1.01 | 1.06  | 1.06  |
| Phase-1 RCT-245 | 1.01  | -1.06 | -1.13 | 1.17  | 1     | 1.11  | 1.11  |
| Phase-1 RCT-246 | 1.07  | -1.07 | -1.1  | 1     | 1.04  | 1.07  | 1.07  |
| Phase-1 RCT-248 | 1.05  | -1.04 | -1.1  | -1.07 | -1.05 | -1.11 | -1.11 |
| Phase-1 RCT-25  | -1.3  | -1.15 | -1.13 | 1.05  | 1.05  | -1.02 | -1.02 |
| Phase-1 RCT-251 | 1.04  | -1.05 | -1.17 | -1    | 1.06  | 1.12  | 1.12  |
| Phase-1 RCT-253 | -1.41 | -1.12 | -1.22 | 1.09  | 1.16  | 1.2   | 1.2   |
| Phase-1 RCT-255 | -1.03 | -1.1  | -1.15 | -1.07 | -1.01 | -1.09 | -1.09 |
| Phase-1 RCT-256 | -1.09 | -1.04 | -1.28 | -1.01 | 1.01  | 1.01  | 1.01  |
| Phase-1 RCT-258 | 1.13  | 1.03  | 1.2   | -1.02 | -1.02 | 1.02  | 1.02  |
| Phase-1 RCT-259 | 1.04  | -1.01 | -1.01 | -1    | 1.01  | -1.12 | -1.12 |
| Phase-1 RCT-26  | -1.15 | -1.12 | -1.21 | -1.01 | 1.05  | 1.08  | 1.08  |
| Phase-1 RCT-260 | -1.07 | -1.08 | -1.17 | 1.02  | 1.11  | -1.07 | -1.07 |
| Phase-1 RCT-261 | 1.1   | 1.02  | -1.08 | 1.04  | 1.03  | 1.1   | 1.1   |
| Phase-1 RCT-262 | -1.01 | -1.14 | -1.16 | -1.01 | 1.02  | -1.04 | -1.04 |
| Phase-1 RCT-263 | -1.02 | 1     | -1.02 | -1.02 | 1.06  | 1.05  | 1.05  |
| Phase-1 RCT-264 | -1.04 | -1.07 | -1.08 | -1.04 | -1.04 | -1.08 | -1.08 |
| Phase-1 RCT-266 | -1    | 1.02  | -1.04 | 1.02  | -1.03 | 1.01  | 1.01  |
| Phase-1 RCT-267 | 1.19  | -1.07 | 1.02  | -1.07 | 1.12  | 1.18  | 1.18  |
| Phase-1 RCT-268 | -1.03 | -1.09 | -1.19 | 1.02  | -1.05 | -1.11 | -1.11 |
| Phase-1 RCT-27  | 1.26  | 1.13  | 1.1   | -1.13 | -1.17 | -1.07 | -1.07 |
| Phase-1 RCT-270 | -1.16 | -1.14 | -1.13 | -1    | 1.06  | -1.02 | -1.02 |
| Phase-1 RCT-271 | -1.39 | -1.1  | -1.26 | 1.08  | 1     | 1.18  | 1.18  |
| Phase-1 RCT-273 | -1.09 | -1.02 | -1.13 | 1.06  | -1    | -1    | -1    |
| Phase-1 RCT-274 | 1.53  | 1.27  | 1.59  | -1.01 | -1.08 | -1.18 | -1.18 |
| Phase-1 RCT-276 | 1.01  | -1.07 | -1.02 | -1.12 | 1.04  | -1.07 | -1.07 |
| Phase-1 RCT-277 | 1.07  | -1.03 | -1.06 | 1.05  | -1.01 | 1.03  | 1.03  |
| Phase-1 RCT-278 | 1.04  | -1.08 | -1.07 | -1.07 | -1.11 | -1.08 | -1.08 |
| Phase-1 RCT-279 | -1.06 | -1.13 | -1.17 | -1.05 | -1.06 | -1.09 | -1.09 |
| Phase-1 RCT-28  | 1.03  | -1.02 | -1.07 | 1.03  | 1     | -1.04 | -1.04 |
| Phase-1 RCT-280 | 1.05  | -1    | -1.06 | 1     | 1.05  | 1.12  | 1.12  |
| Phase-1 RCT-281 | -1.07 | -1.02 | -1.1  | -1.22 | -1.13 | 1.04  | 1.04  |

9/13

Table 45

|                 |       |       |       |       |       |       |
|-----------------|-------|-------|-------|-------|-------|-------|
| Phase-1 RCT-282 | -1.15 | -1.18 | -1.17 | -1.07 | -1.04 | -1.04 |
| Phase-1 RCT-283 | -1.04 | -1.03 | -1.06 | -1.03 | -1.07 | -1.03 |
| Phase-1 RCT-284 | 1.03  | -1.01 | -1.07 | -1.11 | -1.05 | -1.03 |
| Phase-1 RCT-285 | -1.03 | -1.03 | -1.07 | -1.01 | -1.05 | 1.08  |
| Phase-1 RCT-286 | 1.04  | -1.05 | -1.02 | 1.05  | -1    | -1.01 |
| Phase-1 RCT-287 | -1.01 | -1.01 | -1.02 | -1.06 | 1.03  | -1.08 |
| Phase-1 RCT-288 | 1.01  | 1.04  | -1.08 | 1.03  | 1.02  | -1.01 |
| Phase-1 RCT-289 | -1.03 | 1.01  | -1    | -1.01 | 1.05  | 1.14  |
| Phase-1 RCT-290 | -1.08 | -1.16 | -1.18 | -1    | -1.04 | -1.03 |
| Phase-1 RCT-291 | 1.24  | -1.15 | 1.03  | 1.06  | 1.19  | 1.05  |
| Phase-1 RCT-292 | -1.02 | -1.08 | -1.2  | 1.08  | 1.23  | 1.08  |
| Phase-1 RCT-293 | -1.1  | -1.08 | -1.06 | 1.04  | -1    | -1.01 |
| Phase-1 RCT-294 | 1.44  | 1.34  | 1.51  | 1.14  | -1.15 | -1.04 |
| Phase-1 RCT-295 | -1.08 | -1.13 | -1.2  | 1.07  | -1.11 | -1.05 |
| Phase-1 RCT-296 | -1.04 | 1.01  | 1.06  | 1.07  | 1.06  | 1.08  |
| Phase-1 RCT-297 | 1.02  | -1.03 | -1.03 | 1.03  | -1.08 | -1.08 |
| Phase-1 RCT-298 | 1.02  | -1.05 | -1.06 | 1.09  | -1.08 | -1.08 |
| Phase-1 RCT-299 | -1.01 | -1.05 | -1.11 | 1.01  | -1.01 | -1.07 |
| Phase-1 RCT-300 | 1.01  | -1.02 | -1.13 | 1.02  | 1.03  | 1.03  |
| Phase-1 RCT-301 | -1.3  | -1.28 | -1.15 | 1.04  | 1     | 1.03  |
| Phase-1 RCT-302 | 1.05  | 1.02  | -1.03 | -1.08 | -1.07 | 1     |
| Phase-1 RCT-303 | -1.01 | -1.06 | -1.1  | -1.04 | 1.07  | 1.01  |
| Phase-1 RCT-304 | -1.48 | -1.27 | -1.18 | 1.04  | 1.06  | 1.25  |
| Phase-1 RCT-305 | -1.19 | -1.12 | -1.17 | 1.1   | -1    | 1.06  |
| Phase-1 RCT-306 | -1.04 | -1.05 | -1.13 | -1.01 | 1.04  | -1.07 |
| Phase-1 RCT-307 | -1.45 | -1.4  | -1.4  | -1.16 | -1.07 | 1.01  |
| Phase-1 RCT-308 | -1.19 | -1.04 | -1.24 | 1.06  | 1.04  | 1.13  |
| Phase-1 RCT-309 | 1.16  | 1.16  | 1.03  | -1.08 | 1.23  | 1.02  |
| Phase-1 RCT-310 | -1.01 | -1.17 | 1.21  | -1.18 | -1    | -1.04 |
| Phase-1 RCT-311 | -1.07 | -1.06 | -1.22 | 1.01  | -1.03 | -1.12 |
| Phase-1 RCT-312 | -1.3  | -1.07 | -1.29 | 1.11  | 1.13  | 1.04  |
| Phase-1 RCT-313 | -1.02 | -1.01 | -1.03 | -1.01 | -1.06 | -1.06 |
| Phase-1 RCT-314 | 1.09  | 1     | 1.03  | 1.07  | 1.04  | 1.06  |
| Phase-1 RCT-315 | 1     | 1.03  | -1.06 | -1.03 | -1.03 | -1.03 |
| Phase-1 RCT-316 | -1.23 | -1.07 | -1.11 | 1.12  | 1.07  | 1.11  |
| Phase-1 RCT-317 | 1.1   | 1.1   | 1.1   | -1.14 | -1.02 | -1.16 |
| Phase-1 RCT-318 | 1.86  | 1.36  | 1.91  | 1.03  | -1.01 | 1.01  |
| Phase-1 RCT-319 | -1.05 | -1.09 | -1.14 | -1    | -1.01 | 1.04  |
| Phase-1 RCT-320 | -1.08 | -1.15 | -1.14 | -1.16 | 1.05  | 1.04  |
| Phase-1 RCT-321 | -1    | 1.12  | -1.07 | -1.11 | -1.15 | -1.06 |
| Phase-1 RCT-322 | 1.08  | -1.04 | -1.02 | -1.03 | 1.07  | 1.05  |
| Phase-1 RCT-323 | -1.04 | 1.01  | 1.11  | -1.04 | -1.1  | 1.02  |
| Phase-1 RCT-324 | -1.04 | -1.08 | -1.06 | 1.04  | 1.1   | 1.06  |
| Phase-1 RCT-325 | 1.07  | 1.07  | 1.02  | 1.02  | -1.01 | 1.02  |
| Phase-1 RCT-326 | -1.05 | -1.08 | -1.04 | 1.14  | 1.1   | 1.19  |
| Phase-1 RCT-327 | 1.23  | 1.08  | -1.06 | 1.08  | 1.21  | 1.1   |
| Phase-1 RCT-328 | -1.12 | -1.08 | -1.1  | -1.06 | -1.06 | -1.03 |
| Phase-1 RCT-329 | 1.07  | 1.02  | 1.09  | 1.02  | -1.01 | -1.01 |
| Phase-1 RCT-330 | -1.05 | -1.11 | 1.03  | 1.03  | -1    | 1.05  |
| Phase-1 RCT-331 | -1.28 | -1.14 | -1.14 | -1.24 | 1     | 1.15  |
| Phase-1 RCT-332 | 1.04  | 1.01  | -1.03 | -1.17 | -1.18 | -1.14 |
| Phase-1 RCT-333 | -1.16 | 1     | -1.1  | 1.05  | -1.08 | -1.05 |
| Phase-1 RCT-334 | 1.2   | 1.1   | 1.16  | 1.25  | 1.37  | 1.44  |
| Phase-1 RCT-335 | -1.12 | -1    | 1.12  | 1.03  | -1.01 | -1.02 |
| Phase-1 RCT-336 | -1.02 | 1.01  | 1.42  | -1.03 | -1.02 | -1.11 |
| Phase-1 RCT-337 | 1.37  | 1.16  | 1.42  | -1    | 1.05  | 1.04  |
| Phase-1 RCT-338 | 1.1   | 1.13  | 1.13  | -1.16 | -1.13 | 1.04  |

Table 45

10/13



|  |       |       |       |       |       |       |
|--|-------|-------|-------|-------|-------|-------|
| Phase-1 RCT-7                                  | -1.04 | -1.06 | -1.02 | 1.03  | 1.08  | 1.2   |
| Phase-1 RCT-70                                 | 1.04  | -1    | 1.04  | 1.07  | 1.08  | -1    |
| Phase-1 RCT-71                                 | 1.02  | -1.01 | 1.04  | 1.07  | -1.04 | -1.1  |
| Phase-1 RCT-72                                 | 1.13  | 1.04  | 1.22  | 1.06  | -1.02 | 1.05  |
| Phase-1 RCT-73                                 | -1.05 | -1.1  | -1.08 | -1.06 | -1.09 | 1.02  |
| Phase-1 RCT-74                                 | 1.02  | -1.11 | -1.14 | -1.02 | -1.01 | -1.06 |
| Phase-1 RCT-75                                 | 1.09  | 1.03  | 1.1   | -1.04 | 1.14  | 1.19  |
| Phase-1 RCT-76                                 | 1.05  | 1.01  | -1.01 | -1.23 | -1.18 | -1.07 |
| Phase-1 RCT-77                                 | -1.19 | -1.15 | -1.03 | 1.13  | 1.1   | 1.16  |
| Phase-1 RCT-78                                 | -1.4  | -1.37 | -1.42 | 1.19  | -1    | 1.05  |
| Phase-1 RCT-79                                 | -1.06 | -1.16 | -1.04 | 1.03  | 1     | 1.01  |
| Phase-1 RCT-8                                  | -1.16 | -1.13 | -1.1  | -1.12 | -1.01 | -1.01 |
| Phase-1 RCT-80                                 | -1.04 | -1.09 | -1.13 | 1.01  | 1.02  | -1.11 |
| Phase-1 RCT-81                                 | 1.01  | 1.04  | -1.08 | -1.05 | -1.05 | -1.07 |
| Phase-1 RCT-82                                 | -1.01 | -1.14 | -1.1  | -1.01 | 1.01  | -1.08 |
| Phase-1 RCT-83                                 | -1.23 | -1.13 | -1.1  | 1     | 1.05  | -1.06 |
| Phase-1 RCT-84                                 | 1     | -1.05 | -1.1  | -1.06 | -1.09 |       |
| Phase-1 RCT-85                                 | 1.08  | 1.01  | -1.02 | -1.05 | 1.01  | 1.07  |
| Phase-1 RCT-87                                 | -1.15 | -1.13 | -1.04 | 1.02  | 1     | -1.04 |
| Phase-1 RCT-88                                 | 1.25  | 1.21  | 1.08  | 1.06  | 1.07  | -1.03 |
| Phase-1 RCT-89                                 | -1.13 | -1.16 | -1.28 | -1.09 | -1.01 | -1    |
| Phase-1 RCT-9                                  | 1.02  | -1    | 1.04  | -1.07 | -1.6  | -1.2  |
| Phase-1 RCT-90                                 | -1.06 | -1.19 | -1.27 | -1.07 | -1.1  | -1.1  |
| Phase-1 RCT-91                                 | -1.02 | -1.05 | -1.01 | -1.09 | -1.06 | -1.01 |
| Phase-1 RCT-92                                 | 1.09  | -1.07 | -1.03 | 1.06  | 1     | -1.08 |
| Phase-1 RCT-93                                 | -1.13 | -1.17 | -1.24 | -1.03 | 1.04  | -1.08 |
| Phase-1 RCT-94                                 | 1.01  | -1.04 | -1.11 | -1    | 1.02  | -1    |
| Phase-1 RCT-95                                 | -1    | 1.02  | -1.03 | -1.11 | -1.24 | -1.08 |
| Phase-1 RCT-96                                 | 1.08  | 1.06  | 1.03  | -1.03 | 1.06  | 1.05  |
| Phase-1 RCT-97                                 | 1.08  | -1.02 | 1.01  | 1.06  | 1     | 1.02  |
| Phase-1 RCT-99                                 | 1.1   | 1.16  | 1.25  | 1.09  | 1.15  | 1.23  |
| Phenylalanine hydroxylase                      | -1.73 | -1.46 | -1.3  | -1.11 | 1.16  | 1.07  |
| Phosphatidylethanolamine-binding protein       | 1.14  | 1.13  | -1.04 | 1.07  | 1.14  | 1.17  |
| Phosphoglycerate kinase                        | -1.22 | -1.23 | -1.07 | -1.01 | 1.09  | 1.03  |
| Phospholipase D                                | -1.01 | -1.1  | -1.15 | -1    | -1.09 | -1.04 |
| Plin1, proto-oncogene                          | 1.04  | 1.08  | 1.06  | 1.01  | 1.09  | -1.09 |
| Poly(ADP-ribose) polymerase                    | 1.04  | 1.03  | 1.06  | 1.18  | 1.1   | -1.09 |
| Proalbumin                                     | 1.03  | -1.04 | -1.01 | -1.03 | 1.01  | -1.08 |
| Proalbumin, sequence 2                         | 1.08  | -1.02 | -1    | -1.12 | -1.09 | -1.07 |
| Presenilin-1                                   | -1.15 | -1.14 | -1.11 | -1.25 | -1.12 | -1.05 |
| Proliferating cell nuclear antigen gene        | 1     | 1.02  | 1.07  | -1.03 | -1.03 | -1.06 |
| Prostaglandin H synthase                       | -1.05 | -1.02 | -1.05 | 1.11  | 1.09  | 1.05  |
| Protease activator 28 alpha                    | -1.15 | -1.05 | 1.21  | -1.07 | -1.04 | -1.07 |
| Protein disulfide isomerase (PDI)              | -1.08 | -1.05 | -1.01 | -1.05 | 1.02  | -1.02 |
| Protein kinase C alpha                         | -1.09 | -1.02 | -1    | -1.05 | 1.04  | -1.06 |
| Protein kinase C beta1                         | 2.32  | 1.88  | 2.51  | -1.43 | 1.28  | -1.14 |
| Protein tyrosine phosphatase alpha             | -1.06 | -1.01 | -1.08 | 1.02  | -1.06 | -1.08 |
| Protein tyrosine phosphatase, receptor type, D | -1    | 1.02  | -1.09 | -1.07 | 1.08  | -1.03 |
| PTEN/MAC1                                      | -1.15 | -1.06 | -1.07 | -1.2  | -1.04 | 1.02  |
| Putative membrane fatty acid transporter       | -1.04 | -1.11 | -1.38 | -1.03 | -1.38 | -1.13 |
| Pyruvate kinase, muscle                        | 1.25  | 1.11  | 1.11  | 1.16  | -1.17 | -1.05 |
| RAAC protein kinase beta                       | 1.06  | 1.13  | 1.04  | 1.02  | -1.02 | -1.05 |
| RAO  | 1     | 1.03  | 1.01  | 1.17  | 1.04  | 1.14  |
| Raf1   | 1.21  | 1.03  | 1.28  | 1.07  | 1.06  | 1.09  |
| Renal organic anion transporter                | 1.34  | 1.32  | 1.38  | 1.03  | 1.16  | 1.03  |
| Retinoid X receptor alpha                      | -1.03 | 1.04  | -1.01 | 1.01  | 1.06  | -1    |
| Retinol dehydrogenase type III                 | 1.01  | -1.05 | -1.06 | 1.29  | 1.04  | 1.07  |

Table 45

11/13

|   |       |       |       |       |       |       |
|---|-------|-------|-------|-------|-------|-------|
| Retinol-binding protein (RBP)                                       | -1.1  | 1.52  | 1.16  | -1.19 | 1.21  | -1.18 |
| Ribosomal protein L13   | 1.09  | -1    | 1.09  | -1.01 | -1.08 | -1.13 |
| Ribosomal protein L13A  | 1.08  | 1.11  | 1.16  | -1.08 | -1.11 | -1.08 |
| Ribosomal protein L27   | -1.17 | -1.15 | 1.06  | -1.08 | -1.04 | -1.05 |
| Ribosomal protein S17   | -1.11 | -1.15 | 1.02  | 1.05  | 1.01  | 1.05  |
| Ribosomal protein S8  | -1.09 | -1.14 | 1.15  | 1.01  | 1.01  | -1.03 |
| Ribosomal protein S9  | 1.06  | -1.01 | 1.06  | -1.33 | -1.46 | -1.23 |
| S-adenosylmethionine decarboxylase                                  | -1.15 | -1.03 | -1.07 | 1.04  | 1.08  | 1.03  |
| S-adenosylmethionine synthetase                                     | 1.02  | 1.06  | -1.06 | 1.36  | 1.55  | 1.35  |
| Sarcoplasmic reticulum calcium ATPase                               | -1.02 | 1.02  | -1.09 | 1.11  | 1.11  | 1.14  |
| Scavenger receptor class B type I                                   | 1.09  | -1.05 | 1.02  | 1     | -1.04 | -1.05 |
| Scleritin-4   | -1.03 | -1.14 | -1.3  | -1.05 | -1.07 | -1.15 |
| Selenoprotein P   | -1.68 | -1.18 | -1.34 | 1.23  | 1.24  | 1.12  |
| Serine protease marker protein-30                                   | -2.12 | -1.47 | -1.6  | 1.12  | -1.32 | 1.08  |
| Serotonin transporter (SERT)  | -1.25 | -1.21 | -1.17 | 1.05  | 1.05  | -1.05 |
| Sodium/bile acid cotransporter                                      | -1.11 | 1.04  | 1.03  | 1.56  | 1.21  | 1.15  |
| Sodium/glucose cotransporter 1                                      | -1.4  | -1.28 | 1.09  | -1.05 | -1.12 | -1.08 |
| Sorbitol dehydrogenase  | -1.19 | -1.05 | -1.05 | 1.11  | 1.37  | 1.39  |
| Statins   | -1.14 | -1    | -1.02 | -1.15 | -1.1  | -1.03 |
| Stearyl-CoA desaturase, liver                                       | -5.31 | -3.34 | -4.36 | 1.09  | -8.31 | -4.23 |
| Stem cell factor  | -1.63 | -1.29 | -1.46 | 1     | -1.22 | 1.01  |
| Stem cell protein 2   | 1.01  | -1    | 1.04  | 1.04  | 1.13  | 1.09  |
| Sulfotransferase K2   | -2.34 | -1.89 | -1.25 | 1.13  | 1.38  | 1.21  |
| Superoxide dismutase Cu/Zn  | -1.2  | -1.13 | -1.14 | -1.22 | -1.23 | 1.06  |
| Superoxide dismutase Mn   | 1.04  | 1.04  | 1.07  | 1.09  | 1.12  | 1.09  |
| Suppressor of cytokine signaling 3                                  | 1.14  | 1.11  | 1.1   | 1.05  | 1.01  | -1.02 |
| Syndecan-1  | -1.09 | -1.11 | -1.14 | -1.06 | -1.04 | -1.06 |
| T-cell cytoplasmic  | -1.22 | -1.2  | -1.02 | -1.18 | -1.07 | 1.01  |
| TGF-beta receptor type II   | -1.08 | 1.03  | 1.09  | -1.01 | 1.1   | 1.11  |
| Thiol-specific antioxidant (natural killer cell-enhancing factor B) | -1.01 | 1     | 1.06  | -1.08 | -1.09 | -1.03 |
| Thioguanine methyltransferase                                       | -1    | 1.09  | 1.02  | -1.1  | -1.21 | -1.2  |
| Thioredoxin-1 (Trx1)  | 1.16  | 1.18  | 1.27  | -1.12 | -1.12 | -1.03 |
| Thioredoxin-2 (Trx2)  | -1.27 | -1.13 | -1.04 | 1.14  | 1.14  | 1.14  |
| Thrombin receptor (PAR-1)   | 1.04  | 1.09  | 1.1   | 1.09  | 1     | 1.25  |
| Thrombospondin  | 1.13  | 1.14  | 1.32  | 1.05  | 1.03  | 1.03  |
| Thymidylate synthase  | -1.02 | -1.01 | -1.03 | 1.02  | -1.09 | -1.04 |
| Thymosin beta-10  | 1.06  | 1.04  | 1.06  | -1.22 | -1.21 | -1.29 |
| Tissue factor   | 1.08  | 1.09  | 1.19  | 1.16  | 1.02  | 1.07  |
| Tissue factor pathway inhibitor                                     | -1.08 | -1.04 | -1.1  | 1.05  | 1.01  | 1.1   |
| Tissue inhibitor of metalloproteinases-1                            | 1.4   | 1.18  | 1.33  | -1    | 1.01  | -1.05 |
| Tissue inhibitor of metalloproteinases-3                            | -1.09 | 1.03  | -1.03 | 1.07  | -1.08 | 1.06  |
| Tissue plasminogen activator  | 1.13  | 1.1   | 1.15  | -1.09 | -1.1  | -1.1  |
| Transferrin   | 1.83  | 1.71  | 1.8   | 1.24  | -1.09 | -1.1  |
| Transforming growth factor-beta3                                    | -1.04 | 1.06  | -1.05 | 1.04  | 1.04  | -1.04 |
| Transitional endoplasmic reticulum ATPase                           | 1.05  | 1.02  | 1.14  | -1.02 | 1.05  | -1.09 |
| Transferrin   | 1.04  | 1.07  | -1    | 1.05  | -1.12 | 1.06  |
| Tryptophan hydroxylase  | -1.15 | 1.07  | -1.18 | 1.03  | 1.08  | -1.03 |
| Tyrosine aminotransferase   | -1.01 | 1.04  | -1.03 | 1.01  | -1.12 | -1.01 |
| Tyrosine hydroxylase  | -1.13 | -1.04 | -1.09 | -1.01 | -1.03 | -1.04 |
| Ubiquitin protein kinase receptor (UFO)                             | -1.01 | -1.02 | -1.08 | 1.08  | 1.04  | -1.01 |
| Ubiquitin conjugating enzyme (RAD 6 homologue)                      | -1.04 | -1.08 | 1.12  | -1.08 | -1.51 | -1.16 |
| UDP-glucuronosyltransferase   | 1.25  | 1.07  | 2.03  | -1.41 | 1.02  | -1.25 |
| UDP-glucuronosyltransferase 1A6                                     | 1.37  | 1.41  | 1.63  | -1.03 | -1.01 | 1.14  |
| UDP-glucuronosyltransferase 2B                                      | 1.31  | 1.25  | 1.94  | -1.4  | -1.04 | -1.19 |
| Uncoupling protein 2  | -1.2  | -1.09 | -1.06 | -1.18 | -1.24 | -1.14 |
| Urate oxidase   | 1.14  | 1.17  | 1.05  | 1.1   | 1.16  | 1.16  |
| Urokinase plasminogen activator receptor                            | -1.02 | 1.03  | -1.08 | -1.01 | -1.12 | -1.05 |

Table 45

12/13

|  |       |       |       |       |       |       |
|--|-------|-------|-------|-------|-------|-------|
| Vascular cell adhesion molecule 1 (VCAM-1) | 1.13  | 1.04  | 1.09  | 1.02  | -1.05 | 1.02  |
| Vascular endothelial growth factor         | 1.03  | 1.04  | 1.01  | 1.04  | -1.11 | 1.06  |
| Very long-chain acyl-CoA dehydrogenase     | 1.09  | 1.04  | 1.08  | -1.01 | -1.04 | 1.03  |
| Very long-chain acyl-CoA synthetase        | 1.16  | 1.55  | 1.53  | -1.01 | -1.07 | 1.28  |
| Vesicular monoamine transporter (VMAT)     | -1.02 | 1.04  | -1.01 | 1.01  | 1.02  | -1.06 |
| VL30 element                               | 1.4   | 1.75  | 1.24  | 1.71  | -1.4  | 1.04  |
| Wat1                                       | 1.12  | 1.08  | 1.06  | 1.08  | -1    | 1.05  |
| Zinc finger protein                        | 1.71  | 1.42  | 1.89  | 1.12  | 1.13  | 1.08  |
| (Phase-1 RCT-98)                           | 1.02  | -1.17 | -1.24 | -1.08 | -1.23 | 1.09  |
| (Phase-1 RCT-100)                          | 1.3   | 1.2   | 1.03  | 1.21  | 1.01  | -1.07 |
| (Phase-1 RCT-167)                          | 1.06  | -1.01 | 1.09  | -1.17 | -1.03 | 1.1   |
| (Phase-1 RCT-171)                          | -1.27 | -1.05 | -1.1  | 1.07  | 1.02  | -1.05 |
| (Phase-1 RCT-190)                          | -1.38 | -1.37 | -1.19 | 1.01  | -1    | -1.04 |
| (Phase-1 RCT-1)                            | 1.1   | 1.02  | 1.19  | -1.1  | 1.01  | -1.06 |
| (Phase-1 RCT-200)                          | -1.14 | -1.11 | -1.1  | -1.35 | -1.15 | -1.82 |
| (Phase-1 RCT-247)                          | -1.1  | -1.35 | -1.62 | -1.05 | -1.06 | -1.14 |
| (Phase-1 RCT-265)                          | 1.17  | -1.05 | 1.04  | -1.17 | -1.3  | -1.1  |
| (Phase-1 RCT-268)                          | 1.05  | -1.06 | -1.02 | 1.25  | -1    | -1.02 |
| (Phase-1 RCT-272)                          | 1.04  | 1.01  | 1.02  | -1.07 | 1.13  | 1.13  |
| (Phase-1 RCT-275)                          | 1.01  | -1.01 | 1.32  | -1.18 | -1.92 | -1.36 |
| (Phase-1 RCT-5)                            | -1.05 | 1.01  | 1.15  | -1.11 | 1.06  | -1.14 |
| (PST-II)                                   | -1.55 | -1.29 | -1.48 | -1.11 | 1     | -1.02 |
| Ribosomal protein L6                       | 1.04  | -1.03 | 1.18  | -1.04 |       |       |

Table 45

13/13

Table 38. Expression Data for the 0 hour Timepoint

| Compound-Dose | Animal Number | Kidney Toxicity Classification | Gene Name | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 | 526 | 527 | 528 | 529 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 538 | 539 | 540 | 541 | 542 | 543 | 544 | 545 | 546 | 547 | 548 | 549 | 550 | 551 | 552 | 553 | 554 | 555 | 556 | 557 | 558 | 559 | 560 | 561 | 562 | 563 | 564 | 565 | 566 | 567 | 568 | 569 | 570 | 571 | 572 | 573 | 574 | 575 | 576 | 577 | 578 | 579 | 580 | 581 | 582 | 583 | 584 | 585 | 586 | 587 | 588 | 589 | 590 | 591 | 592 | 593 | 594 | 595 | 596 | 597 | 598 | 599 | 600 | 601 | 602 | 603 | 604 | 605 | 606 | 607 | 608 | 609 | 610 | 611 | 612 | 613 | 614 | 615 | 616 | 617 | 618 | 619 | 620 | 621 | 622 | 623 | 624 | 625 | 626 | 627 | 628 | 629 | 630 | 631 | 632 | 633 | 634 | 635 | 636 | 637 | 638 | 639 | 640 | 641 | 642 | 643 | 644 | 645 | 646 | 647 | 648 | 649 | 650 | 651 | 652 | 653 | 654 | 655 | 656 | 657 | 658 | 659 | 660 | 661 | 662 | 663 | 664 | 665 | 666 | 667 | 668 | 669 | 670 | 671 | 672 | 673 | 674 | 675 | 676 | 677 | 678 | 679 | 680 | 681 | 682 | 683 | 684 | 685 | 686 | 687 | 688 | 689 | 690 | 691 | 692 | 693 | 694 | 695 | 696 | 697 | 698 | 699 | 700 | 701 | 702 | 703 | 704 | 705 | 706 | 707 | 708 | 709 | 710 | 711 | 712 | 713 | 714 | 715 | 716 | 717 | 718 | 719 | 720 | 721 | 722 | 723 | 724 | 725 | 726 | 727 | 728 | 729 | 730 | 731 | 732 | 733 | 734 | 735 | 736 | 737 | 738 | 739 | 740 | 741 | 742 | 743 | 744 | 745 | 746 | 747 | 748 | 749 | 750 | 751 | 752 | 753 | 754 | 755 | 756 | 757 | 758 | 759 | 760 | 761 | 762 | 763 | 764 | 765 | 766 | 767 | 768 | 769 | 770 | 771 | 772 | 773 | 774 | 775 | 776 | 777 | 778 | 779 | 780 | 781 | 782 | 783 | 784 | 785 | 786 | 787 | 788 | 789 | 790 | 791 | 792 | 793 | 794 | 795 | 796 | 797 | 798 | 799 | 800 | 801 | 802 | 803 | 804 | 805 | 806 | 807 | 808 | 809 | 810 | 811 | 812 | 813 | 814 | 815 | 816 | 817 | 818 | 819 | 820 | 821 | 822 | 823 | 824 | 825 | 826 | 827 | 828 | 829 | 830 | 831 | 832 | 833 | 834 | 835 | 836 | 837 | 838 | 839 | 840 | 841 | 842 | 843 | 844 | 845 | 846 | 847 | 848 | 849 | 850 | 851 | 852 | 853 | 854 | 855 | 856 | 857 | 858 | 859 | 860 | 861 | 862 | 863 | 864 | 865 | 866 | 867 | 868 | 869 | 870 | 871 | 872 | 873 | 874 | 875 | 876 | 877 | 878 | 879 | 880 | 881 | 882 | 883 | 884 | 885 | 886 | 887 | 888 | 889 | 890 | 891 | 892 | 893 | 894 | 895 | 896 | 897 | 898 | 899 | 900 | 901 | 902 | 903 | 904 | 905 | 906 | 907 | 908 | 909 | 910 | 911 | 912 | 913 | 914 | 915 | 916 | 917 | 918 | 919 | 920 | 921 | 922 | 923 | 924 | 925 | 926 | 927 | 928 | 929 | 930 | 931 | 932 | 933 | 934 | 935 | 936 | 937 | 938 | 939 | 940 | 941 | 942 | 943 | 944 | 945 | 946 | 947 | 948 | 949 | 950 | 951 | 952 | 953 | 954 | 955 | 956 | 957 | 958 | 959 | 960 | 961 | 962 | 963 | 964 | 965 | 966 | 967 | 968 | 969 | 970 | 971 | 972 | 973 | 974 | 975 | 976 | 977 | 978 | 979 | 980 | 981 | 982 | 983 | 984 | 985 | 986 | 987 | 988 | 989 | 990 | 991 | 992 | 993 | 994 | 995 | 996 | 997 | 998 | 999 | 1000 | 1001 | 1002 | 1003 | 1004 | 1005 | 1006 | 1007 | 1008 | 1009 | 1010 | 1011 | 1012 | 1013 | 1014 | 1015 | 1016 | 1017 | 1018 | 1019 | 1020 | 1021 | 1022 | 1023 | 1024 | 1025 | 1026 | 1027 | 1028 | 1029 | 1030 | 1031 | 1032 | 1033 | 1034 | 1035 | 1036 | 1037 | 1038 | 1039 | 1040 | 1041 | 1042 | 1043 | 1044 | 1045 | 1046 | 1047 | 1048 | 1049 | 1050 | 1051 | 1052 | 1053 | 1054 | 1055 | 1056 | 1057 | 1058 | 1059 | 1060 | 1061 | 1062 | 1063 | 1064 | 1065 | 1066 | 1067 | 1068 | 1069 | 1070 | 1071 | 1072 | 1073 | 1074 | 1075 | 1076 | 1077 | 1078 | 1079 | 1080 | 1081 | 1082 | 1083 | 1084 | 1085 | 1086 | 1087 | 1088 | 1089 | 1090 | 1091 | 1092 | 1093 | 1094 | 1095 | 1096 | 1097 | 1098 | 1099 | 1100 | 1101 | 1102 | 1103 | 1104 | 1105 | 1106 | 1107 | 1108 | 1109 | 1110 | 1111 | 1112 | 1113 | 1114 | 1115 | 1116 | 1117 | 1118 | 1119 | 1120 | 1121 | 1122 | 1123 | 1124 | 1125 | 1126 | 1127 | 1128 | 1129 | 1130 | 1131 | 1132 | 1133 | 1134 | 1135 | 1136 | 1137 | 1138 | 1139 | 1140 | 1141 | 1142 | 1143 | 1144 | 1145 | 1146 | 1147 | 1148 | 1149 | 1150 | 1151 | 1152 | 1153 | 1154 | 1155 | 1156 | 1157 | 1158 | 1159 | 1160 | 1161 | 1162 | 1163 | 1164 | 1165 | 1166 | 1167 | 1168 | 1169 | 1170 | 1171 | 1172 | 1173 | 1174 | 1175 | 1176 | 1177 | 1178 | 1179 | 1180 | 1181 | 1182 | 1183 | 1184 | 1185 | 1186 | 1187 | 1188 | 1189 | 1190 | 1191 | 1192 | 1193 | 1194 | 1195 | 1196 | 1197 | 1198 | 1199 | 1200 | 1201 | 1202 | 1203 | 1204 | 1205 | 1206 | 1207 | 1208 | 1209 | 1210 | 1211 | 1212 | 1213 | 1214 | 1215 | 1216 | 1217 | 1218 | 1219 | 1220 | 1221 | 1222 | 1223 | 1224 | 1225 | 1226 | 1227 | 1228 | 1229 | 1230 | 1231 | 1232 | 1233 | 1234 | 1235 | 1236 | 1237 | 1238 | 1239 | 1240 | 1241 | 1242 | 1243 | 1244 | 1245 | 1246 | 1247 | 1248 | 1249 | 1250 | 1251 | 1252 | 1253 | 1254 | 1255 | 1256 | 1257 | 1258 | 1259 | 1260 | 1261 | 1262 | 1263 | 1264 | 1265 | 1266 | 1267 | 1268 | 1269 | 1270 | 1271 | 1272 | 1273 | 1274 | 1275 | 1276 | 1277 | 1278 | 1279 | 1280 | 1281 | 1282 | 1283 | 1284 | 1285 | 1286 | 1287 | 1288 | 1289 | 1290 | 1291 | 1292 | 1293 | 1294 | 1295 | 1296 | 1297 | 1298 | 1299 | 1300 | 1301 | 1302 | 1303 | 1304 | 1305 | 1306 | 1307 | 1308 | 1309 | 1310 | 1311 | 1312 | 1313 | 1314 | 1315 | 1316 | 1317 | 1318 | 1319 | 1320 | 1321 | 1322 | 1323 | 1324 | 1325 | 1326 | 1327 | 1328 | 1329 | 1330 | 1331 | 1332 | 1333 | 1334 | 1335 | 1336 | 1337 | 1338 | 1339 | 1340 | 1341 | 1342 | 1343 | 1344 | 1345 | 1346 | 1347 | 1348 | 1349 | 1350 | 1351 | 1352 | 1353 | 1354 | 1355 | 1356 | 1357 | 1358 | 1359 | 1360 | 1361 | 1362 | 1363 | 1364 | 1365 | 1366 | 1367 | 1368 | 1369 | 1370 | 1371 | 1372 | 1373 | 1374 | 1375 | 1376 | 1377 | 1378 | 1379 | 1380 | 1381 | 1382 | 1383 | 1384 | 1385 | 1386 | 1387 | 1388 | 1389 | 1390 | 1391 | 1392 | 1393 | 1394 | 1395 | 1396 | 1397 | 1398 | 1399 | 1400 | 1401 | 1402 | 1403 | 1404 | 1405 | 1406 | 1407 | 1408 | 1409 | 1410 | 1411 | 1412 | 1413 | 1414 | 1415 | 1416 | 1417 | 1418 | 1419 | 1420 | 1421 | 1422 | 1423 | 1424 | 1425 | 1426 | 1427 | 1428 | 1429 | 1430 | 1431 | 1432 | 1433 | 1434 | 1435 | 1436 | 1437 | 1438 | 1439 | 1440 | 1441 | 1442 | 1443 | 1444 | 1445 | 1446 | 1447 | 1448 | 1449 | 1450 | 1451 | 1452 | 1453 | 1454 | 1455 | 1456 | 1457 | 1458 | 1459 | 1460 | 1461 | 1462 | 1463 | 1464 | 1465 | 1466 | 1467 | 1468 | 1469 | 1470 | 1471 | 1472 | 1473 | 1474 | 1475 | 1476 | 1477 | 1478 | 1479 | 1480 | 1481 | 1482 | 1483 | 1484 | 1485 | 1 |
|---------------|---------------|--------------------------------|-----------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---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|---------------|---------------|--------------------------------|-----------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---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Page 34

|   |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|---|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| CD44 transmembrane adhesion protein       | 0.8873562 | 0.8978942 | 1.0011665 | 0.9236263 | 1.0090098 | 0.9811188 | 0.9205001 | 0.8774257 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Phase 1 RCT-387                           | 0.9132789 | 0.9249865 | 1.0228072 | 0.9324965 | 0.94444   | 0.9804072 | 0.9468776 | 0.8809058 | 1.1935623 | 0.8354142 | 0.8735653 | 1.2867781 | 1.0534588 | 0.9225440 | 0.9204649 | 0.9204649 | 0.9204649 | 0.9204649 |
| Phase 1 RCT-314                           | 0.9118106 | 0.9249862 | 1.0228072 | 0.9324965 | 0.94444   | 0.9804072 | 0.9468776 | 0.8809058 | 1.1935623 | 0.8354142 | 0.8735653 | 1.2867781 | 1.0534588 | 0.9225440 | 0.9204649 | 0.9204649 | 0.9204649 | 0.9204649 |
| Transitional endoplasmic reticulum ATPase | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Sevconin translocator (SERT)              | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Phase 1 RCT-305                           | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Phase 1 RCT-4                             | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Phase 1 RCT-6                             | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Hydroxyl-oxidizable factor 1 alpha        | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Phase 1 RCT-194                           | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Transferrin                               | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Alpha-fetoprotein                         | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Phosphorylating protein-2                 | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Phosphorylating protein-3                 | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Phase 1 RCT-40                            | 0.9084299 | 0.9087716 | 1.0071028 | 0.9172763 | 1.0272335 | 0.9811037 | 0.9471034 | 0.8917038 | 1.2620505 | 1.0533487 | 0.8736152 | 0.9107233 | 1.1813260 | 1.0653468 | 0.9887607 | 0.9306419 | 0.8887402 | 0.9145020 |
| Phase 1 RCT-41                            | 0.9084299 | 0.9087716 |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |

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Table 39

[illegible]









[illegible]



|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| 0.8457345 | 0.5904134 | 1.0027861 | 2.3602249 | 0.8211078 | 0.9544874 | 1.0270458 | 1.2049045 | 0.5304575 | 1.0087186 | 0.8611919 | 0.8714237 | 0.8115005 | 0.7223705 | 0.8762791 | 1.0115206 | 0.8718873 | 0.8053509 | 0.8119017 | 0.8847859 | 0.9471254 | 1.1024452 | 1.4594895 | 0.9874007 |
| 1.1782583 | 0.8752403 | 1.1208177 | 1.3572324 | 1.0712660 | 0.7372860 | 0.9572940 | 0.9258782 | 1.3333796 | 1.2333796 | 1.0075480 | 0.7803144 | 1.2167807 | 1.1658927 | 1.2595881 | 0.8147275 | 0.8017937 | 0.8053509 | 0.8119017 | 0.8847859 | 0.9471254 | 1.1024452 | 1.4594895 | 0.9874007 |
| 0.8734020 | 0.8718605 | 0.8176668 | 1.0086477 | 0.9702569 | 0.9572940 | 0.9258782 | 1.3333796 | 1.2333796 | 1.0075480 | 0.7803144 | 1.2167807 | 1.1658927 | 1.2595881 | 0.8147275 | 0.8017937 | 0.8053509 | 0.8119017 | 0.8847859 | 0.9471254 | 1.1024452 | 1.4594895 | 0.9874007 |           |
| 0.8715007 | 0.8170184 | 1.0471064 | 0.8021820 | 0.8243477 | 0.8946455 | 0.9400218 | 1.1944091 | 0.8973005 | 1.1201869 | 0.8337305 | 1.011324  | 1.0753284 | 1.0115338 | 1.0713560 | 0.8085233 | 1.1737327 | 1.2731078 | 1.1732529 | 1.2875118 | 1.7934823 | 1.10128   | 0.8940875 | 1.0118064 |
| 0.7711520 | 0.5905556 | 0.9310096 | 0.8247137 | 0.9074654 | 0.9400218 | 1.1944091 | 0.8973005 | 1.1201869 | 0.8337305 | 1.011324  | 1.0753284 | 1.0115338 | 1.0713560 | 0.8085233 | 1.1737327 | 1.2731078 | 1.1732529 | 1.2875118 | 1.7934823 | 1.10128   | 0.8940875 | 1.0118064 |           |
| 0.6265822 | 0.8775314 | 1.7004262 | 0.9400901 | 0.8977655 | 0.9400901 | 0.8977655 | 0.9400901 | 0.8977655 | 0.9400901 | 0.8977655 | 0.9400901 | 0.8977655 | 0.9400901 | 0.8977655 | 0.9400901 | 0.8977655 | 0.9400901 | 0.8977655 | 0.9400901 | 0.8977655 | 0.9400901 | 0.8977655 | 0.9400901 |
| 0.3455553 | 0.2841172 | 0.3125358 | 0.8403735 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 |
| 0.6456994 | 0.8524248 | 1.164487  | 0.9202783 | 0.8947738 | 0.880441  | 0.9138733 | 1.0106955 | 0.9782614 | 1.1841927 | 0.7924707 | 0.8509404 | 1.0819532 | 1.2276198 | 1.2601918 | 1.251428  | 1.452384  | 1.2617852 | 1.2706538 | 1.2421463 | 1.0889133 | 1.0889133 | 1.0889133 | 1.0889133 |
| 0.9801014 | 0.84273   | 1.7500255 | 0.3716803 | 0.9547037 | 0.8947738 | 0.880441  | 0.9138733 | 1.0106955 | 0.9782614 | 1.1841927 | 0.7924707 | 0.8509404 | 1.0819532 | 1.2276198 | 1.2601918 | 1.251428  | 1.452384  | 1.2617852 | 1.2706538 | 1.2421463 | 1.0889133 | 1.0889133 | 1.0889133 |
| 0.5454027 | 0.0524583 | 0.0254068 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 |
| 0.8772438 | 0.0524583 | 0.0254068 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 |
| 0.8772438 | 0.0524583 | 0.0254068 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 | 0.9400901 |
| 0.8427414 | 1.1537765 | 0.9716678 | 0.9400901 |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |













[illegible]

Table 38

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| 1.017937  | 0.972504  | 0.544267  | 1.002613  | 0.867964  | 0.724262  | 0.6221762 | 0.6357132 | 1.0520075 | 0.8671623 | 1.0002084 | 1.0426455 | 0.9176731 | 1.0480468 | 1.0094457 | 1.0400432 | 1.2527760 | 0.8771460 | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.9539194 | 1.126002  | 1.016946  | 0.8118301 | 1.180446  | 1.180773  | 0.9077039 | 1.0327716 | 1.0262781 | 1.0326718 | 1.0762016 | 1.1371768 | 1.012137  | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.82347   | 1.076060  | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.9815429 | 0.7876269 | 0.9132003 |
| 0.853237  | 1.0760616 | 0.9525004 | 0.9825004 | 1.1766574 | 1.1407797 | 0.9486926 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 1.0760616 | 0.9891407 | 1.0291158 | 0.9405003 | 1.0342205 | 1.5420269 | 1.648122  | 0.        |           |           |









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| 0.8752527 | 0.8835301 | 0.8853409 | 0.8871498 | 0.8890104 | 0.8909164 | 0.8928629 | 0.8948550 | 0.8968986 | 0.8989900 | 0.9011259 | 0.9033022 | 0.9055149 | 0.9077699 | 0.9100133 | 0.9123412 | 0.9147595 | 0.9172732 | 0.9197871 | 0.9223059 | 0.9248346 | 0.9273681 | 0.9299016 | 0.9324399 | 0.9349870 | 0.9375388 | 0.9400903 | 0.9426464 | 0.9452021 | 0.9477624 | 0.9503223 | 0.9528868 | 0.9554510 | 0.9580200 | 0.9605888 | 0.9631524 | 0.9657158 | 0.9682740 | 0.9708321 | 0.9733951 | 0.9759580 | 0.9785258 | 0.9810885 | 0.9836510 | 0.9862184 | 0.9887857 | 0.9913479 | 0.9939099 | 0.9964668 | 0.9990236 | 1.0015753 | 1.0041269 | 1.0066784 | 1.0092249 | 1.0117714 | 1.0143130 | 1.0168545 | 1.0193959 | 1.0219373 | 1.0244787 | 1.0270199 | 1.0295611 | 1.0321023 | 1.0346435 | 1.0371847 | 1.0397259 | 1.0422671 | 1.0448083 | 1.0473495 | 1.0498907 | 1.0524319 | 1.0549731 | 1.0575143 | 1.0600555 | 1.0625967 | 1.0651379 | 1.0676791 | 1.0702203 | 1.0727615 | 1.0753027 | 1.0778439 | 1.0803851 | 1.0829263 | 1.0854675 | 1.0880087 | 1.0905499 | 1.0930911 | 1.0956323 | 1.0981735 | 1.1007147 | 1.1032559 | 1.1057971 | 1.1083383 | 1.1108795 | 1.1134207 | 1.1159619 | 1.1185031 | 1.1210443 | 1.1235855 | 1.1261267 | 1.1286679 | 1.1312091 | 1.1337503 | 1.1362915 | 1.1388327 | 1.1413739 | 1.1439151 | 1.1464563 | 1.1489975 | 1.1515387 | 1.1540799 | 1.1566211 | 1.1591623 | 1.1617035 | 1.1642447 | 1.1667859 | 1.1693271 | 1.1718683 | 1.1744095 | 1.1769507 | 1.1794919 | 1.1820331 | 1.1845743 | 1.1871155 | 1.1896567 | 1.1921979 | 1.1947391 | 1.1972803 | 1.1998215 | 1.2023627 | 1.2049039 | 1.2074451 | 1.2100000 | 1.2125441 | 1.2150882 | 1.2176323 | 1.2201764 | 1.2227205 | 1.2252646 | 1.2278087 | 1.2303528 | 1.2328969 | 1.2354410 | 1.2379851 | 1.2405292 | 1.2430733 | 1.2456174 | 1.2481615 | 1.2507056 | 1.2532497 | 1.2557938 | 1.2583379 | 1.2608820 | 1.2634261 | 1.2659702 | 1.2685143 | 1.2710584 | 1.2736025 | 1.2761466 | 1.2786907 | 1.2812348 | 1.2837789 | 1.2863230 | 1.2888671 | 1.2914112 | 1.2939553 | 1.2964994 | 1.2990435 | 1.3015876 | 1.3041317 | 1.3066758 | 1.3092199 | 1.3117640 | 1.3143081 | 1.3168522 | 1.3193963 | 1.3219404 | 1.3244845 | 1.3270286 | 1.3295727 | 1.3321168 | 1.3346609 | 1.3372050 | 1.3397491 | 1.3422932 | 1.3448373 | 1.3473814 | 1.3499255 | 1.3524696 | 1.3550137 | 1.3575578 | 1.3601019 | 1.3626460 | 1.3651901 | 1.3677342 | 1.3702783 | 1.3728224 | 1.3753665 | 1.3779106 | 1.3804547 | 1.3829988 | 1.3855429 | 1.3880870 | 1.3906311 | 1.3931752 | 1.3957193 | 1.3982634 | 1.4008075 | 1.4033516 | 1.4058957 | 1.4084398 | 1.4109839 | 1.4135280 | 1.4160721 | 1.4186162 | 1.4211603 | 1.4237044 | 1.4262485 | 1.4287926 | 1.4313367 | 1.4338808 | 1.4364249 | 1.4389690 | 1.4415131 | 1.4440572 | 1.4466013 | 1.4491454 | 1.4516895 | 1.4542336 | 1.4567777 | 1.4593218 | 1.4618659 | 1.4644100 | 1.4669541 | 1.4694982 | 1.4720423 | 1.4745864 | 1.4771305 | 1.4796746 | 1.4822187 | 1.4847628 | 1.4873069 | 1.4898510 | 1.4923951 | 1.4949392 | 1.4974833 | 1.4999274 | 1.5024715 | 1.5050156 | 1.5075597 | 1.5101038 | 1.5126479 | 1.5151920 | 1.5177361 | 1.5202802 | 1.5228243 | 1.5253684 | 1.5279125 | 1.5304566 | 1.5329907 | 1.5355348 | 1.5380789 | 1.5406230 | 1.5431671 | 1.5457112 | 1.5482553 | 1.5507994 | 1.5533435 | 1.5558876 | 1.5584317 | 1.5609758 | 1.5635199 | 1.5660640 | 1.5686081 | 1.5711522 | 1.5736963 | 1.5762404 | 1.5787845 | 1.5813286 | 1.5838727 | 1.5864168 | 1.5889609 | 1.5915050 | 1.5940491 | 1.5965932 | 1.5991373 | 1.6016814 | 1.6042255 | 1.6067696 | 1.6093137 | 1.6118578 | 1.6144019 | 1. |
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[illegible]

|         |          |           |          |          |          |          |          |          |          |          |          |          |         |           |          |
|---------|----------|-----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|---------|-----------|----------|
| 0.02561 | 1.045458 | 0.0864117 | 1.077116 | 1.161172 | 1.005006 | 1.179426 | 1.005346 | 1.005127 | 1.087513 | 1.006457 | 1.009453 | 1.013373 | 1.10336 | 1.0811626 | 0.886444 |
| 0.02562 | 1.045459 | 0.0864118 | 1.077117 | 1.161173 | 1.005007 | 1.179427 | 1.005347 | 1.005128 | 1.087514 | 1.006458 | 1.009454 | 1.013374 | 1.10337 | 1.0811627 | 0.886445 |
| 0.02563 | 1.045460 | 0.0864119 | 1.077118 | 1.161174 | 1.005008 | 1.179428 | 1.005348 | 1.005129 | 1.087515 | 1.006459 | 1.009455 | 1.013375 | 1.10338 | 1.0811628 | 0.886446 |
| 0.02564 | 1.045461 | 0.0864120 | 1.077119 | 1.161175 | 1.005009 | 1.179429 | 1.005349 | 1.005130 | 1.087516 | 1.006460 | 1.009456 | 1.013376 | 1.10339 | 1.0811629 | 0.886447 |
| 0.02565 | 1.045462 | 0.0864121 | 1.077120 | 1.161176 | 1.005010 | 1.179430 | 1.005350 | 1.005131 | 1.087517 | 1.006461 | 1.009457 | 1.013377 | 1.10340 | 1.0811630 | 0.886448 |
| 0.02566 | 1.045463 | 0.0864122 | 1.077121 | 1.161177 | 1.005011 | 1.179431 | 1.005351 | 1.005132 | 1.087518 | 1.006462 | 1.009458 | 1.013378 | 1.10341 | 1.0811631 | 0.886449 |
| 0.02567 | 1.045464 | 0.0864123 | 1.077122 | 1.161178 | 1.005012 | 1.179432 | 1.005352 | 1.005133 | 1.087519 | 1.006463 | 1.009459 | 1.013379 | 1.10342 | 1.0811632 | 0.886450 |
| 0.02568 | 1.045465 | 0.0864124 | 1.077123 | 1.161179 | 1.005013 | 1.179433 | 1.005353 | 1.005134 | 1.087520 | 1.006464 | 1.009460 | 1.013380 | 1.10343 | 1.0811633 | 0.886451 |
| 0.02569 | 1.045466 | 0.0864125 | 1.077124 | 1.161180 | 1.005014 | 1.179434 | 1.005354 | 1.005135 | 1.087521 | 1.006465 | 1.009461 | 1.013381 | 1.10344 | 1.0811634 | 0.886452 |
| 0.02570 | 1.045467 | 0.0864126 | 1.077125 | 1.161181 | 1.005015 | 1.179435 | 1.005355 | 1.005136 | 1.087522 | 1.006466 | 1.009462 | 1.013382 | 1.10345 | 1.0811635 | 0.886453 |
| 0.02571 | 1.045468 | 0.0864127 | 1.077126 | 1.161182 | 1.005016 | 1.179436 | 1.005356 | 1.005137 | 1.087523 | 1.006467 | 1.009463 | 1.013383 | 1.10346 | 1.0811636 | 0.886454 |
| 0.02572 | 1.045469 | 0.0864128 | 1.077127 | 1.161183 | 1.005017 | 1.179437 | 1.005357 | 1.005138 | 1.087524 | 1.006468 | 1.009464 | 1.013384 | 1.10347 | 1.0811637 | 0.886455 |
| 0.02573 | 1.045470 | 0.0864129 | 1.077128 | 1.161184 | 1.005018 | 1.179438 | 1.005358 | 1.005139 | 1.087525 | 1.006469 | 1.009465 | 1.013385 | 1.10348 | 1.0811638 | 0.886456 |
| 0.02574 | 1.045471 | 0.0864130 | 1.077129 | 1.161185 | 1.005019 | 1.179439 | 1.005359 | 1.005140 | 1.087526 | 1.006470 | 1.009466 | 1.013386 | 1.10349 | 1.0811639 | 0.886457 |
| 0.02575 | 1.045472 | 0.0864131 | 1.077130 | 1.161186 | 1.005020 | 1.179440 | 1.005360 | 1.005141 | 1.087527 | 1.006471 | 1.009467 | 1.013387 | 1.10350 | 1.0811640 | 0.886458 |
| 0.02576 | 1.045473 | 0.0864132 | 1.077131 | 1.161187 | 1.005021 | 1.179441 | 1.005361 | 1.005142 | 1.087528 | 1.006472 | 1.009468 | 1.013388 | 1.10351 | 1.0811641 | 0.886459 |
| 0.02577 | 1.045474 | 0.0864133 | 1.077132 | 1.161188 | 1.005022 | 1.179442 | 1.005362 | 1.005143 | 1.087529 | 1.006473 | 1.009469 | 1.013389 | 1.10352 | 1.0811642 | 0.886460 |
| 0.02578 | 1.045475 | 0.0864134 | 1.077133 | 1.161189 | 1.005023 | 1.179443 | 1.005363 | 1.005144 | 1.087530 | 1.006474 | 1.009470 | 1.013390 | 1.10353 | 1.0811643 | 0.886461 |
| 0.02579 | 1.045476 | 0.0864135 | 1.077134 | 1.161190 | 1.005024 | 1.179444 | 1.005364 | 1.005145 | 1.087531 | 1.006475 | 1.009471 | 1.013391 | 1.10354 | 1.0811644 | 0.886462 |
| 0.02580 | 1.045477 | 0.0864136 | 1.077135 | 1.161191 |          |          |          |          |          |          |          |          |         |           |          |



[illegible]







**1**



|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |            |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|
| 0.6258046 | 0.8552536 | 0.4077281 | 1.0523718 | 0.960480  | 1.1542115 | 0.9943306 | 1.0057715 | 1.2601155 | 1.532064  | 1.2553578 | 1.2353308 | 1.3180014 | 1.5653512 | 0.6533978 | 1.4620334 | 1.0203963 | 0.8460584 | 1.0822298  | 1.4084976 | 1.3210005 | 1.3252330 |
| 1.2318105 | 1.1258864 | 0.6294874 | 1.2820525 | 0.9750417 | 1.0307180 | 0.8743794 | 0.8688263 | 0.8781161 | 0.8386767 | 0.5151461 | 0.8077010 | 1.1287934 | 0.8043365 | 0.0034271 | 1.8467817 | 0.9547473 | 0.8824454 | 0.80779114 | 0.8711312 | 0.8188324 | 0.7985699 |
| 0.7175804 | 1.0530032 | 0.5387419 | 1.3113964 | 0.9277075 | 0.9735718 | 1.0002028 | 0.9488252 | 0.8081160 | 1.1335751 | 1.0204480 | 0.472833  | 0.7783014 | 0.8620279 | 0.7502774 | 1.2352218 | 0.6411811 | 0.8027755 | 1.0182299  | 0.8707855 | 1.0182299 | 0.8000242 |
| 0.8752581 | 1.171802  | 1.081836  | 1.0240265 | 0.8016018 | 1.0383527 | 1.171802  | 1.081836  | 1.0240265 | 0.8016018 | 1.0383527 | 0.472833  | 0.7783014 | 0.8620279 | 0.7502774 | 1.2352218 | 0.6411811 | 0.8027755 | 1.0182299  | 0.8707855 | 1.0182299 | 0.8000242 |
| 0.9438205 | 1.0884132 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684 | 1.0406684  | 1.0406684 | 1.0406684 | 1.0406684 |
| 0.8435271 | 0.810002  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513  | 0.878513   | 0.878513  | 0.878513  |           |
| 0.8000168 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504 | 1.0814504  | 1.0814504 | 1.0814504 | 1.0814504 |
| 0.9505563 | 0.861102  | 0.86391   | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845  | 0.801307  | 0.7876561 | 2.44509   |
| 0.8537883 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727  | 0.7531727 | 0.7531727 | 0.7531727 |
| 0.9505563 | 0.861102  | 0.86391   | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845  | 0.801307  | 0.7876561 | 2.44509   |
| 0.8537883 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727  | 0.7531727 | 0.7531727 | 0.7531727 |
| 0.9505563 | 0.861102  | 0.86391   | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845  | 0.801307  | 0.7876561 | 2.44509   |
| 0.8537883 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727 | 0.7531727  | 0.7531727 | 0.7531727 | 0.7531727 |
| 0.9505563 | 0.861102  | 0.86391   | 0.7718845 | 0.801307  | 0.7876561 | 2.44509   | 1.087758  | 0.7718845 | 0.801307  |           |           |           |           |           |           |           |           |            |           |           |           |

|  | 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | 2101 | 2102 | 2103 | 2104 | 2105 | 2106 | 2107 | 2108 | 2109 | 2110 | 2111 | 2112 | 2113 | 2114 | 2115 | 2116 | 2117 | 2118 | 2119 | 2120 | 2121 | 2122 | 2123 | 2124 | 2125 | 2126 | 2127 | 2128 | 2129 | 2130 | 2131 | 2132 | 2133 | 2134 | 2135 | 2136 | 2137 | 2138 | 2139 | 2140 | 2141 | 2142 | 2143 | 2144 | 2145 | 2146 | 2147 | 2148 | 2149 | 2150 | 2151 | 2152 | 2153 | 2154 | 2155 | 2156 | 2157 | 2158 | 2159 | 2160 | 2161 | 2162 | 2163 | 2164 | 2165 | 2166 | 2167 | 2168 | 2169 | 2170 | 2171 | 2172 | 2173 | 2174 | 2175 | 2176 | 2177 | 2178 | 2179 | 2180 | 2181 | 2182 | 2183 | 2184 | 2185 | 2186 | 2187 | 2188 | 2189 | 2190 | 2191 | 2192 | 2193 | 2194 | 2195 | 2196 | 2197 | 2198 | 2199 | 2200 | 2201 | 2202 | 2203 | 2204 | 2205 | 2206 | 2207 | 2208 | 2209 | 2210 | 2211 | 2212 | 2213 | 2214 | 2215 | 2216 | 2217 | 2218 | 2219 | 2220 | 2221 | 2222 | 2223 | 2224 | 2225 | 2226 | 2227 | 2228 | 2229 | 2230 | 2231 | 2232 | 2233 | 2234 | 2235 | 2236 | 2237 | 2238 | 2239 | 2240 | 2241 | 2242 | 2243 | 2244 | 2245 | 2246 | 2247 | 2248 | 2249 | 2250 | 2251 | 2252 | 2253 | 2254 | 2255 | 2256 | 2257 | 2258 | 2259 | 2260 | 2261 | 2262 | 2263 | 2264 | 2265 | 2266 | 2267 | 2268 | 2269 | 2270 | 2271 | 2272 | 2273 | 2274 | 2275 | 2276 | 2277 | 2278 | 2279 | 2280 | 2281 | 2282 | 2283 | 2284 | 2285 | 2286 | 2287 | 2288 | 2289 | 2290 | 2291 | 2292 | 2293 | 2294 | 2295 | 2296 | 2297 | 2298 | 2299 | 2300 | 2301 | 2302 | 2303 | 2304 | 2305 | 2306 | 2307 | 2308 | 2309 | 2310 | 2311 | 2312 | 2313 | 2314 | 2315 | 2316 | 2317 | 2318 | 2319 | 2320 | 2321 | 2322 | 2323 | 2324 | 2325 | 2326 | 2327 | 2328 | 2329 | 2330 | 2331 | 2332 | 2333 | 2334 | 2335 | 2336 | 2337 | 2338 | 2339 | 2340 | 2341 | 2342 | 2343 | 2344 | 2345 | 2346 | 2347 | 2348 | 2349 | 2350 | 2351 | 2352 | 2353 | 2354 | 2355 | 2356 | 2357 | 2358 | 2359 | 2360 | 2361 | 2362 | 2363 | 2364 | 2365 | 2366 | 2367 | 2368 | 2369 | 2370 | 2371 | 2372 | 2373 | 2374 | 2375 | 2376 | 2377 | 2378 | 2379 | 2380 | 2381 | 2382 | 2383 | 2384 | 2385 | 2386 | 2387 | 2388 | 2389 | 2390 | 2391 | 2392 | 2393 | 2394 | 2395 | 2396 | 2397 | 2398 | 2399 | 2400 | 2401 | 2402 | 2403 | 2404 | 2405 | 2406 | 2407 | 2408 | 2409 | 2410 | 2411 | 2412 | 2413 | 2414 | 2415 | 2416 | 2417 | 2418 | 2419 | 2420 | 2421 | 2422 | 2 |
|--|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|---|
|--|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|---|

Table 3a

[illegible]

|           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|
| 1.3237672 | 1.3735267 | 1.2461341 | 1.4328167 | 1.3400446 | 1.4300629 |
| 0.6249002 | 0.6143099 | 0.6989414 | 0.7101815 | 0.5670633 | 0.7203101 |
| 0.6468006 | 0.602078  | 0.6710008 | 0.6435904 | 0.5980202 | 0.7715324 |
| 0.5705126 | 0.4971365 | 0.5143716 | 0.4840021 | 0.5003567 | 0.6763624 |
| 0.7803626 | 0.78138   | 0.6420978 | 0.7245778 | 0.8404385 | 0.646002  |
| 1.2545227 | 1.204551  | 0.6115252 | 1.0711714 | 0.7860586 | 0.9380002 |
| 0.8911785 | 0.7148865 | 0.691026  | 0.6072468 | 0.7107518 | 0.609016  |
| 1.3718953 | 1.401782  | 1.4460182 | 1.4489818 | 1.6180836 | 1.5018754 |
| 0.721250  | 0.7558277 | 0.7429448 | 0.800005  | 0.8132002 | 0.6774609 |
| 1.453508  | 1.3697316 | 1.6779169 | 1.3108477 | 1.5777268 | 1.6048713 |
| 2.4684154 | 0.451435  | 2.3018032 | 1.4528069 | 4.000231  | 1.8480339 |
| 1.0000005 | 1.6794656 | 1.4222185 | 1.832911  | 1.7933801 | 1.7208549 |
| 0.7803059 | 0.6371271 | 0.7750253 | 0.6917979 | 0.7857282 | 0.7038868 |
| 0.6048812 | 0.6580811 | 0.700069  | 0.7829375 | 0.6920598 | 0.6300794 |
| 1.4082903 | 1.4762482 | 2.0222338 | 1.4021622 | 1.4866877 | 1.8250424 |
| 1.0884403 | 1.1186555 | 1.2365091 | 1.0509493 | 1.0800406 | 1.0387206 |
| 0.8151884 | 0.8704302 | 0.7991324 | 1.2626273 | 0.7149716 | 1.2813915 |
| 1.158019  | 0.884108  | 0.715817  | 1.0007035 | 1.178812  | 1.0700862 |
| 1.2440881 | 1.6175728 | 1.6080555 | 1.6530942 | 1.5559281 | 1.8525383 |
| 1.517721  | 1.3981485 | 1.240711  | 1.4615456 | 1.680456  | 1.802207  |
| 1.8005383 | 1.6278172 | 1.804756  | 1.5748639 | 1.5481868 | 1.411242  |
| 2.0003845 | 1.383464  | 1.6100759 | 1.1871212 | 1.4300166 | 1.3411088 |
| 1.2934758 | 1.6531104 | 0.680108  | 1.0074342 | 1.077839  | 1.212468  |
| 1.4922355 | 1.454171  | 1.3118942 | 1.1959335 | 1.1781089 | 1.2558216 |
| 1.8108107 | 1.3285682 | 1.4817168 | 1.2629668 | 1.4411106 | 1.3144860 |
| 1.7181105 | 1.055859  | 1.0881105 | 1.058585  | 1.058585  | 1.7171147 |
| 0.5248539 | 0.8031178 | 0.8002088 | 0.830422  | 0.84865   | 0.627147  |
| 0.7880081 | 1.0028853 | 0.8068114 | 0.8807257 | 0.6188207 | 0.7520664 |
| 0.8047008 | 1.0012128 | 0.8045557 | 0.8500804 | 0.8557852 | 0.7100091 |
| 0.7231862 | 0.7862049 | 0.7898382 | 1.0529654 | 0.4788785 | 0.8527374 |
| 0.6458081 | 0.6900528 | 0.6326387 | 0.6111851 | 0.6738132 | 0.8038862 |
| 1.0734531 | 1.4984289 | 1.3376552 | 1.7788491 | 1.4613973 | 1.9038468 |
| 1.284516  | 1.222181  | 1.0070911 | 1.0509710 | 1.0652460 | 0.8824903 |
| 1.4243812 | 1.2311059 | 1.3511877 | 1.6007297 | 1.3218912 | 1.1285125 |
| 1.2544501 | 0.8362875 | 1.0262622 | 0.6400472 | 1.1237753 | 1.1088967 |

Compound-Dose  
Animal Number  
Kidney Toxicity Classification  
Dose Name

[illegible]

[illegible]



|                                       |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|---------------------------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Hepatoocyte nuclear factor 4          | 0.8312101 | 1.0544459 | 0.5201465 | 1.1573004 | 1.1833981 | 1.0374170 | 0.5301693 | 1.0170409 | 0.8245453 | 0.801184  | 1.0142113 | 1.2006410 | 0.8102002 | 0.8003979 | 0.8707238 | 0.8107003 | 0.7794060 | 0.9638846 | 1.0000337 |
| Sarcoplasmic reticulum calcium ATPase | 0.5730256 | 1.0433205 | 1.0422102 | 0.9801419 | 0.8343735 | 1.2054374 | 1.0545336 | 1.0185055 | 1.0109422 | 1.0352585 | 0.9450773 | 0.8311298 | 0.8303089 | 1.0554227 | 1.490070  | 1.0430785 | 1.0480551 | 1.1077125 | 0.7800088 |
| Oxidative mitochondrial               | 1.0707512 | 1.2291703 | 0.8721638 | 0.9490002 | 0.7869702 | 1.0743883 | 0.1687942 | 1.1302037 | 0.9184864 | 0.8071383 | 0.8922774 | 0.8887604 | 1.2003865 | 1.2771634 | 1.2543448 | 0.8111284 | 1.2084544 | 1.1823268 | 1.202327  |
| Aspartate kinase                      | 0.8698148 | 0.8664742 | 1.0878302 | 0.777863  | 0.7473777 | 1.0754570 | 0.4102125 | 0.9525179 | 0.8979002 | 0.8794366 | 1.0495290 | 0.7050772 | 1.0500479 | 1.1523325 | 1.1543334 | 1.2310486 | 1.0073002 | 1.1818005 | 1.1200068 |
| Phase-1 PCT-5                         | 1.0476638 | 0.8592269 | 1.1455015 | 0.777604  | 1.0804427 | 1.1883140 | 0.6459817 | 0.5228559 | 1.128042  | 0.8801155 | 0.861781  | 0.8050309 | 1.0094339 | 1.1227792 | 1.0813863 | 1.2797171 | 1.0477801 | 1.1778942 | 1.0337873 |
| Phase-1 PCT-5                         | 1.4005989 | 1.1873364 | 0.790288  | 1.1713331 | 0.8178860 | 0.4418845 | 3.0774088 | 0.8807448 | 0.8234345 | 0.8361868 | 0.8383842 | 0.8389145 | 0.1812349 | 0.1488390 | 0.7130078 | 0.4480134 | 0.1680047 | 0.0444559 | 0.9404219 |
| Penicillin alpha 1 chain              | 1.7010319 | 1.1855783 | 0.7945451 | 1.1800005 | 0.8124716 | 0.6240205 | 2.2007818 | 0.7200718 | 0.9554259 | 0.839432  | 0.6427804 | 0.8167601 | 0.1388853 | 0.1541187 | 0.73714   | 0.4814717 | 0.1320048 | 0.047177  | 0.7302802 |
| Penicillin alpha 1 chain              | 1.0332017 | 1.1168809 | 1.0055008 | 0.820414  | 0.89072   | 0.8688872 | 1.0540946 | 1.2185047 | 0.8971856 | 0.7778037 | 1.0339439 | 0.8110001 | 0.8975441 | 0.8519188 | 0.8508819 | 1.2204785 | 0.8632748 | 1.0314003 | 0.8789415 |
| Cytoplasmic phosphatase alpha         | 1.0116203 | 1.1438546 | 1.0620282 | 1.2401917 | 1.2634022 | 1.2881731 | 1.2382222 | 1.1116885 | 0.8704803 | 1.1622587 | 1.0440885 | 0.8570784 | 0.8641319 | 1.0152629 | 0.8021882 | 0.9784578 | 0.8955431 | 1.0288435 | 0.7742648 |
| Phase-1 PCT-300                       | 1.0357481 | 1.1817816 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 | 1.0357481 |
| Phase-1 PCT-181                       | 0.8800003 | 0.8146035 | 1.0590428 | 1.1081481 | 0.8817708 | 1.0830308 | 0.4301459 | 1.1088574 | 0.8827740 | 0.8872237 | 1.0201088 | 1         | 0.8430003 | 1.0857358 | 0.8818735 | 1.1013401 | 1.0812878 | 0.8343408 | 0.8301119 |

4/4

Table 40







[illegible]











1.032560 1.025208 0.908167 1.276072 1.215090 0.890983 0.851891 0.818094 1.050035 1.054108 1.048102 1.107437 1.100778 1.100817 1.008776 1.012404 1.014864 1.211484 1.110053 0.008433 0.0403194 0.8704239 1.1454818  
 1.132560 0.873825 1.250319 1.250319 1.250319 0.844070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823  
 1.307294 0.873825 1.250319 1.250319 1.250319 0.844070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823  
 0.881724 1.016874 1.183440 1.203119 0.908167 1.276072 1.215090 0.890983 0.851891 0.818094 1.050035 1.054108 1.048102 1.107437 1.100778 1.100817 1.008776 1.012404 1.014864 1.211484 1.110053 0.008433 0.0403194 0.8704239 1.1454818  
 1.093307 1.205072 0.873825 1.250319 1.250319 0.844070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823  
 0.3053162 0.101572 0.711305 0.351913 0.505013 0.811201 1.015475 1.223072 1.003441 1.013122 1.044059 1.041007 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071  
 0.3053162 0.101572 0.711305 0.351913 0.505013 0.811201 1.015475 1.223072 1.003441 1.013122 1.044059 1.041007 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071 1.010071  
 1.000761 0.873825 1.250319 1.250319 1.250319 0.844070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823  
 1.100735 1.271317 0.842002 0.873825 1.250319 1.250319 0.844070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823  
 1.007600 0.842002 1.015508 0.873825 1.250319 1.250319 0.844070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823 1.000423 0.840070 1.070720 1.048070 0.841823  
 1.040504 1.127760 1.076013 1.165045 1.191007 0.808169



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|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| 0.61798   | 0.691720  | 0.684723  | 1.0174106 | 0.9704611 | 0.8877972 | 0.626417  | 0.9162003 | 0.861146  | 0.8702574 | 1.0564073 | 0.2081278 | 1.0712482 | 1.0656067 | 1.1150426 | 1.1688349 | 1.1752224 | 0.7654808 | 0.7752805 | 1.0468364 | 0.8347653 | 0.7003683 | 1.0481102 | 0.8075445 |
| 1.020720  | 0.8950186 | 1.0784005 | 0.7861309 | 1.0801130 | 1.0844277 | 1.1073534 | 1.0100867 | 1.1020869 | 1.0897297 | 1.2428846 | 0.9897137 | 1.1833282 | 1.0460358 | 1.3509104 | 1.0955228 | 1.4238242 | 0.8091235 | 0.8436416 | 1.2745302 | 1.1382187 | 0.8355887 | 1.3165372 | 1.4323258 |
| 1.1478238 | 1.2381809 | 0.9809335 | 0.7545232 | 0.8625688 | 0.8986554 | 0.8945887 | 0.8334215 | 0.9432631 | 0.8822394 | 1.0051117 | 1.0024108 | 0.8333382 | 1.0042764 | 1.3045503 | 1.611945  | 1.3715208 | 0.8520682 | 0.8473186 | 0.7445329 | 0.5300014 | 0.890042  | 1.0129032 |           |
| 1.0253523 | 0.8203119 | 1.6440309 | 1.6540773 | 1.4190488 | 1.2401073 | 1.1023968 | 1.0505935 | 0.8617442 | 0.8503197 | 0.8008644 | 1.0764181 | 0.8432423 | 0.8011327 | 1.8682207 | 2.1073383 | 1.1183253 | 0.9982545 | 0.7394538 | 0.8626402 | 0.735401  | 0.7065447 | 1.2587183 |           |
| 1.1411103 | 1.1168146 | 1.0284530 | 1.2811646 | 1.0162289 | 1.2430351 | 0.8932386 | 1.2847881 | 1.2681128 | 0.8435047 | 0.8879517 | 1.1111141 | 0.40137   | 0.7182478 | 1.4184103 | 1.4387866 | 1.1470267 | 0.8843219 | 0.7630264 | 0.8174653 | 0.8433068 | 0.8700005 | 1.0047624 |           |
| 0.8151329 | 0.8208331 | 1.1168145 | 0.8625409 | 0.8111807 | 0.7882047 | 0.7714693 | 0.8914732 | 0.8145182 | 0.7881845 | 1.3044827 | 1.0232478 | 1.1442873 | 0.7407905 | 0.7970414 | 1.0037351 | 2.0288464 | 0.7117282 | 0.8989498 | 1.0277183 | 0.3517138 | 0.2409005 | 0.5190421 | 0.0913354 |
| 0.8188061 | 0.8208331 | 1.1168145 | 0.8625409 | 0.8111807 | 0.7882047 | 0.7714693 | 0.8914732 | 0.8145182 | 0.7881845 | 1.3044827 | 1.0232478 | 1.1442873 | 0.7407905 | 0.7970414 | 1.0037351 | 2.0288464 | 0.7117282 | 0.8989498 | 1.0277183 | 0.3517138 | 0.2409005 | 0.5190421 | 0.0913354 |
| 0.7773153 | 0.7951801 | 0.8723118 | 0.8161082 | 1.021887  | 1.577051  | 0.8535483 | 0.8629532 | 0.8158230 | 0.821812  | 0.800101  | 1.2883773 | 1.1402532 | 1.1288432 | 0.4454158 | 0.5982085 | 0.6201487 | 0.8042903 | 0.8422431 | 1.0515287 | 0.8894484 | 0.8077453 | 0.8448368 | 1.404818  |
| 1.2589407 | 1.2585309 | 0.865374  | 1.2461487 | 1.0320183 | 0.9217757 | 0.7720801 | 0.9468718 | 1.0508338 | 1.0338889 | 1.050511  | 1.2883773 | 1.1402532 | 1.1288432 | 0.4454158 | 0.5982085 | 0.6201487 | 0.8042903 | 0.8422431 | 1.0515287 | 0.8894484 | 0.8077453 | 0.8448368 | 1.404818  |
| 0.8553374 | 0.8213871 | 0.9396545 | 0.8522335 | 1.0393028 | 0.8644865 | 0.801009  | 0.8631871 | 1.010651  | 0.8184055 | 0.8080757 | 0.8082714 | 0.812702  | 0.5003423 | 0.8303242 | 0.7395535 | 0.8730716 | 1.0093503 | 0.8380063 | 0.6823175 | 1.1327832 | 0.0103881 | 0.8474814 | 0.8896007 |
| 0.9916861 | 0.8846179 | 1.0200280 | 1.2382269 | 0.893076  | 0.9132222 | 0.8882882 | 1.0165074 | 1.2174488 | 0.9830885 | 1.0338538 | 1.0233264 | 1.0114285 | 1.0041814 | 1.2380288 | 1.1181446 | 1.0051223 | 0.9813473 | 0.8798733 | 0.9488421 | 1.127077  | 0.8333578 | 0.6935887 | 0.8254159 |



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|           |          |          |          |          |          |          |          |          |           |          |          |          |          |          |          |          |           |          |           |          |          |          |
|-----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|----------|----------|----------|----------|----------|----------|----------|-----------|----------|-----------|----------|----------|----------|
| 0.948009  | 0.940527 | 0.284475 | 0.452086 | 0.847810 | 0.628170 | 0.628157 | 0.579105 | 0.611581 | 0.862021  | 0.724158 | 0.251009 | 1.007702 | 0.892007 | 0.815782 | 0.542581 | 1.116744 | 0.899008  | 0.848308 | 1.070183  | 1.606551 | 1.263179 | 0.614831 |
| 0.877501  | 1.185653 | 0.834688 | 0.851574 | 0.698373 | 1.023307 | 1.211729 | 1.407344 | 1.011385 | 1.011385  | 0.764158 | 0.251009 | 1.007702 | 0.892007 | 0.815782 | 0.542581 | 1.116744 | 0.899008  | 0.848308 | 1.070183  | 1.606551 | 1.263179 | 0.614831 |
| 0.844004  | 1.220051 | 0.702777 | 0.874790 | 0.865185 | 0.706520 | 0.729479 | 0.828138 | 0.828138 | 0.828138  | 0.764158 | 0.251009 | 1.007702 | 0.892007 | 0.815782 | 0.542581 | 1.116744 | 0.899008  | 0.848308 | 1.070183  | 1.606551 | 1.263179 | 0.614831 |
| 1.011314  | 1.111065 | 0.822293 | 1.285269 | 0.55978  | 0.828138 | 0.828138 | 0.828138 | 0.828138 | 0.828138  | 0.764158 | 0.251009 | 1.007702 | 0.892007 | 0.815782 | 0.542581 | 1.116744 | 0.899008  | 0.848308 | 1.070183  | 1.606551 | 1.263179 | 0.614831 |
| 1.047659  | 1.078400 | 0.713588 | 1.198800 | 0.811800 | 0.828138 | 0.828138 | 0.828138 | 0.828138 | 0.828138  | 0.764158 | 0.251009 | 1.007702 | 0.892007 | 0.815782 | 0.542581 | 1.116744 | 0.899008  | 0.848308 | 1.070183  | 1.606551 | 1.263179 | 0.614831 |
| 0.052867  | 0.062179 | 0.692077 | 1.123872 | 0.822258 | 0.671539 | 0.695156 | 0.670049 | 0.783374 | 0.341191  | 0.945163 | 0.622009 | 0.336678 | 0.329447 | 2.35471  | 1.862543 | 1.152058 | 1.020079  | 2.59521  | 1.383268  | 1.308454 | 2.18542  | 0.151268 |
| 0.053008  | 0.041143 | 0.887401 | 1.282541 | 0.871289 | 0.681108 | 0.673868 | 0.515514 | 0.790403 | 0.306511  | 0.503164 | 0.510101 | 0.371727 | 0.323899 | 2.307313 | 1.162083 | 1.07124  | 1.020079  | 1.807718 | 1.887984  | 1.418023 | 1.394818 | 1.462319 |
| 0.271481  | 0.898043 | 0.892588 | 1.010215 | 0.994781 | 0.770084 | 0.884515 | 0.794788 | 1.109236 | 1.097698  | 1.078008 | 1.008698 | 1.210444 | 0.892007 | 0.815782 | 0.542581 | 1.116744 | 0.899008  | 0.848308 | 1.070183  | 1.606551 | 1.263179 | 0.614831 |
| 1.045008  | 1.119901 | 0.810277 | 0.810277 | 0.810277 | 0.810277 | 0.810277 | 0.810277 | 0.810277 | 0.810277  | 0.810277 | 0.810277 | 0.810277 | 0.810277 | 0.810277 | 0.810277 | 0.810277 | 0.810277  | 0.810277 | 0.810277  | 0.810277 | 0.810277 | 0.810277 |
| 0.894328  | 0.811847 | 1.211473 | 1.081358 | 1.408873 | 2.048882 | 2.078431 | 1.208077 | 1.102163 | 1.0204702 | 1.131899 | 1.158416 | 1.305905 | 1.116002 | 0.794987 | 0.779155 | 0.780524 | 0.834338  | 0.872086 | 0.868354  | 0.898848 | 0.750813 | 1.071553 |
| 0.7771478 | 0.508881 | 0.878101 | 1.168884 | 1.052378 | 1.125634 | 1.148183 | 1.020153 | 1.068678 | 1.041837  | 1.077338 | 1.072728 | 1.17963  | 0.838870 | 0.864798 | 1.244026 | 1.021241 | 0.8201128 | 1.041401 | 1.2829188 | 1.171528 | 1.473982 | 1.047887 |

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Table 40







11/66

|           |           |           |           |           |           |           |           |           |          |           |           |           |           |          |          |           |           |           |          |           |          |          |          |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|----------|----------|-----------|-----------|-----------|----------|-----------|----------|----------|----------|
| 0.325441  | 0.981328  | 0.959397  | 0.971894  | 0.770738  | 0.917807  | 0.973381  | 0.964378  | 0.939454  | 0.935433 | 0.942218  | 0.878215  | 1.17521   | 0.990513  | 0.844818 | 1.148433 | 0.953887  | 1.005788  | 0.488065  | 0.955572 | 0.473282  | 0.812281 | 0.958991 | 0.581127 |
| 1.115823  | 0.921185  | 1.178204  | 1.432899  | 0.977325  | 0.971237  | 0.973381  | 0.964378  | 0.939454  | 0.935433 | 0.942218  | 0.878215  | 1.17521   | 0.990513  | 0.844818 | 1.148433 | 0.953887  | 1.005788  | 0.488065  | 0.955572 | 0.473282  | 0.812281 | 0.958991 | 0.581127 |
| 0.871178  | 0.509161  | 0.914382  | 0.625568  | 0.448233  | 0.818182  | 0.739201  | 0.949702  | 0.729272  | 0.729272 | 0.729272  | 0.729272  | 0.729272  | 0.729272  | 0.729272 | 0.729272 | 0.729272  | 0.729272  | 0.729272  | 0.729272 | 0.729272  | 0.729272 | 0.729272 |          |
| 0.701044  | 1.153789  | 1.111003  | 0.6158428 | 1.0910812 | 1.295882  | 0.988178  | 0.988178  | 0.988178  | 0.988178 | 0.988178  | 0.988178  | 0.988178  | 0.988178  | 0.988178 | 0.988178 | 0.988178  | 0.988178  | 0.988178  | 0.988178 | 0.988178  | 0.988178 | 0.988178 |          |
| 1.3515285 | 0.423114  | 1.011550  | 0.717098  | 0.995253  | 1.129818  | 1.074628  | 1.065794  | 0.746815  | 0.653887 | 0.489441  | 0.948284  | 1.027218  | 0.821451  | 1.204453 | 1.043719 | 0.943719  | 0.943719  | 0.943719  | 0.943719 | 0.943719  | 0.943719 | 0.943719 |          |
| 0.191415  | 0.552901  | 0.654458  | 0.138246  | 0.428186  | 0.328655  | 0.3184185 | 0.681387  | 0.6807123 | 0.470782 | 0.6813784 | 0.445492  | 0.944158  | 0.981984  | 0.782827 | 0.462205 | 0.457883  | 0.625765  | 0.483071  | 0.817782 | 0.387081  | 0.857748 | 0.957285 |          |
| 0.056254  | 0.5721727 | 0.6655074 | 0.138629  | 0.480175  | 0.3412949 | 0.3211157 | 0.680325  | 0.567387  | 0.461439 | 0.6813784 | 0.445492  | 0.944158  | 0.981984  | 0.782827 | 0.462205 | 0.457883  | 0.625765  | 0.483071  | 0.817782 | 0.387081  | 0.857748 | 0.957285 |          |
| 0.898181  | 1.0228835 | 1.087454  | 0.85005   | 0.895741  | 0.8213311 | 1.052085  | 1.108876  | 1.188448  | 0.888578 | 0.73204   | 0.657748  | 1.0776473 | 1.189287  | 0.981984 | 0.805118 | 0.4420713 | 0.8545297 | 0.9545293 | 0.918084 | 0.9297258 | 0.845054 | 0.748314 |          |
| 0.970283  | 0.974688  | 0.786488  | 0.895588  | 0.856364  | 0.877955  | 0.982287  | 0.982287  | 0.982287  | 0.982287 | 0.982287  | 0.982287  | 0.982287  | 0.982287  | 0.982287 | 0.982287 | 0.982287  | 0.982287  | 0.982287  | 0.982287 | 0.982287  | 0.982287 | 0.982287 |          |
| 1.172158  | 0.885362  | 0.837118  | 0.814355  | 0.7504787 | 0.629284  | 0.6435258 | 0.6387258 | 0.7185044 | 0.835896 | 0.7148848 | 0.7712549 | 0.945008  | 1.1882786 | 1.083347 | 0.94488  | 1.025448  | 0.878318  | 1.128339  | 1.048213 | 1.207287  | 0.900382 | 0.813184 |          |
|           |           |           |           |           |           |           |           |           |          |           |           |           |           |          |          |           |           |           |          |           |          |          |          |

Table 40

24/44

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|          |          |          |          |          |          |          |          |           |           |           |          |          |          |          |          |          |          |          |          |          |          |          |          |
|----------|----------|----------|----------|----------|----------|----------|----------|-----------|-----------|-----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| 1.094575 | 1.014453 | 0.924349 | 1.157475 | 1.126701 | 1.145278 | 0.960250 | 1.122200 | 1.045077  | 1.110910  | 0.888278  | 0.93779  | 0.877190 | 1.770004 | 0.024781 | 1.227603 | 0.635015 | 0.506515 | 0.374075 | 0.783415 | 0.771374 | 0.758174 | 1.145036 | 0.860581 |
| 0.874751 | 1.095124 | 1.078070 | 1.403003 | 1.338106 | 1.262443 | 1.172873 | 1.077804 | -1.120827 | 1.124585  | -1.218012 | 1.769004 | 0.860274 | 1.357006 | 0.018414 | 0.987200 | 0.740254 | 1.204150 | 1.178433 | 1.112570 | 1.001746 | 1.218431 | 0.872116 | 1.516504 |
| 1.152707 | 1.250625 | 1.028072 | 1.155383 | 1.043887 | 0.894187 | 3.807585 | 1.104348 | 0.625543  | -0.007585 | -1.075167 | 1.228800 | 1.218700 | 1.130482 | 1.201378 | 1.385217 | 1        | 1.102718 | 1.487461 | 3.780458 | 1.016807 | 1.114172 | 1.586801 | 0.747769 |
| 1.000176 | 1.138290 | 1.028072 | 1.171623 | 0.702727 | 1.003754 | 0.789166 | 0.737135 | 0.780211  | 0.876504  | 0.918874  | 0.779280 | 1.632691 | 1.282720 | 1.787842 | 1.972033 | 1.252818 | 1.635223 | 0.850286 | 1.142252 | 0.072257 | 1.032241 | 1.000942 | 0.835168 |
| 0.865648 | 0.828778 | 0.804246 | 0.747044 | 0.498038 | 0.73706  | 0.855008 | 1.084845 | 1.184538  | 1.000474  | 0.860759  | -1.19312 | 1.080382 | 0.888709 | 1.718417 | 1.817167 | 1.232078 | 0.818453 | 0.748168 | 1.889094 | 1.177382 | 0.780792 | 1.278235 | 0.760662 |
| 1.393854 | 0.872752 | 0.594468 | 0.822647 | 0.350583 | 1.123285 | 0.724578 | 0.198069 | 0.320501  | 0.830219  | 1.310188  | 0.330875 | 0.308133 | 0.935998 | 1.132811 | 1.524128 | 0.218024 | 0.831268 | 0.538802 | 0.538802 | 0.602378 | 1.207253 | 0.8783   | 0.880028 |
| 1.879164 | 0.887728 | 0.870368 | 0.870158 | 0.350583 | 1.153348 | 0.662377 | 0.200879 | 0.818612  | 0.803188  | 1.225488  | 0.228018 | 0.338038 | 0.31483  | 1.348178 | 1.238687 | 0.216482 | 0.850015 | 0.814459 | 0.509437 | 0.660589 | 1.204188 | 0.804536 | 0.718189 |
| 1.879164 | 0.887728 | 0.870368 | 0.870158 | 0.350583 | 1.153348 | 0.662377 | 0.200879 | 0.818612  | 0.803188  | 1.225488  | 0.228018 | 0.338038 | 0.31483  | 1.348178 | 1.238687 | 0.216482 | 0.850015 | 0.814459 | 0.509437 | 0.660589 | 1.204188 | 0.804536 | 0.718189 |
| 0.842187 | 1.080188 | 0.818754 | 0.798251 | 0.888883 | 0.832717 | 0.882207 | 0.101845 | 0.818588  | 1.078824  | 1.044078  | 0.840349 | 1.811371 | 0.812087 | 1.444138 | 0.925175 | 1.344891 | 0.841889 | 0.801353 | 1.603374 | 0.808711 | 0.874454 | 1.200684 | 1.014815 |
| 0.86013  | 0.890328 | 0.880118 | 1.158945 | 1.051885 | 0.894538 | 0.878479 | 0.885549 | 1.047175  | 0.879483  | 0.867281  | 1.086721 | 0.978139 | 1.877481 | 0.248312 | 0.845582 | 0.785208 | 0.8885   | 0.813843 | 0.871387 | 0.884388 | 0.819137 | 0.847582 | 1.023475 |
| 1.020481 | 0.888438 | 0.815723 | 0.840521 | 0.729151 | 1.084178 | 0.854287 | 0.880784 | 1.030844  | 1.089407  | 1.003284  | 1.018822 | 1.033248 | 0.885726 | 1.002813 | 1.152838 | 0.832578 | 0.734081 | 0.722787 | 1.058681 | 1.044885 | 0.850702 | 1        | 0.830743 |

2944

Table 40



|          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----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| 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
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| 0.86297689 | 0.8744604 | 0.8796733 | 0.8849318 | 0.8902476 | 0.8956194 | 0.9010048 | 0.9064048 | 0.9118194 | 0.9172486 | 0.9226924 | 0.9281506 | 0.9336232 | 0.9391102 | 0.9446116 | 0.9501274 | 0.9556576 | 0.9612022 | 0.9667614 | 0.9723352 | 0.9779236 | 0.9835266 | 0.9891442 | 0.9947764 | 1.0004232 | 1.0060846 | 1.0117606 | 1.0174512 | 1.0231564 | 1.0288762 | 1.0346106 | 1.0403594 | 1.0461226 | 1.0518902 | 1.0576722 | 1.0634686 | 1.0692794 | 1.0751046 | 1.0809442 | 1.0867982 | 1.0926666 | 1.0985494 | 1.1044466 | 1.1103582 | 1.1162842 | 1.1222246 | 1.1281794 | 1.1341486 | 1.1401322 | 1.1461302 | 1.1521426 | 1.1581694 | 1.1642106 | 1.1702662 | 1.1763362 | 1.1824206 | 1.1885194 | 1.1946326 | 1.2007502 | 1.2068822 | 1.2130286 | 1.2191894 | 1.2253646 | 1.2315542 | 1.2377582 | 1.2439766 | 1.2502094 | 1.2564566 | 1.2627182 | 1.2689942 | 1.2752846 | 1.2815894 | 1.2879086 | 1.2942422 | 1.2999902 | 1.3057526 | 1.3115294 | 1.3173206 | 1.3231262 | 1.3289462 | 1.3347806 | 1.3406294 | 1.3464926 | 1.3523602 | 1.3582422 | 1.3641386 | 1.3700494 | 1.3759746 | 1.3819142 | 1.3878682 | 1.3938366 | 1.3998194 | 1.4058166 | 1.4118282 | 1.4178542 | 1.4238946 | 1.4299494 | 1.4360186 | 1.4420922 | 1.4481702 | 1.4542626 | 1.4603694 | 1.4664906 | 1.4726262 | 1.4787762 | 1.4849406 | 1.4911194 | 1.4973126 | 1.5035202 | 1.5097422 | 1.5159786 | 1.5222294 | 1.5284946 | 1.5347742 | 1.5410682 | 1.5473766 | 1.5536994 | 1.5600366 | 1.5663882 | 1.5727542 | 1.5791346 | 1.5855294 | 1.5919386 | 1.5983622 | 1.6048002 | 1.6112526 | 1.6177194 | 1.6241906 | 1.6306762 | 1.6371762 | 1.6436906 | 1.6502186 | 1.6567602 | 1.6633154 | 1.6698842 | 1.6764666 | 1.6830626 | 1.6896722 | 1.6962954 | 1.7029322 | 1.7095826 | 1.7162466 | 1.7229242 | 1.7296154 | 1.7363202 | 1.7430386 | 1.7497706 | 1.7565162 | 1.7632754 | 1.7700482 | 1.7768346 | 1.7836346 | 1.7904482 | 1.7972752 | 1.8041154 | 1.8109686 | 1.8178346 | 1.8247134 | 1.8316052 | 1.8385102 | 1.8454282 | 1.8523594 | 1.8593036 | 1.8662606 | 1.8732306 | 1.8802134 | 1.8872092 | 1.8942176 | 1.9012386 | 1.9082722 | 1.9153186 | 1.9223776 | 1.9294492 | 1.9365334 | 1.9436302 | 1.9507396 | 1.9578616 | 1.9649956 | 1.9721416 | 1.9792996 | 1.9864696 | 1.9936516 | 2.0008454 | 2.0080512 | 2.0152686 | 2.0224976 | 2.0297386 | 2.0369914 | 2.0442556 | 2.0515312 | 2.0588186 | 2.0661176 | 2.0734286 | 2.0807514 | 2.0880856 | 2.0954312 | 2.1027886 | 2.1101576 | 2.1175386 | 2.1249312 | 2.1323354 | 2.1397512 | 2.1471782 | 2.1546166 | 2.1620662 | 2.1695276 | 2.1769996 | 2.1844826 | 2.1919766 | 2.1994816 | 2.2069976 | 2.2145246 | 2.2220626 | 2.2296116 | 2.2371716 | 2.2447426 | 2.2523246 | 2.2599176 | 2.2675216 | 2.2751366 | 2.2827626 | 2.2903996 | 2.2980476 | 2.3057066 | 2.3133766 | 2.3210576 | 2.3287496 | 2.3364526 | 2.3441666 | 2.3518916 | 2.3596276 | 2.3673746 | 2.3751326 | 2.3829016 | 2.3906816 | 2.3984726 | 2.4062746 | 2.4140876 | 2.4219116 | 2.4297466 | 2.4375926 | 2.4454496 | 2.4533176 | 2.4611966 | 2.4690866 | 2.4769876 | 2.4848996 | 2.4928226 | 2.5007566 | 2.5087016 | 2.5166576 | 2.5246246 | 2.5326026 | 2.5405916 | 2.5485916 | 2.5566026 | 2.5646246 | 2.5726576 | 2.5807016 | 2.5887566 | 2.5968226 | 2.6048996 | 2.6129876 | 2.6210866 | 2.6291966 | 2.6373176 | 2.6454496 | 2.6535926 | 2.6617466 | 2.6699116 | 2.6780876 | 2.6862746 | 2.6944726 | 2.7026816 | 2.7108916 | 2.7191126 | 2.7273446 | 2.7355876 | 2.7438416 | 2.7521066 | 2.7603826 | 2.7686696 | 2.7769676 | 2.7852766 | 2.7935966 | 2.8019276 | 2.8102696 | 2.8186226 | 2.8269866 | 2.8353616 | 2.8437476 | 2.852144 |
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| 1.047102 | 0.864375 | 0.8417025 | 0.8171025 | 0.8116114 | 0.8045230 | 0.8042538 | 0.8037454 | 0.8032164 | 0.8026910 | 0.8021744 | 0.8016578 | 0.8011412 | 0.8006246 | 0.8001080 | 0.7995914 | 0.7990748 | 0.7985582 | 0.7980416 | 0.7975250 | 0.7970084 | 0.7964918 | 0.7959752 | 0.7954586 | 0.7949420 | 0.7944254 | 0.7939088 | 0.7933922 | 0.7928756 | 0.7923590 | 0.7918424 | 0.7913258 | 0.7908092 | 0.7902926 | 0.7897760 | 0.7892594 | 0.7887428 | 0.7882262 | 0.7877096 | 0.7871930 | 0.7866764 | 0.7861598 | 0.7856432 | 0.7851266 | 0.7846100 | 0.7840934 | 0.7835768 | 0.7830602 | 0.7825436 | 0.7820270 | 0.7815104 | 0.7809938 | 0.7804772 | 0.7799606 | 0.7794440 | 0.7789274 | 0.7784108 | 0.7778942 | 0.7773776 | 0.7768610 | 0.7763444 | 0.7758278 | 0.7753112 | 0.7747946 | 0.7742780 | 0.7737614 | 0.7732448 | 0.7727282 | 0.7722116 | 0.7716950 | 0.7711784 | 0.7706618 | 0.7701452 | 0.7696286 | 0.7691120 | 0.7685954 | 0.7680788 | 0.7675622 | 0.7670456 | 0.7665290 | 0.7660124 | 0.7654958 | 0.7649792 | 0.7644626 | 0.7639460 | 0.7634294 | 0.7629128 | 0.7623962 | 0.7618796 | 0.7613630 | 0.7608464 | 0.7603298 | 0.7598132 | 0.7592966 | 0.7587800 | 0.7582634 | 0.7577468 | 0.7572302 | 0.7567136 | 0.7561970 | 0.7556804 | 0.7551638 | 0.7546472 | 0.7541306 | 0.7536140 | 0.7530974 | 0.7525808 | 0.7520642 | 0.7515476 | 0.7510310 | 0.7505144 | 0.7499978 | 0.7494812 | 0.7489646 | 0.7484480 | 0.7479314 | 0.7474148 | 0.7468982 | 0.7463816 | 0.7458650 | 0.7453484 | 0.7448318 | 0.7443152 | 0.7437986 | 0.7432820 | 0.7427654 | 0.7422488 | 0.7417322 | 0.7412156 | 0.7406990 | 0.7401824 | 0.7396658 | 0.7391492 | 0.7386326 | 0.7381160 | 0.7375994 | 0.7370828 | 0.7365662 | 0.7360496 | 0.7355330 | 0.7350164 | 0.7344998 | 0.7339832 | 0.7334666 | 0.7329500 | 0.7324334 | 0.7319168 | 0.7314002 | 0.7308836 | 0.7303670 | 0.7298504 | 0.7293338 | 0.7288172 | 0.7283006 | 0.7277840 | 0.7272674 | 0.7267508 | 0.7262342 | 0.7257176 | 0.7252010 | 0.7246844 | 0.7241678 | 0.7236512 | 0.7231346 | 0.7226180 | 0.7221014 | 0.7215848 | 0.7210682 | 0.7205516 | 0.7200350 | 0.7195184 | 0.7190018 | 0.7184852 | 0.7179686 | 0.7174520 | 0.7169354 | 0.7164188 | 0.7159022 | 0.7153856 | 0.7148690 | 0.7143524 | 0.7138358 | 0.7133192 | 0.7128026 | 0.7122860 | 0.7117694 | 0.7112528 | 0.7107362 | 0.7102196 | 0.7097030 | 0.7091864 | 0.7086698 | 0.7081532 | 0.7076366 | 0.7071200 | 0.7066034 | 0.7060868 | 0.7055702 | 0.7050536 | 0.7045370 | 0.7040204 | 0.7035038 | 0.7029872 | 0.7024706 | 0.7019540 | 0.7014374 | 0.7009208 | 0.7004042 | 0.6998876 | 0.6993710 | 0.6988544 | 0.6983378 | 0.6978212 | 0.6973046 | 0.6967880 | 0.6962714 | 0.6957548 | 0.6952382 | 0.6947216 | 0.6942050 | 0.6936884 | 0.6931718 | 0.6926552 | 0.6921386 | 0.6916220 | 0.6911054 | 0.6905888 | 0.6900722 | 0.6895556 | 0.6890390 | 0.6885224 | 0.6880058 | 0.6874892 | 0.6869726 | 0.6864560 | 0.6859394 | 0.6854228 | 0.6849062 | 0.6843896 | 0.6838730 | 0.6833564 | 0.6828398 | 0.6823232 | 0.6818066 | 0.6812900 | 0.6807734 | 0.6802568 | 0.6797402 | 0.6792236 | 0.6787070 | 0.6781904 | 0.6776738 | 0.6771572 | 0.6766406 | 0.6761240 | 0.6756074 | 0.6750908 | 0.6745742 | 0.6740576 | 0.6735410 | 0.6730244 | 0.6725078 | 0.6719912 | 0.6714746 | 0.6709580 | 0.6704414 | 0.6699248 | 0.6694082 | 0.6688916 | 0.6683750 | 0.6678584 | 0.6673418 | 0.6668252 | 0.6663086 | 0.6657920 | 0.6652754 | 0.6647588 | 0.6642422 | 0.6637256 | 0.6632090 | 0.6626924 | 0.6621758 | 0.6616592 | 0.6611426 | 0.6606260 | 0.6601094 | 0.6595928 | 0.6590762 | 0.6585596 | 0.6580430 | 0.6575264 | 0.6570098 | 0.6564932 | 0.6559766 | 0.6554600 | 0.6549434 | 0.6544268 | 0.6539102 | 0.6533936 | 0.6528770 | 0.6523604 | 0.6518438 | 0.6513272 | 0.6508106 | 0.6502940 | 0.6497774 | 0.6492608 | 0.6487442 | 0.6482276 | 0.6477110 | 0.6471944 | 0.6466778 | 0.6461612 | 0.6456446 | 0.6451280 | 0.6446114 | 0.6440948 | 0.6435782 | 0.6430616 | 0.6425450 | 0.6420284 | 0.6415118 | 0.6409952 | 0.6404786 | 0.6399620 | 0.6394454 | 0.6389288 | 0.6384122 | 0.6378956 | 0.6373790 | 0.6368624 | 0.6363458 | 0.6358292 | 0.6353126 | 0.6347960 | 0.6342794 | 0.6337628 | 0.6332462 | 0.6327296 | 0.6322130 | 0.6316964 | 0.6311798 | 0.6306632 | 0.6301466 | 0.6296300 | 0.6291134 | 0.6285968 | 0.6280802 | 0.6275636 | 0.6270470 | 0.6265304 | 0.6260138 | 0.6254972 | 0.6249806 | 0.6244640 | 0.6239474 | 0.6234308 | 0.6229142 | 0.6223976 | 0.6218810 | 0.6213644 | 0.6208478 | 0.6203312 | 0.6198146 | 0.6192980 | 0.6187814 | 0.6182648 | 0.6177482 | 0.6172316 | 0.6167150 | 0.6161984 | 0.6156818 | 0.6151652 | 0.6146486 | 0.6141320 | 0.6136154 | 0.6130988 | 0.6125822 | 0.6120656 | 0.6115490 | 0.6110324 | 0.6105158 | 0.6099992 | 0.6094826 | 0.6089660 | 0.6084494 | 0.6079328 | 0.6074162 | 0.6068996 | 0.6063830 | 0.6058664 | 0.6053498 | 0.6048332 | 0.6043166 | 0.6038000 | 0.6032834 | 0.6027668 | 0.6022502 | 0.6017336 | 0.6012170 | 0.6007004 | 0.6001838 | 0.5996672 | 0.5991506 | 0.5986340 | 0.5981174 | 0.5976008 | 0.5970842 | 0.5965676 | 0.5960510 | 0.5955344 | 0.5950178 | 0.5945012 | 0.5939846 | 0.5934680 | 0.5929514 | 0.5924348 | 0.5919182 | 0.5914016 | 0.5908850 | 0.5903684 | 0.5898518 | 0.5893352 | 0.5888186 | 0.5883020 | 0.5877854 | 0.5872688 | 0.5867522 | 0.5862356 | 0.5857190 | 0.5852024 | 0.5846858 | 0.5841692 | 0.5836526 | 0.5831360 | 0.5826194 | 0.5821028 | 0.5815862 | 0.5810696 | 0.5805530 | 0.5800364 | 0.5795198 | 0.5790032 | 0.5784866 | 0.5779700 | 0.5774534 | 0.5769368 | 0.5764202 | 0.5759036 | 0.5753870 | 0.5748704 | 0.5743538 | 0.5738372 | 0.5733206 | 0.5728040 | 0.5722874 | 0.5717708 | 0.5712542 | 0.5707376 | 0.5702210 | 0.5697044 | 0.5691878 | 0.5686712 | 0.5681546 | 0.5676380 | 0.5671214 | 0.5666048 | 0.5660882 | 0.5655716 | 0.5650550 | 0.5645384 | 0.5640218 | 0.5635052 | 0.5629886 | 0.5624720 | 0.5619554 | 0.5614388 | 0.5609222 | 0.5604056 | 0.5598890 | 0.5593724 | 0.5588558 | 0.5583392 | 0.5578226 | 0.5573060 | 0.5567894 | 0.5562728 | 0.5557562 | 0.5552396 | 0.5547230 | 0.5542064 | 0.5536898 | 0.5531732 | 0.5526566 | 0.5521400 | 0.5516234 | 0.5511068 | 0.5505902 | 0.5500736 | 0.5495570 | 0.5490404 | 0.5485238 | 0.5480072 | 0.5474906 | 0.5469740 | 0.5464574 | 0.5459408 | 0.5454242 | 0.5449076 | 0.5443910 | 0.5438744 | 0.5433578 | 0.5428412 | 0.5423246 | 0.5418080 | 0.5412914 | 0.5407748 | 0.5402582 | 0.5397416 | 0.5392250 | 0.5387084 | 0.5381918 | 0.5376752 | 0.5371586 | 0.5366420 | 0.5361254 | 0.5356088 | 0.5350922 | 0.5345756 | 0.5340590 | 0.5335424 | 0.5330258 | 0.5325092 | 0.5319926 | 0.5314760 | 0.5309594 | 0.5304428 | 0.5299262 | 0.5294096 | 0.5288930 | 0.5283764 | 0.5278598 | 0.5273432 | 0.5268266 | 0.5263100 | 0.5257934 | 0.5252768 | 0.5247602 | 0.5242436 | 0.5237270 | 0.5232104 | 0.5226938 | 0.5221772 | 0.5216606 | 0.5211440 | 0.5206274 | 0.5201108 | 0.5195942 | 0.5190776 | 0.5185610 | 0.5180444 | 0.5175278 | 0.5170112 | 0.5164946 | 0.5159780 | 0.5154614 | 0.5149448 | 0.5144282 | 0.5139116 | 0.5133950 | 0.5128784 | 0.5123618 | 0.5118452 | 0.5113286 | 0.5108120 | 0.5102954 | 0.5097788 | 0.5092622 | 0.5087456 | 0.5082290 | 0.5077124 | 0.5071958 | 0.5066792 | 0.5061626 | 0.5056460 | 0.5051294 | 0.5046128 | 0.5040962 | 0.5035796 | 0.5030630 | 0.5025464 | 0.5020298 | 0.5015132 | 0.5009966 | 0.5004800 | 0.4999634 | 0.4994468 | 0.4989302 | 0.4984136 | 0.4978970 | 0.4973804 | 0.4968638 | 0.4963472 | 0.4958306 | 0.4953140 | 0.4947974 | 0.4942808 | 0.4937642 | 0.4932476 | 0.4927310 | 0.4922144 | 0.4916978 | 0.4911812 | 0.4906646 | 0.4901480 | 0.4896314 | 0.4891148 | 0.4885982 | 0.4880816 | 0.4875650 | 0.4870484 | 0.4865318 | 0.4860152 | 0.4854986 | 0.4849820 | 0.4844654 | 0.4839488 | 0.4834322 | 0.4829156 | 0.4823990 | 0.4818824 | 0.4813658 | 0.4808492 | 0.4803326 | 0.4798160 | 0.4792994 | 0.4787828 | 0.4782662 | 0.4777496 | 0.4772330 | 0.4767164 | 0.4761998 | 0.4756832 | 0.4751666 | 0.4746500 | 0.4741334 | 0.4736168 | 0.4731002 | 0.4725836 | 0.4720670 | 0.4715504 | 0.4710338 | 0.4705172 | 0.4699999 | 0.4694826 | 0.4689653 | 0.4684480 | 0.4679307 | 0.4674134 | 0.4668961 | 0.4663788 | 0.4658615 | 0.4653442 | 0.4648269 | 0.4643096 | 0.4637923 | 0.4632750 | 0.4627577 | 0.4622404 | 0.4617231 | 0.4612058 | 0.4606885 | 0.4601712 | 0.4596539 | 0.4591366 | 0.4586193 | 0.4581020 | 0.4575847 | 0.4570674 | 0.4565501 | 0.4560328 | 0.4555155 | 0.4549982 | 0.4544809 | 0.4539636 | 0.4534463 | 0.4529290 | 0.4524117 | 0.4518944 | 0.4513771 | 0.4508598 | 0.4503425 | 0.4498252 | 0.4493079 | 0.4487906 | 0.4482733 | 0.4477560 | 0.4472387 | 0.4467214 | 0.4462041 | 0.4456868 | 0.4451695 | 0.4446522 | 0.4441349 | 0.4436176 | 0.4431003 | 0.4425830 | 0.4420657 | 0.4415484 | 0.4410311 | 0.4405138 | 0.4399965 | 0.4394792 | 0.4389619 | 0.4384446 | 0.4379273 | 0.4374100 | 0.4368927 | 0.4363754 | 0.4358581 | 0.4353408 | 0.4348235 | 0.4343062 | 0.4337889 | 0.4332716 | 0.4327543 | 0.4322370 | 0.4317197 | 0.4312024 | 0.4306851 | 0.4301678 | 0.4296505 | 0.4291332 | 0.4286159 | 0.4280986 | 0.4275813 | 0.4270640 | 0.4265467 | 0.4260294 | 0.4255121 | 0.4249948 | 0.4244775 | 0.4239602 | 0.4234429 | 0.4229256 | 0.4224083 | 0.4218910 | 0.4213737 | 0.4208564 | 0.4203391 | 0.4198218 | 0.4193045 | 0.4187872 | 0.4182699 | 0.4177526 | 0.4172353 | 0.4167180 | 0.4162007 | 0.4156834 | 0.4151661 | 0.4146488 | 0.4141315 | 0.4136142 | 0.4130969 | 0.4125796 | 0.4120623 | 0.4115450 | 0.4110277 | 0.4105104 | 0.4099931 | 0.4094758 | 0.4089585 | 0.4084412 | 0.4079239 | 0.4074066 | 0.4068893 | 0.4063720 | 0.4058547 | 0.4053374 | 0.4048201 | 0.4043028 | 0.4037855 | 0.4032682 | 0.4027509 | 0.4022336 | 0.4017163 | 0.4011990 | 0.4006817 | 0.4001644 | 0.3996471 | 0.3991298 | 0.3986125 | 0.3980952 | 0.3975779 | 0.3970606 | 0.3965433 | 0.3960260 | 0.3955087 | 0.3949914 | 0.3944741 | 0.3939568 | 0.3934395 | 0.3929222 | 0.3924049 | 0.3918876 | 0.3913703 | 0.3908530 | 0.3903357 | 0.3898184 | 0.3893011 | 0.3887838 | 0.3882665 | 0.3877492 | 0.3872319 | 0.3867146 | 0.3861973 | 0.3856800 | 0.3851627 | 0.3846454 | 0.3841281 | 0.3836108 | 0.3830935 | 0.3825762 | 0.3820589 | 0.3815416 | 0.3810243 | 0.3805070 | 0.3799897 | 0.3794724 | 0.3789551 | 0.3784378 | 0.3779205 | 0.3774032 | 0.3768859 | 0.3763686 | 0.3758513 | 0.3753340 | 0.3748167 | 0.3742994 | 0.3737821 | 0.3732648 | 0.3727475 | 0.3722302 | 0.3717129 | 0.3711956 | 0.3706783 | 0.3701610 | 0.3696437 | 0.3691264 | 0.3686091 | 0.3680918 | 0.3675745 | 0.3670572 | 0.3665399 | 0.3660226 | 0.3655053 | 0.3649880 | 0.3644707 | 0.3639534 | 0.3634361 | 0.3629188 | 0.3624015 | 0.3618842 | 0.3613669 | 0.3608496 | 0.3603323 | 0.3598150 | 0.3592977 | 0.3587804 | 0.3582631 | 0.3577458 | 0.3572285 | 0.3567112 | 0.3561939 | 0.3556766 | 0.3551593 | 0.354 |
|----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-------|



[illegible]

|          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| 1.276402 | 1.283714 | 1.307704 | 1.051220 | 0.960652 | 1.191212 | 1.080189 | 0.878114 | 1.113247 | 0.81106  | 0.825467 | 1.078838 | 0.864501 | 0.862478 | 0.536783 | 1.014624 | 0.877289 | 0.824583 | 0.801803 | 0.875433 | 0.794053 | 0.851483 | 0.888079 | 0.819449 |
| 1.020789 | 1.276338 | 1.355021 | 1.080088 | 0.974654 | 0.945657 | 1.044088 | 1.044382 | 1.317234 | 1.004248 | 1.158035 | 1.007787 | 0.807707 | 0.803365 | 1.213138 | 0.980015 | 1.237172 | 1.021324 | 0.802748 | 1.023068 | 0.802883 | 1.053708 | 0.868338 | 0.825407 |
| 1.290093 | 1.291425 | 1.525075 | 0.936320 | 0.847442 | 0.800482 | 0.724070 | 0.786332 | 0.857686 | 1.005787 | 0.895704 | 1.457314 | 1.195478 | 1.067817 | 0.935188 | 0.920066 | 0.927547 | 0.825394 | 0.847528 | 0.840182 | 0.740068 | 0.717808 | 0.817835 | 0.825407 |
| 0.873210 | 0.861584 | 0.812311 | 0.843834 | 0.823977 | 0.707734 | 0.776954 | 0.811489 | 0.887172 | 0.808245 | 0.875443 | 1.250054 | 0.825474 | 0.804478 | 0.777158 | 0.968589 | 0.818623 | 1.008859 | 0.877288 | 1.016494 | 1.088858 | 0.745883 | 0.817141 | 0.825407 |
| 0.800149 | 0.800313 | 0.700159 | 0.847188 | 0.894531 | 0.806244 | 0.806511 | 0.892788 | 0.818388 | 0.830284 | 0.818037 | 1.078187 | 0.860478 | 0.817828 | 0.811032 | 0.728342 | 0.801183 | 1.008183 | 1.022085 | 1.424701 | 1.468787 | 0.841829 | 0.251563 | 0.343942 |
| 1.444686 | 1.853416 | 0.903548 | 0.711279 | 0.871682 | 0.822479 | 1.004874 | 0.797319 | 0.743188 | 0.839375 | 0.838485 | 0.817832 | 0.835782 | 0.229132 | 1.189189 | 1.079254 | 1.101748 | 1.189189 | 1.488028 | 1.413039 | 0.832788 | 0.252558 | 0.132801 | 0.338708 |
| 1.308539 | 1.890073 | 1.872961 | 0.700088 | 0.878502 | 0.867289 | 1.031645 | 0.830785 | 0.830785 | 0.838275 | 0.838275 | 0.838275 | 0.838275 | 0.229132 | 1.189189 | 1.079254 | 1.101748 | 1.189189 | 1.488028 | 1.413039 | 0.832788 | 0.252558 | 0.132801 | 0.338708 |
| 0.840752 | 1.081808 | 1.051382 | 1.015270 | 1.008384 | 1.014643 | 1.014643 | 0.834721 | 0.834721 | 0.834721 | 0.834721 | 0.834721 | 0.834721 | 0.229132 | 1.189189 | 1.079254 | 1.101748 | 1.189189 | 1.488028 | 1.413039 | 0.832788 | 0.252558 | 0.132801 | 0.338708 |
| 0.108484 | 1.181763 | 1.187541 | 1.067742 | 0.844432 | 0.784849 | 0.838485 | 0.838485 | 0.838485 | 0.838485 | 0.838485 | 0.838485 | 0.838485 | 0.229132 | 1.189189 | 1.079254 | 1.101748 | 1.189189 | 1.488028 | 1.413039 | 0.832788 | 0.252558 | 0.132801 | 0.338708 |
| 0.728432 | 0.844338 | 0.778231 | 1.015782 | 0.844432 | 0.784849 | 0.838485 | 0.838485 | 0.838485 | 0.838485 | 0.838485 | 0.838485 | 0.838485 | 0.229132 | 1.189189 | 1.079254 | 1.101748 | 1.189189 | 1.488028 | 1.413039 | 0.832788 | 0.252558 | 0.132801 | 0.338708 |
| 0.887171 | 0.848881 | 0.888010 | 1.104338 | 1.020143 | 1.106488 | 0.888010 | 0.888010 | 0.888010 | 0.888010 | 0.888010 | 0.888010 | 0.888010 | 0.229132 | 1.189189 | 1.079254 | 1.101748 | 1.189189 | 1.488028 | 1.413039 | 0.832788 | 0.252558 | 0.132801 | 0.338708 |

30/44

Table 45



[illegible]

[illegible]



|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| 0.763744  | 0.4450084 | 0.4817844 | 0.2390853 | 0.9591186 | 0.9807302 | 1.2495508 | 0.9304822 | 1.0544446 | 0.7817251 | 1.0488188 | 0.6581384 | 0.4486424 | 0.3102115 | 0.7380006 | 0.5407167 | 0.8804113 | 0.87247   | 0.8343477 | 0.8171825 | 1.2045568 | 0.2300415 | 0.8316751 | 0.8303751 |
| 0.8715523 | 0.7805654 | 0.7880308 |           | 0.9512727 | 0.9400880 | 1.1433883 | 1.1275308 | 1.1775583 | 0.8454549 | 0.8282782 | 0.8840471 | 1.1331828 | 1.0947841 | 1.0068476 | 0.8160431 | 0.8880714 | 1.0416587 | 0.8686947 | 0.8279405 | 0.8786338 | 0.8487055 | 1.2818605 | 0.8302798 |
| 0.3574278 | 0.8187886 | 0.8186578 | 0.580341  | 0.2001345 | 0.2009912 | 1.2245574 | 1.0064518 | 1.10255   | 1.2143105 | 1.1859415 | 0.8803487 | 1.0280738 | 0.8840249 | 0.925287  | 0.8737509 | 0.7325231 | 0.7550231 | 0.7591185 | 0.8817748 | 0.7110281 | 0.2571384 | 0.3124877 | 1.0283152 |
| 0.8214383 | 1.0472438 | 1.2386002 | 0.9186773 | 0.2768814 | 0.3743007 | 1.2445705 | 1.1229984 | 1.3178222 | 0.9422387 | 1.3407183 | 1.3812278 | 0.7028181 | 0.8575284 | 0.725287  | 0.8705037 | 0.8142384 | 0.8451484 | 0.8811804 | 0.7818811 | 1.0782001 | 1.1844873 | 0.4487073 | 0.5484281 |
| 0.6958479 | 1.238294  | 1.2942783 | 0.9058131 | 0.0052005 | 0.0055532 | 1.3004596 | 1.2288246 | 1.3711418 | 0.8385114 | 1.1888659 | 0.82882   | 0.7788344 | 1.8872289 | 0.7181145 | 0.8811788 | 0.8811788 | 0.8811788 | 0.8811788 | 0.8811788 | 0.8811788 | 0.8811788 | 0.8811788 | 0.8811788 |
| 0.3803522 | 0.4971376 | 0.4984836 | 0.3377064 | 0.0348809 | 0.038247  | 0.4803865 | 0.2982572 | 0.4484832 | 0.4517838 | 0.4520378 | 0.2707867 | 0.1481183 | 0.1328577 | 0.8382119 | 0.8577822 | 0.8588498 | 0.1178544 | 2.1340172 | 0.800779  | 0.800779  | 0.800779  | 0.800779  | 0.800779  |
| 0.4052138 | 0.2434519 | 0.3722536 | 0.2372586 | 0.0284659 | 0.0287873 | 0.4834889 | 0.2982572 | 0.4484832 | 0.4517838 | 0.4520378 | 0.2707867 | 0.1481183 | 0.1328577 | 0.8382119 | 0.8577822 | 0.8588498 | 0.1178544 | 2.1340172 | 0.800779  | 0.800779  | 0.800779  | 0.800779  | 0.800779  |
| 0.8877425 | 0.8895152 | 0.8873971 | 0.7828157 | 0.8855222 | 0.8725405 | 1.051031  | 0.9238442 | 0.7910219 | 0.4553388 | 0.4562484 | 0.6388208 | 0.8894155 | 0.7442049 | 0.5078725 | 0.8577822 | 0.8588498 | 0.1178544 | 2.1340172 | 0.800779  | 0.800779  | 0.800779  | 0.800779  | 0.800779  |
| 0.8877425 | 0.8895152 | 0.8873971 | 0.7828157 | 0.8855222 | 0.8725405 | 1.051031  | 0.9238442 | 0.7910219 | 0.4553388 | 0.4562484 | 0.6388208 | 0.8894155 | 0.7442049 | 0.5078725 | 0.8577822 | 0.8588498 | 0.1178544 | 2.1340172 | 0.800779  | 0.800779  | 0.800779  | 0.800779  | 0.800779  |
| 0.811484  | 0.8517421 | 0.7283143 | 0.7224723 | 0.7789818 | 0.7844673 | 0.9788207 | 0.9111817 | 0.8807042 | 0.8088437 | 0.7482288 | 0.5333365 | 0.8022238 | 0.5729027 | 0.8811503 | 0.8487059 | 0.8807005 | 1.2326510 | 0.7347853 | 0.8150859 | 0.8040388 | 0.8452854 | 0.8282291 | 0.7379487 |
| 0.8648128 | 0.9108844 | 0.8428643 | 0.8658089 | 0.7288006 | 0.7284681 | 0.9855553 | 0.8528848 | 0.8408167 | 0.6543408 | 0.8884819 | 0.0833187 | 0.8188538 | 0.824862  | 0.785888  | 0.8104126 | 0.8310086 | 1.0081178 | 0.8283889 | 1.035598  | 0.8888314 | 0.8847889 | 0.7854188 | 0.8256573 |

20/44

Table 40

[illegible]

Table 40

|           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|
| 1.0225332 | 0.6711041 | 1.1664054 | 1.0151938 | 1.0864264 |
| 1.2741681 | 2.0087132 | 0.9801279 | 1.1013382 | 1.2107404 |
| 1.4726807 | 1.4375141 | 2.112342  | 1.497975  | 1.180372  |
| 0.531433  | 0.6790027 | 1.0206972 | 1.0728172 | 0.6385269 |
| 1.0481082 | 1.1764889 | 1.6111604 | 0.8664061 | 1.2719484 |
| 1.0031862 | 0.7953332 | 1.2103113 | 0.9414526 | 1.5712287 |
| 0.9799978 | 1.1761812 | 1.0265511 | 0.8579782 | 1.0797925 |
| 1.0902004 | 0.9048123 | 1.6162318 | 1.0253811 | 1.0087723 |
| 1.3447317 | 1.0294884 | 0.8452539 | 1.1285587 | 1.2759129 |
| 0.8310282 | 0.6904957 | 0.5867237 | 0.5076339 | 1.122645  |
| 0.9621115 | 0.8233084 | 0.7574283 | 1.0301216 | 0.8541618 |
| 1.3476212 | 1.4671688 | 1.2076024 | 0.8757291 | 0.7044516 |
| 1.1025569 | 1.0433348 | 0.7489397 | 0.8954943 | 0.8934955 |
| 0.7844987 | 0.7290408 | 0.8411234 | 0.3575784 | 0.8068955 |
| 1.033351  | 0.8911682 | 1.3626357 | 1.0376023 | 0.8603065 |
| 0.8034014 | 1.0510287 | 1.2785445 | 1.250172  | 0.8603065 |
| 0.8715523 | 1.0444088 | 0.9085357 | 0.9862722 | 1.0081412 |
| 0.7118053 | 0.8146087 | 1.0870958 | 0.8245274 | 0.9812877 |
| 0.8163590 | 0.7953555 | 0.7503078 | 0.8033811 | 0.7826458 |
| 0.8112444 | 0.7285118 | 1.0286082 | 1.1713282 | 1.1805584 |
| 0.5812858 | 0.5471168 | 0.4749798 | 0.4856718 | 0.6094425 |
| 0.5125542 | 0.8225075 | 0.2954088 | 0.4394908 | 0.4531148 |
| 0.2921913 | 0.2938955 | 0.2317613 | 0.3180387 | 0.2503304 |
| 0.6894223 | 0.4533237 | 0.4712185 | 0.6877435 | 0.7488178 |
| 0.7475791 | 0.8545121 | 0.8545121 | 0.8545121 | 0.8545121 |
| 0.4340548 | 0.4834005 | 0.3327018 | 0.5484116 | 0.4544884 |
| 0.7400954 | 0.6746091 | 0.8165075 | 0.7166591 | 0.7481885 |
| 0.5817857 | 0.8352048 | 0.3658858 | 0.5759404 | 0.6783383 |
| 0.6365003 | 0.8516388 | 0.4857523 | 0.7223917 | 0.7854893 |
| 0.4948641 | 0.5011558 | 0.214347  | 0.431143  | 0.3408145 |
| 0.8628539 | 0.7071778 | 0.4654437 | 0.8674858 | 0.7015221 |
| 0.4850502 | 0.4968883 | 0.3305503 | 0.5387159 | 0.4539442 |
| 0.8187183 | 0.5898128 | 0.4894044 | 0.8448537 | 0.5713387 |
| 0.8002436 | 0.8871647 | 0.6327334 | 0.6327313 | 0.7577694 |
| 0.7773272 | 0.8186081 | 0.8762648 | 0.8676211 | 0.8873384 |
| 0.7502151 | 0.8186081 | 0.8762648 | 0.8676211 | 0.8873384 |
| 0.4315989 | 0.8787048 | 0.3788787 | 0.5897778 | 0.8148205 |
| 0.7082215 | 0.7386589 | 0.4855557 | 0.5496282 | 0.7082283 |
| 0.3517973 | 0.6581711 | 0.2758174 | 0.3215801 | 0.3816505 |
| 0.8510088 | 0.6720629 | 0.5803282 | 0.7615128 | 0.7180887 |
| 0.8970284 | 0.9623401 | 0.6958624 | 0.8033127 | 0.9418278 |
| 0.5200774 | 0.8180528 | 0.3785144 | 0.8418498 | 0.8745787 |
| 0.7584358 | 0.7330387 | 0.5038387 | 0.7584484 | 0.5505945 |
| 0.8631284 | 0.8222148 | 0.408033  | 0.5396052 | 0.781884  |
| 0.3271151 | 0.3271844 | 0.4864323 | 0.5955113 | 0.5359715 |
| 0.8485151 | 0.8485151 | 0.8485151 | 0.8485151 | 0.8485151 |
| 1.4284492 | 1.2460493 | 1.8094165 | 1.7553001 | 1.8888772 |
| 1.097217  | 0.8794893 | 0.7382837 | 0.5290401 | 0.4883113 |
| 1.537842  | 1.5717488 | 1.7806877 | 1.3550488 | 1.3883848 |
| 1.05847   | 2.846288  | 1.2050375 | 0.7273913 | 1.2613772 |
| 0.7073104 | 0.7872804 | 1.4276912 | 0.8538778 | 1.1281005 |
| 0.9483072 | 0.6311447 | 0.84375   | 0.9051537 | 0.8338179 |
| 1.3082553 | 1.3000055 | 2.811017  | 1.4657851 | 1.4539353 |
| 1.2612242 | 1.0813739 | 1.7545382 | 1.3857788 | 1.0141889 |
| 1.7098875 | 1.1206872 | 2.428777  | 1.4223511 | 1.4184071 |
| 1.4716835 | 1.1648287 | 1.8603107 | 1.6848138 | 1.2839781 |
| 1.0811481 | 0.8513253 | 1.7878188 | 1.0565078 | 1.1812825 |
| 1.3842252 | 1.1251033 | 1.1097153 | 1.0474487 | 1.1880182 |
| 1.0208851 | 0.8013427 | 1.088722  | 1.0412169 | 0.8784831 |
| 1.0323848 | 1.2588104 | 0.8882102 | 0.8786585 | 0.9432382 |
| 0.8994242 | 0.7848753 | 1         | 0.9547893 | 0.9444429 |
| 2.056707  | 1.0053723 | 7.1878804 | 2.7887724 | 4.1687284 |
| 2.3737142 | 2.4912834 | 3.0823188 | 3.3052789 | 3.3213405 |
| 1.0118841 | 1.0534718 | 1.1831509 | 1.2307571 | 1.2875587 |
| 1.7048554 | 1.5089558 | 4.310225  | 1.944081  | 2.4543848 |
| 1.4239421 | 1.2055928 | 0.8863524 | 1.1913681 | 1.2808887 |
| 1.3283125 | 1.3899781 | 1.111187  | 1.1181825 | 1.2808887 |
| 1.3842252 | 1.1251033 | 1.201125  | 1.27248   | 1.2247165 |
| 1.0014804 | 0.8288148 | 1.354117  | 1.0280068 | 1.1188222 |
| 1.0328818 | 1.1161283 | 1.2007034 | 1.0294839 | 1.1813882 |
| 1.5827553 | 1.5733842 | 1.8741285 | 1.5071115 | 1.8955001 |
| 1.2016883 | 1.0475208 | 1.8890028 | 1.2157887 | 1.8786558 |
| 1.2158318 | 1.154575  | 1.8082788 | 1.3882273 | 1.2830775 |

Table 40

|         |          |          |           |          |
|---------|----------|----------|-----------|----------|
| 7339891 | 1.044325 | 0.701148 | 1.180107  | 1.174443 |
| 7339900 | 0.610635 | 0.290186 | 1.180107  | 1.174443 |
| 7339909 | 1.222626 | 0.707564 | -0.515462 | 1.243984 |
| 7339918 | 0.494377 | 1.250298 | 1.250378  | 1.089142 |
| 7339927 | 1.114464 | 0.300391 | 1.153458  | 1.058369 |
| 7339936 | 0.381015 | 0.727140 | 0.504319  | 1.053087 |
| 7339945 | 0.826394 | 0.750505 | 1.204362  | 1.062681 |
| 7339954 | 0.906527 | 0.706003 | 1.204362  | 1.062681 |
| 7339963 | 0.706003 | 1.204362 | 1.062681  | 1.062681 |
| 7339972 | 1.142926 | 0.200772 | 0.850203  | 0.735939 |
| 7339981 | 1.081167 | 1.081167 | 0.850203  | 0.735939 |
| 7339990 | 1.320416 | 1.085558 | 1.085558  | 1.040533 |
| 7339999 | 0.83582  | 0.83582  | 1.085558  | 1.077948 |
| 7340008 | 0.728107 | 1.386327 | 1.105718  | 0.877576 |
| 7340017 | 0.833986 | 0.833986 | 1.046054  | 0.877576 |
| 7340026 | 1.742545 | 0.356954 | 0.846814  | 0.846814 |
| 7340035 | 0.846814 | 0.356954 | 1.046054  | 0.877576 |
| 7340044 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340053 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340062 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340071 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340080 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340089 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340098 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340107 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340116 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340125 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340134 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340143 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340152 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340161 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340170 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340179 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340188 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340197 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340206 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340215 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340224 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340233 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340242 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340251 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340260 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340269 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340278 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340287 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340296 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340305 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340314 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340323 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340332 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340341 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340350 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340359 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340368 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340377 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340386 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340395 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340404 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340413 | 1.046054 | 0.356954 | 1.046054  | 0.877576 |
| 7340422 | 1.046    |          |           |          |

Table 40

0.7570747 0.8435643 0.4501891 1.0706486 0.6726457  
0.6000563 0.8618107 0.5300079 0.7944230 0.8278391  
0.8271123 0.8610186 0.4142682 0.7008382 0.6373302  
0.8333177 0.6547929 0.7364771 0.7237851 0.7732212  
0.7938132 0.7818136 0.4263798 0.7451182 0.7181182  
0.7486746 0.7781136 0.5382020 0.4406332 0.3158108  
0.7811530 0.7739401 0.8244317 0.4569778 0.3151818  
0.6791398 0.7945385 0.8446084 0.8118372 0.8877117  
0.70803 0.7901425 0.9443180 0.8138829 0.8822805  
0.8150902 0.8294805 0.7335849 0.8138854 0.7782223  
1.023880 0.8872711 0.8887547 1.0010151 1.041412

Table 40

44/44



1

**Table 39**



[illegible]

0.000167 0.7610049 0.753829 0.816732 0.814189 0.800025 0.872917 0.943339 0.717325 0.816492 0.878449 0.841321 1.035456 1.127401 1.028114 0.853984 0.810204 1.029137  
 0.881059 1.04472 0.94859 0.85789 0.810140 0.815233 0.888251 0.834785 1.108732 1.074492 1.00227 0.830068 0.832233 0.876777 0.876318 1.132052 0.835165 1.017982

Total cyclophillin  
 Permeable profilin for activated receptor alpha

444

Table 39

|          |          |          |          |          |          |           |           |          |          |           |           |          |          |          |          |          |          |          |          |           |          |           |          |
|----------|----------|----------|----------|----------|----------|-----------|-----------|----------|----------|-----------|-----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|----------|-----------|----------|
| 1.300386 | 1.381760 | 1.400722 | 1.410712 | 1.400835 | 1.073158 | 1.0205179 | 1.113655  | 1.272543 | 1.177626 | 1.245176  | 1.300763  | 1.226095 | 1.645485 | 0.967372 | 1.136026 | 1.222081 | 1.194004 | 1.02092  | 1.125689 | 0.9584028 | 0.818242 | 0.9678084 | 0.825357 |
| 1.300757 | 1.350072 | 0.855549 | 0.830878 | 1.047391 | 0.739818 | 0.712687  | 0.8377965 | 0.877965 | 0.703091 | 0.920587  | 0.7190809 | 1.188673 | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853  | 0.766853 | 0.766853  | 0.766853 |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.188673  | 1.020168 | 0.902328 | 0.986739 | 0.894394 | 0.874879 | 0.894398 | 0.766853 | 0.766853 | 0.766853  | 0.766853 | 0.766853  |          |
| 1.300757 | 1.350072 | 0.855549 | 1.047391 | 0.739818 | 0.712687 | 0.8377965 | 0.877965  | 0.703091 | 0.920587 | 0.7190809 | 1.18867   |          |          |          |          |          |          |          |          |           |          |           |          |

ॐ नमो भगवते वासुदेवाय

[illegible]



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| 1.000001 | 1.000002 | 1.000003 | 1.000004 | 1.000005 | 1.000006 | 1.000007 | 1.000008 | 1.000009 | 1.000010 | 1.000011 | 1.000012 | 1.000013 | 1.000014 | 1.000015 | 1.000016 | 1.000017 | 1.000018 | 1.000019 | 1.000020 | 1.000021 | 1.000022 | 1.000023 | 1.000024 | 1.000025 | 1.000026 | 1.000027 | 1.000028 | 1.000029 | 1.000030 | 1.000031 | 1.000032 | 1.000033 | 1.000034 | 1.000035 | 1.000036 | 1.000037 | 1.000038 | 1.000039 | 1.000040 | 1.000041 | 1.000042 | 1.000043 | 1.000044 | 1.000045 | 1.000046 | 1.000047 | 1.000048 | 1.000049 | 1.000050 | 1.000051 | 1.000052 | 1.000053 | 1.000054 | 1.000055 | 1.000056 | 1.000057 | 1.000058 | 1.000059 | 1.000060 | 1.000061 | 1.000062 | 1.000063 | 1.000064 | 1.000065 | 1.000066 | 1.000067 | 1.000068 | 1.000069 | 1.000070 | 1.000071 | 1.000072 | 1.000073 | 1.000074 | 1.000075 | 1.000076 | 1.000077 | 1.000078 | 1.000079 | 1.000080 | 1.000081 | 1.000082 | 1.000083 | 1.000084 | 1.000085 | 1.000086 | 1.000087 | 1.000088 | 1.000089 | 1.000090 | 1.000091 | 1.000092 | 1.000093 | 1.000094 | 1.000095 | 1.000096 | 1.000097 | 1.000098 | 1.000099 | 1.000100 | 1.000101 | 1.000102 | 1.000103 | 1.000104 | 1.000105 | 1.000106 | 1.000107 | 1.000108 | 1.000109 | 1.000110 | 1.000111 | 1.000112 | 1.000113 | 1.000114 | 1.000115 | 1.000116 | 1.000117 | 1.000118 | 1.000119 | 1.000120 | 1.000121 | 1.000122 | 1.000123 | 1.000124 | 1.000125 | 1.000126 | 1.000127 | 1.000128 | 1.000129 | 1.000130 | 1.000131 | 1.000132 | 1.000133 | 1.000134 | 1.000135 | 1.000136 | 1.000137 | 1.000138 | 1.000139 | 1.000140 | 1.000141 | 1.000142 | 1.000143 | 1.000144 | 1.000145 | 1.000146 | 1.000147 | 1.000148 | 1.000149 | 1.000150 | 1.000151 | 1.000152 | 1.000153 | 1.000154 | 1.000155 | 1.000156 | 1.000157 | 1.000158 | 1.000159 | 1.000160 | 1.000161 | 1.000162 | 1.000163 | 1.000164 | 1.000165 | 1.000166 | 1.000167 | 1.000168 | 1.000169 | 1.000170 | 1.000171 | 1.000172 | 1.000173 | 1.000174 | 1.000175 | 1.000176 | 1.000177 | 1.000178 | 1.000179 | 1.000180 | 1.000181 | 1.000182 | 1.000183 | 1.000184 | 1.000185 | 1.000186 | 1.000187 | 1.000188 | 1.000189 | 1.000190 | 1.000191 | 1.000192 | 1.000193 | 1.000194 | 1.000195 | 1.000196 | 1.000197 | 1.000198 | 1.000199 | 1.000200 | 1.000201 | 1.000202 | 1.000203 | 1.000204 | 1.000205 | 1.000206 | 1.000207 | 1.000208 | 1.000209 | 1.000210 | 1.000211 | 1.000212 | 1.000213 | 1.000214 | 1.000215 | 1.000216 | 1.000217 | 1.000218 | 1.000219 | 1.000220 | 1.000221 | 1.000222 | 1.000223 | 1.000224 | 1.000225 | 1.000226 | 1.000227 | 1.000228 | 1.000229 | 1.000230 | 1.000231 | 1.000232 | 1.000233 | 1.000234 | 1.000235 | 1.000236 | 1.000237 | 1.000238 | 1.000239 | 1.000240 | 1.000241 | 1.000242 | 1.000243 | 1.000244 | 1.000245 | 1.000246 | 1.000247 | 1.000248 | 1.000249 | 1.000250 | 1.000251 | 1.000252 | 1.000253 | 1.000254 | 1.000255 | 1.000256 | 1.000257 | 1.000258 | 1.000259 | 1.000260 | 1.000261 | 1.000262 | 1.000263 | 1.000264 | 1.000265 | 1.000266 | 1.000267 | 1.000268 | 1.000269 | 1.000270 | 1.000271 | 1.000272 | 1.000273 | 1.000274 | 1.000275 | 1.000276 | 1.000277 | 1.000278 | 1.000279 | 1.000280 | 1.000281 | 1.000282 | 1.000283 | 1.000284 | 1.000285 | 1.000286 | 1.000287 | 1.000288 | 1.000289 | 1.000290 | 1.000291 | 1.000292 | 1.000293 | 1.000294 | 1.000295 | 1.000296 | 1.000297 | 1.000298 | 1.000299 | 1.000300 | 1.000301 | 1.000302 | 1.000303 | 1.000304 | 1.000305 | 1.000306 | 1.000307 | 1.000308 | 1.000309 | 1.000310 | 1.000311 | 1.000312 | 1.000313 | 1.000314 | 1.000315 | 1.000316 | 1.000317 | 1.000318 | 1.000319 | 1.000320 | 1.000321 | 1.000322 | 1.000323 | 1.000324 | 1.000325 | 1.000326 | 1.000327 | 1.000328 | 1.000329 | 1.000330 | 1.000331 | 1.000332 | 1.000333 | 1.000334 | 1.000335 | 1.000336 | 1.000337 | 1.000338 | 1.000339 | 1.000340 | 1.000341 | 1.000342 | 1.000343 | 1.000344 | 1.000345 | 1.000346 | 1.000347 | 1.000348 | 1.000349 | 1.000350 | 1.000351 | 1.000352 | 1.000353 | 1.000354 | 1.000355 | 1.000356 | 1.000357 | 1.000358 | 1.000359 | 1.000360 | 1.000361 | 1.000362 | 1.000363 | 1.000364 | 1.000365 | 1.000366 | 1.000367 | 1.000368 | 1.000369 | 1.000370 | 1.000371 | 1.000372 | 1.000373 | 1.000374 | 1.000375 | 1.000376 | 1.000377 | 1.000378 | 1.000379 | 1.000380 | 1.000381 | 1.000382 | 1.000383 | 1.000384 | 1.000385 | 1.000386 | 1.000387 | 1.000388 | 1.000389 | 1.000390 | 1.000391 | 1.000392 | 1.000393 | 1.000394 | 1.000395 | 1.000396 | 1.000397 | 1.000398 | 1.000399 | 1.000400 | 1.000401 | 1.000402 | 1.000403 | 1.000404 | 1.000405 | 1.000406 | 1.000407 | 1.000408 | 1.000409 | 1.000410 | 1.000411 | 1.000412 | 1.000413 | 1.000414 | 1.000415 | 1.000416 | 1.000417 | 1.000418 | 1.000419 | 1.000420 | 1.000421 | 1.000422 | 1.000423 | 1.000424 | 1.000425 | 1.000426 | 1.000427 | 1.000428 | 1.000429 | 1.000430 | 1.000431 | 1.000432 | 1.000433 | 1.000434 | 1.000435 | 1.000436 | 1.000437 | 1.000438 | 1.000439 | 1.000440 | 1.000441 | 1.000442 | 1.000443 | 1.000444 | 1.000445 | 1.000446 | 1.000447 | 1.000448 | 1.000449 | 1.000450 | 1.000451 | 1.000452 | 1.000453 | 1.000454 | 1.000455 | 1.000456 | 1.000457 | 1.000458 | 1.000459 | 1.000460 | 1.000461 | 1.000462 | 1.000463 | 1.000464 | 1.000465 | 1.000466 | 1.000467 | 1.000468 | 1.000469 | 1.000470 | 1.000471 | 1.000472 | 1.000473 | 1.000474 | 1.000475 | 1.000476 | 1.000477 | 1.000478 | 1.000479 | 1.000480 | 1.000481 | 1.000482 | 1.000483 | 1.000484 | 1.000485 | 1.000486 | 1.000487 | 1.000488 | 1.000489 | 1.000490 | 1.000491 | 1.000492 | 1.000493 | 1.000494 | 1.000495 | 1.000496 | 1.000497 | 1.000498 | 1.000499 | 1.000500 | 1.000501 | 1.000502 | 1.000503 | 1.000504 | 1.000505 | 1.000506 | 1.000507 | 1.000508 | 1.000509 | 1.000510 | 1.000511 | 1.000512 | 1.000513 | 1.000514 | 1.000515 | 1.000516 | 1.000517 | 1.000518 | 1.000519 | 1.000520 | 1.000521 | 1.000522 | 1.000523 | 1.000524 | 1.000525 | 1.000526 | 1.000527 | 1.000528 | 1.000529 | 1.000530 | 1.000531 | 1.000532 | 1.000533 | 1.000534 | 1.000535 | 1.000536 | 1.000537 | 1.000538 | 1.000539 | 1.000540 | 1.000541 | 1.000542 | 1.000543 | 1.000544 | 1.000545 | 1.000546 | 1.000547 | 1.000548 | 1.000549 | 1.000550 | 1.000551 | 1.000552 | 1.000553 | 1.000554 | 1.000555 | 1.000556 | 1.000557 | 1.000558 | 1.000559 | 1.000560 | 1.000561 | 1.000562 | 1.000563 | 1.000564 | 1.000565 | 1.000566 | 1.000567 | 1.000568 | 1.000569 | 1.000570 | 1.000571 | 1.000572 | 1.000573 | 1.000574 | 1.000575 | 1.000576 | 1.000577 | 1.000578 | 1.000579 | 1.000580 | 1.000581 | 1.000582 | 1.000583 | 1.000584 | 1.000585 | 1.000586 | 1.000587 | 1.000588 | 1.000589 | 1.000590 | 1.000591 | 1.000592 | 1.000593 | 1.000594 | 1.000595 | 1.000596 | 1.000597 | 1.000598 | 1.000599 | 1.000600 | 1.000601 | 1.000602 | 1.000603 | 1.000604 | 1.000605 | 1.000606 | 1.000607 | 1.000608 | 1.000609 | 1.000610 | 1.000611 | 1.000612 | 1.000613 | 1.000614 | 1.000615 | 1.000616 | 1.000617 | 1.000618 | 1.000619 | 1.000620 | 1.000621 | 1.000622 | 1.000623 | 1.000624 | 1.000625 | 1.000626 | 1.000627 | 1.000628 | 1.000629 | 1.000630 | 1.000631 | 1.000632 | 1.000633 | 1.000634 | 1.000635 | 1.000636 | 1.000637 | 1.000638 | 1.000639 | 1.000640 | 1.000641 | 1.000642 | 1.000643 | 1.000644 | 1.000645 | 1.000646 | 1.000647 | 1.000648 | 1.000649 | 1.000650 | 1.000651 | 1.000652 | 1.000653 | 1.000654 | 1.000655 | 1.000656 | 1.000657 | 1.000658 | 1.000659 | 1.000660 | 1.000661 | 1.000662 | 1.000663 | 1.000664 | 1.000665 | 1.000666 | 1.000667 | 1.000668 | 1.000669 | 1.000670 | 1.000671 | 1.000672 | 1.000673 | 1.000674 | 1.000675 | 1.000676 | 1.000677 | 1.000678 | 1.000679 | 1.000680 | 1.000681 | 1.000682 | 1.000683 | 1.000684 | 1.000685 | 1.000686 | 1.000687 | 1.000688 | 1.000689 | 1.000690 | 1.000691 | 1.000692 | 1.000693 | 1.000694 | 1.000695 | 1.000696 | 1.000697 | 1.000698 | 1.000699 | 1.000700 | 1.000701 | 1.000702 | 1.000703 | 1.000704 | 1.000705 | 1.000706 | 1.000707 | 1.000708 | 1.000709 | 1.000710 | 1.000711 | 1.000712 | 1.000713 | 1.000714 | 1.000715 | 1.000716 | 1.000717 | 1.000718 | 1.000719 | 1.000720 | 1.000721 | 1.000722 | 1.000723 | 1.000724 | 1.000725 | 1.000726 | 1.000727 | 1.000728 | 1.000729 | 1.000730 | 1.000731 | 1.000732 | 1.000733 | 1.000734 | 1.000735 | 1.000736 | 1.000737 | 1.000738 | 1.000739 | 1.000740 | 1.000741 | 1.000742 | 1.000743 | 1.000744 | 1.000745 | 1.000746 | 1.000747 | 1.000748 | 1.000749 | 1.000750 | 1.000751 | 1.000752 | 1.000753 | 1.000754 | 1.000755 | 1.000756 | 1.000757 | 1.000758 | 1.000759 | 1.000760 | 1.000761 | 1.000762 | 1.000763 | 1.000764 | 1.000765 | 1.000766 | 1.000767 | 1.000768 | 1.000769 | 1.000770 | 1.000771 | 1.000772 | 1.000773 | 1.000774 | 1.000775 | 1.000776 | 1.000777 | 1.000778 | 1.000779 | 1.000780 | 1.000781 | 1.000782 | 1.000783 | 1.000784 | 1.000785 | 1.000786 | 1.000787 | 1.000788 | 1.000789 | 1.000790 | 1.000791 | 1.000792 | 1.000793 | 1.000794 | 1.000795 | 1.000796 | 1.000797 | 1.000798 | 1.000799 | 1.000800 | 1.000801 | 1.000802 | 1.000803 | 1.000804 | 1.000805 | 1.000806 | 1.000807 | 1.000808 | 1.000809 | 1.000810 | 1.000811 | 1.000812 | 1.000813 | 1.000814 | 1.000815 | 1.000816 | 1.000817 | 1.000818 | 1.000819 | 1.000820 | 1.000821 | 1.000822 | 1.000823 | 1.000824 | 1.000825 | 1.000826 | 1.000827 | 1.000828 | 1.000829 | 1.000830 | 1.000831 | 1.000832 | 1.000833 | 1.000834 | 1.000835 | 1.000836 | 1.000837 | 1.000838 | 1.000839 | 1.000840 | 1.000841 | 1.000842 | 1.000843 | 1.000844 | 1.000845 | 1.000846 | 1.000847 | 1.000848 | 1.000849 | 1.000850 | 1.000851 | 1.000852 | 1.000853 | 1.000854 | 1.000855 | 1.000856 | 1.000857 | 1.000858 | 1.000859 | 1.000860 | 1.000861 | 1.000862 | 1.000863 | 1.000864 | 1.000865 | 1.000866 | 1.000867 | 1.000868 | 1.000869 | 1.000870 | 1.000871 | 1.000872 | 1.000873 | 1.000874 | 1.000875 | 1.000876 | 1.000877 | 1.000878 | 1.000879 | 1.000880 | 1.000881 | 1.000882 | 1.000883 | 1.000884 | 1.000885 | 1.000886 | 1.000887 | 1.000888 | 1.000889 | 1.000890 | 1.000891 | 1.000892 | 1.000893 | 1.000894 | 1.000895 | 1.000896 | 1.000897 | 1.000898 | 1.000899 | 1.000900 | 1.000901 | 1.000902 | 1.000903 | 1.000904 | 1.000905 | 1.000906 | 1.000907 | 1.000908 | 1.000909 | 1.000910 | 1.000911 | 1.000912 | 1.000913 | 1.000914 | 1.000915 | 1.000916 | 1.000917 | 1.000918 | 1.000919 | 1.000920 | 1.000921 | 1.000922 | 1.000923 | 1.000924 | 1.000925 | 1.000926 | 1.000927 | 1.000928 | 1.000929 | 1.000930 | 1.000931 | 1.000932 | 1.000933 | 1.000934 | 1.000935 | 1.000936 | 1.000937 | 1.000938 | 1.000939 | 1.000940 | 1.000941 | 1.000942 | 1.000943 | 1.000944 | 1.000945 | 1.000946 | 1.000947 | 1.000948 | 1.000949 | 1.000950 | 1.000951 | 1.000952 | 1. |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----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[illegible]

0.7534875 1.020225 0.732857 0.854407 0.833085 1.032450 0.844031 0.822500 0.875539 0.825425 1.278023 0.910240 0.825794 1.295273 0.891611 0.883398 0.850189 0.888210 1.244053 0.804701 1.153732 0.824403 0.890071 0.897127  
 1.220483 -1.003977 1.096609 0.798408 0.843078 0.794832 0.863398 1.108772 1.027812 1.444105 1.133876 1.148378 1.088016 1.190287 1.234402 0.861188 0.812544 0.862850 1.261050 0.827034 0.717031 0.853028 0.796316 1.153386

12/44

Table 3D

|          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |       |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-------|
| 1.007008 | 1.006109 | 1.005805 | 1.005458 | 1.005113 | 1.004774 | 1.004444 | 1.004124 | 1.003814 | 1.003514 | 1.003224 | 1.002944 | 1.002674 | 1.002414 | 1.002164 | 1.001924 | 1.001694 | 1.001474 | 1.001264 | 1.001064 | 1.000874 | 1.000694 | 1.000524 | 1.000364 | 1.000214 | 1.000074 | 0.999944 | 0.999824 | 0.999714 | 0.999614 | 0.999524 | 0.999444 | 0.999374 | 0.999314 | 0.999264 | 0.999224 | 0.999194 | 0.999174 | 0.999164 | 0.999164 | 0.999174 | 0.999194 | 0.999224 | 0.999264 | 0.999314 | 0.999374 | 0.999444 | 0.999524 | 0.999614 | 0.999694 | 0.999794 | 0.999914 | 0.999994 | 1.000074 | 1.000164 | 1.000264 | 1.000374 | 1.000494 | 1.000624 | 1.000764 | 1.000914 | 1.001074 | 1.001244 | 1.001424 | 1.001614 | 1.001814 | 1.002024 | 1.002244 | 1.002474 | 1.002714 | 1.002964 | 1.003224 | 1.003494 | 1.003774 | 1.004064 | 1.004364 | 1.004674 | 1.004994 | 1.005324 | 1.005664 | 1.006014 | 1.006374 | 1.006744 | 1.007124 | 1.007514 | 1.007914 | 1.008324 | 1.008744 | 1.009174 | 1.009614 | 1.009994 | 1.010394 | 1.010814 | 1.011244 | 1.011684 | 1.012134 | 1.012594 | 1.013064 | 1.013544 | 1.014034 | 1.014534 | 1.015044 | 1.015564 | 1.016094 | 1.016634 | 1.017184 | 1.017744 | 1.018314 | 1.018894 | 1.019484 | 1.020084 | 1.020694 | 1.021314 | 1.021944 | 1.022584 | 1.023234 | 1.023894 | 1.024564 | 1.025244 | 1.025934 | 1.026634 | 1.027344 | 1.028064 | 1.028794 | 1.029534 | 1.030284 | 1.031044 | 1.031814 | 1.032594 | 1.033384 | 1.034184 | 1.034994 | 1.035814 | 1.036644 | 1.037484 | 1.038334 | 1.039194 | 1.040064 | 1.040944 | 1.041834 | 1.042734 | 1.043644 | 1.044564 | 1.045494 | 1.046434 | 1.047384 | 1.048344 | 1.049314 | 1.050294 | 1.051284 | 1.052284 | 1.053294 | 1.054314 | 1.055344 | 1.056384 | 1.057434 | 1.058494 | 1.059564 | 1.060644 | 1.061734 | 1.062834 | 1.063944 | 1.065064 | 1.066194 | 1.067334 | 1.068484 | 1.069644 | 1.070814 | 1.071994 | 1.073184 | 1.074384 | 1.075594 | 1.076814 | 1.078044 | 1.079284 | 1.080534 | 1.081794 | 1.083064 | 1.084344 | 1.085634 | 1.086934 | 1.088244 | 1.089564 | 1.090894 | 1.092234 | 1.093584 | 1.094944 | 1.096314 | 1.097694 | 1.099084 | 1.100484 | 1.101894 | 1.103314 | 1.104744 | 1.106184 | 1.107634 | 1.109094 | 1.110564 | 1.112044 | 1.113534 | 1.115034 | 1.116544 | 1.118064 | 1.119594 | 1.121134 | 1.122684 | 1.124244 | 1.125814 | 1.127394 | 1.128984 | 1.130584 | 1.132194 | 1.133814 | 1.135444 | 1.137084 | 1.138734 | 1.140394 | 1.142064 | 1.143744 | 1.145434 | 1.147134 | 1.148844 | 1.150564 | 1.152294 | 1.154034 | 1.155784 | 1.157544 | 1.159314 | 1.161094 | 1.162884 | 1.164684 | 1.166494 | 1.168314 | 1.170144 | 1.171984 | 1.173834 | 1.175694 | 1.177564 | 1.179444 | 1.181334 | 1.183234 | 1.185144 | 1.187064 | 1.189 |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-------|

[illegible]





0.7087613 0.5953007 0.7007169 1.0787328 0.7315663 0.7327857 1.1727872 1.1548872 1.0760527 1.0376784 1.2022715 1.0344188 0.8422717 0.7046209 0.9500944 0.8818374 0.8470119 0.6250662 0.7463376 0.8323774 0.6884178 1.0035818 1.1724354 1.0225513  
1.2050854 1.0179003 0.9009119 0.8234679 0.9414569 1.2208302 1.0071785 0.9886951 1.0562556 1.1214382 1.0883303 0.9503358 0.8508114 1.1818522 0.8473186 1.0603282 1.0534348 1.0600867 1.2282522 1.1827241 1.0701689 1.2030885 1.1153306 1.1218444

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Table 39





[illegible]

|          |          |          |          |          |          |          |          |           |           |          |          |          |          |          |          |          |          |
|----------|----------|----------|----------|----------|----------|----------|----------|-----------|-----------|----------|----------|----------|----------|----------|----------|----------|----------|
| 1.215007 | 0.632405 | 1.181302 | 0.944200 | 0.988997 | 0.941320 | 1.181323 | 0.974427 | -1.022356 | -1.377356 | 2.250397 | 0.784023 | 0.864208 | 0.853738 | 2.351325 | 0.471731 | 1.184512 | 2.727470 |
| 1.084062 | 3.732629 | 0.763467 | 2.382163 | 1.244031 | 0.656977 | 0.914320 | 1.181323 | 0.974427  | -1.022356 | 2.250397 | 0.784023 | 0.864208 | 0.853738 | 2.351325 | 0.471731 | 1.184512 | 2.727470 |
| 1.028675 | 1.028675 | 1.028675 | 1.028675 | 1.028675 | 1.028675 | 1.028675 | 1.028675 | 1.028675  | 1.028675  | 1.028675 | 1.028675 | 1.028675 | 1.028675 | 1.028675 | 1.028675 | 1.028675 | 1.028675 |
| 0.874068 | 0.874068 | 0.874068 | 0.874068 | 0.874068 | 0.874068 | 0.874068 | 0.874068 | 0.874068  | 0.874068  | 0.874068 | 0.874068 | 0.874068 | 0.874068 | 0.874068 | 0.874068 | 0.874068 | 0.874068 |
| 1.161175 | 1.161293 | 0.880442 | 0.705467 | 0.800718 | 0.811712 | 0.825305 | 0.820019 | 0.817724  | 0.855677  | 0.811639 | 0.865401 | 0.811639 | 0.865401 | 0.811639 | 0.865401 | 0.811639 | 0.865401 |
| 1.011705 | 1.312401 | 0.800000 | 1.350007 | 1.495437 | 1.223816 | 1.011712 | 0.800000 | 1.350007  | 1.495437  | 1.223816 | 1.011712 | 0.800000 | 1.350007 | 1.495437 | 1.223816 | 1.011712 | 0.800000 |
| 0.011307 | 0.414758 | 1.336213 | 1.237164 | 1.377164 | 1.336213 | 1.113251 | 1.001132 | 1.278242  | 1.278242  | 1.113251 | 1.001132 | 1.278242 | 1.278242 | 1.113251 | 1.001132 | 1.278242 | 1.278242 |
| 0.712552 | 0.712552 | 0.712552 | 0.712552 | 0.712552 | 0.712552 | 0.712552 | 0.712552 | 0.712552  | 0.712552  | 0.712552 | 0.712552 | 0.712552 | 0.712552 | 0.712552 | 0.712552 | 0.712552 | 0.712552 |
| 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000  | 0.000000  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| 1.011339 | 0.846412 | 0.777146 | 0.827016 | 0.827016 | 0.846412 | 0.777146 | 0.827016 | 0.827016  | 0.846412  | 0.777146 | 0.827016 | 0.827016 | 0.846412 | 0.777146 | 0.827016 | 0.827016 | 0.846412 |
| 1.201359 | 0.968772 | 0.760414 | 0.737611 | 0.830645 | 0.830645 | 1.214547 | 0.830645 | 0.830645  | 1.214547  | 0.830645 | 0.830645 | 1.214547 | 0.830645 | 0.830645 | 1.214547 | 0.830645 | 0.830645 |
| 0.070224 | 0.845312 | 0.645022 | 0.300207 | 0.205651 | 1.780318 | 0.960831 | 1.257479 | 1.040033  | 1.040033  | 1.780318 | 0.960831 | 1.257479 | 1.040033 | 1.040033 | 1.780318 | 0.960831 | 1.257479 |
| 0.873142 | 1.167043 | 0.650641 | 1.183014 | 1.376075 | 0.300138 | 1.251543 | 0.811675 | 0.811675  | 1.376075  | 0.300138 | 1.251543 | 0.811675 | 0.811675 | 1.376075 | 0.300138 | 1.251543 | 0.811675 |
| 1.118697 | 0.884136 | 0.757025 | 0.674527 | 0.674527 | 0.884136 | 0.757025 | 0.674527 | 0.674527  | 0.884136  | 0.757025 | 0.674527 | 0.674527 | 0.884136 | 0.757025 | 0.674527 | 0.674527 | 0.884136 |
| 0.803015 | 0.811470 | 0.597723 | 1.040011 | 1.131379 | 1.145264 | 1.144276 | 1.040011 | 1.131379  | 1.145264  | 1.144276 | 1.040011 | 1.131379 | 1.145264 | 1.144276 | 1.040011 | 1.131379 | 1.145264 |
| 0.873145 | 1.150659 | 0.28282  | 1.180478 | 1.28282  | 1.150659 | 0.28282  | 1.180478 | 1.28282   | 1.150659  | 0.28282  | 1.180478 | 1.28282  | 1.150659 | 0.28282  | 1.180478 | 1.28282  | 1.150659 |
| 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000  | 0.000000  | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| 1.138202 | 1.594721 | 0.009359 | 0.781672 |          |          |          |          |           |           |          |          |          |          |          |          |          |          |

1.051287 0.702744 0.041171 0.648845 0.675507 0.702611 0.673158 0.671954 0.707173 1.158772 1.048114 1.437827 1.054582 1.117236 0.606724 1.230511 1.104813 1.224237 1.302504 0.620727 1.214158 0.820417 0.560854  
0.637033 0.406345 1.382104 0.000886 0.711681 0.705783 0.662215 1.301328 1.028286 1.071374 1.048114 1.437827 1.054582 1.117236 0.606724 1.230511 1.104813 1.224237 0.711464 0.702582 1.072872 1.130403 1.227187



|           |           |          |           |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |
|-----------|-----------|----------|-----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| 1.130532  | 0.9051821 | 1.241012 | 1.204129  | 1.373133 | 0.860294 | 0.912130 | 0.917767 | 0.862906 | 0.944108 | 0.824059 | 1.021322 | 0.877705 | 1.000489 | 0.079822 | 2.056437 | 0.862375 | 0.416828 | 0.842584 | 0.806029 | 0.813811 |
| 1.184415  | 0.845439  | 1.174762 | 0.953714  | 1.307151 | 1.140500 | 0.908778 | 1.041506 | 0.897070 | 0.920726 | 1.042221 | 1.175912 | 1.110103 | 0.950779 | 1.315715 | 1.214533 | 0.020275 | 0.105749 | 0.955314 | 1.229447 | 0.806509 |
| 0.993526  | 0.846458  | 0.945351 | 0.773227  | 0.868897 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 | 0.830272 |
| 0.927165  | 0.803004  | 0.973811 | 0.835865  | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 | 0.835865 |
| 1.185454  | 0.874507  | 1.251479 | 1.274424  | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 | 1.274424 |
| 0.91087   | 0.937443  | 0.965079 | 1.026144  | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 | 1.026144 |
| 1.14072   | 0.971914  | 1.084307 | 1.182327  | 0.952158 | 1.014071 | 1.080718 | 1.020148 | 1.154561 | 0.930138 | 0.850403 | 0.782323 | 0.726238 | 0.692564 | 0.669214 | 0.646558 | 0.624077 | 0.601671 | 0.579265 | 0.556859 | 0.534453 |
| 1.177778  | 0.758089  | 0.828017 | 1.381535  | 1.241517 | 1.021187 | 1.015231 | 1.032445 | 0.930219 | 0.850403 | 0.782323 | 0.726238 | 0.692564 | 0.669214 | 0.646558 | 0.624077 | 0.601671 | 0.579265 | 0.556859 | 0.534453 | 0.512047 |
| 0.921395  | 0.841185  | 1.007561 | 0.964445  | 0.925769 | 0.870889 | 0.815961 | 0.761033 | 0.706105 | 0.651177 | 0.596249 | 0.541321 | 0.486393 | 0.431465 | 0.376537 | 0.321609 | 0.266681 | 0.211753 | 0.156825 | 0.101897 | 0.046969 |
| 0.711806  | 0.871314  | 0.917618 | 0.782327  | 0.815769 | 0.848712 | 0.881655 | 0.914598 | 0.947541 | 0.980484 | 1.013427 | 1.046370 | 1.079313 | 1.112256 | 1.145199 | 1.178142 | 1.211085 | 1.244028 | 1.276971 | 1.309914 | 1.342857 |
| 0.508023  | 0.394003  | 0.653277 | 0.805157  | 0.843701 | 0.882244 | 0.920787 | 0.959330 | 0.997873 | 1.036416 | 1.074959 | 1.113502 | 1.152045 | 1.190588 | 1.229131 | 1.267674 | 1.306217 | 1.344760 | 1.383303 | 1.421846 | 1.460389 |
| 0.048891  | 0.017134  | 0.017886 | 0.022701  | 0.027516 | 0.032331 | 0.037146 | 0.041961 | 0.046776 | 0.051591 | 0.056406 | 0.061221 | 0.066036 | 0.070851 | 0.075666 | 0.080481 | 0.085296 | 0.090111 | 0.094926 | 0.099741 | 0.104556 |
| 0.460911  | 0.558122  | 0.614271 | 0.69477   | 0.804182 | 0.941187 | 1.081181 | 1.241001 | 1.415138 | 1.604468 | 1.809018 | 2.039018 | 2.294018 | 2.574018 | 2.879018 | 3.209018 | 3.564018 | 3.944018 | 4.349018 | 4.779018 | 5.234018 |
| 0.077943  | 0.144119  | 0.19121  | 0.253514  | 0.323514 | 0.403514 | 0.493514 | 0.593514 | 0.703514 | 0.823514 | 0.953514 | 1.093514 | 1.243514 | 1.403514 | 1.573514 | 1.753514 | 1.943514 | 2.143514 | 2.353514 | 2.573514 | 2.803514 |
| 0.563004  | 0.370769  | 0.90118  | 0.453053  | 0.723768 | 1.016107 | 1.323768 | 1.647171 | 1.986818 | 2.349818 | 2.734818 | 3.140818 | 3.568818 | 4.018818 | 4.490818 | 4.984818 | 5.499818 | 6.034818 | 6.589818 | 7.164818 | 7.759818 |
| 0.597188  | 0.222148  | 0.501919 | 0.076439  | 0.765021 | 1.474711 | 0.802311 | 1.090338 | 1.011214 | 0.709134 | 0.321347 | 0.108134 | 0.031347 | 0.008134 | 0.001347 | 0.000134 | 0.000013 | 0.000001 | 0.000000 | 0.000000 | 0.000000 |
| 1.180404  | 0.483347  | 1.205464 | 1.190084  | 0.255142 | 0.925244 | 0.873512 | 0.950329 | 1.023316 | 1.081347 | 1.126347 | 1.160347 | 1.184347 | 1.200347 | 1.209347 | 1.213347 | 1.214347 | 1.214847 | 1.215047 | 1.215147 | 1.215247 |
| 0.787408  | 0.678365  | 0.635368 | 0.623328  | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 | 0.623328 |
| 0.7053175 | 0.678093  | 0.788237 | 0.823372  | 0.856859 | 1.251186 | 1.075541 | 1.204188 | 1.342188 | 1.489188 | 1.645188 | 1.810188 | 1.984188 | 2.167188 | 2.358188 | 2.557188 | 2.764188 | 2.988188 | 3.229188 | 3.487188 | 3.763188 |
| 0.1079453 | 0.094523  | 0.277018 | 0.960879  | 0.603843 | 0.977513 | 0.920273 | 0.846818 | 0.751818 | 0.640818 | 0.510818 | 0.370818 | 0.220818 | 0.060818 | 0.000818 | 0.000018 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| 0.758850  | 0.477581  | 0.745053 | 0.727697  | 0.623553 | 0.607513 | 0.582513 | 0.557513 | 0.532513 | 0.507513 | 0.482513 | 0.457513 | 0.432513 | 0.407513 | 0.382513 | 0.357513 | 0.332513 | 0.307513 | 0.282513 | 0.257513 | 0.232513 |
| 0.733168  | 0.576116  | 0.677755 | 0.543229  | 0.635371 | 0.741723 | 0.853071 | 0.969423 | 1.090775 | 1.217127 | 1.348479 | 1.484831 | 1.626183 | 1.772535 | 1.923887 | 2.080239 | 2.242591 | 2.410943 | 2.585295 | 2.765647 | 2.951999 |
| 0.568465  | 0.36437   | 0.768422 | 0.765438  | 0.828198 | 1.277491 | 1.182891 | 1.128291 | 1.073691 | 1.019091 | 0.964491 | 0.909891 | 0.855291 | 0.800691 | 0.746091 | 0.691491 | 0.636891 | 0.582291 | 0.527691 | 0.473091 | 0.418491 |
| 1.102975  | 0.980614  | 1.27114  | 1.208013  | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 | 1.208013 |
| 0.711726  | 0.306918  | 0.76904  | 0.833178  | 0.844804 | 0.850378 | 0.855952 | 0.861526 | 0.867100 | 0.872674 | 0.878248 | 0.883822 | 0.889396 | 0.894970 | 0.900544 | 0.906118 | 0.911692 | 0.917266 | 0.922840 | 0.928414 | 0.933988 |
| 0.889093  | 0.820048  | 0.804545 | 0.811557  | 0.816404 | 0.821251 | 0.826098 | 0.830945 | 0.835792 | 0.840639 | 0.845486 | 0.850333 | 0.855180 | 0.860027 | 0.864874 | 0.869721 | 0.874568 | 0.879415 | 0.884262 | 0.889109 | 0.893956 |
| 0.810507  | 0.810507  | 0.810507 | 0.810507  | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 | 0.810507 |
| 0.474753  | 0.454137  | 0.636868 | 0.708270  | 0.806353 | 1.250418 | 1.186918 | 1.213378 | 1.239838 | 1.266298 | 1.292758 | 1.319218 | 1.345678 | 1.372138 | 1.398598 | 1.425058 | 1.451518 | 1.477978 | 1.504438 | 1.530898 | 1.557358 |
| 0.919237  | 0.377086  | 0.676459 | 0.708595  | 0.847479 | 1.017045 | 1.128891 | 1.266298 | 1.425058 | 1.604468 | 1.804468 | 2.024468 | 2.264468 | 2.524468 | 2.804468 | 3.104468 | 3.424468 | 3.764468 | 4.124468 | 4.504468 | 4.904468 |
| 1.805115  | 0.787087  | 1.42972  | 1.27130   | 1.01823  | 1.409721 | 1.062753 | 0.828358 | 0.623758 | 0.450758 | 0.309758 | 0.189758 | 0.099758 | 0.049758 | 0.024758 | 0.012379 | 0.006189 | 0.003094 | 0.001547 | 0.000773 | 0.000387 |
| 1.200772  | 1.723519  | 0.927593 | 0.781312  | 0.832228 | 0.850737 | 0.865737 | 0.878737 | 0.890737 | 0.901737 | 0.911737 | 0.921737 | 0.931737 | 0.941737 | 0.951737 | 0.961737 | 0.971737 | 0.981737 | 0.991737 | 1.001737 | 1.011737 |
| 0.776184  | 0.641058  | 0.884239 | 0.884239  | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 | 0.884239 |
| 1.105042  | 0.777511  | 0.841556 | 0.813442  | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 | 0.800455 |
| 1.007715  | 0.254268  | 0.859441 | 0.800265  | 0.840404 | 1.006254 | 1.050561 | 1.093437 | 1.135813 | 1.177189 | 1.218565 | 1.259941 | 1.301317 | 1.342693 | 1.384069 | 1.425445 | 1.466821 | 1.508197 | 1.549573 | 1.590949 | 1.632325 |
| 0.723091  | 0.683741  | 0.828869 | 0.877748  | 0.941458 | 1.135317 | 1.202882 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 | 0.971230 |
| 1.216153  | 1.277118  | 1.385511 | 1.305168  | 1.175171 | 0.757778 | 0.441534 | 0.943332 | 0.971418 | 1.004448 | 1.041978 | 1.084448 | 1.131978 | 1.184448 | 1.241978 | 1.304448 | 1.371978 | 1.444448 | 1.521978 | 1.604448 | 1.691978 |
| 0.250041  | 1.00844   | 0.644901 | 1.008476  | 0.625811 | 0.981418 | 1.004448 | 0.971418 | 0.944448 | 0.917418 | 0.890448 | 0.863448 | 0.836448 | 0.809448 | 0.782448 | 0.755448 | 0.728448 | 0.701448 | 0.674448 | 0.647448 | 0.620448 |
| 0.819523  | 0.801134  | 0.833105 | 0.848118  | 0.863072 | 0.878085 | 0.893098 | 0.908111 | 0.923124 | 0.938137 | 0.953150 | 0.968163 | 0.983176 | 0.998189 | 1.013202 | 1.028215 | 1.043228 | 1.058241 | 1.073254 | 1.088267 | 1.103280 |
| 1.18423   | 1.10174   | 1.133108 | 1.004168  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  | 1.07943  |
| 0.342122  | 0.207547  | 0.458372 | 0.420748  | 0.477543 | 0.483714 | 0.489885 | 0.496056 | 0.502227 | 0.508398 | 0.514569 | 0.520740 | 0.526911 | 0.533082 | 0.539253 | 0.545424 | 0.551595 | 0.557766 | 0.563937 | 0.570108 | 0.576279 |
| 0.418753  | 0.200877  | 0.645819 | 0.643141  | 0.722386 | 0.917225 | 1.044964 | 1.217203 | 1.521913 | 1.868268 | 2.258018 | 2.692268 | 3.170518 | 3.692768 | 4.259018 | 4.869268 | 5.523518 | 6.222768 | 6.967018 | 7.756268 | 8.590518 |
| 1.271692  | 0.464604  | 1.040737 | 1.043948  | 0.970354 | 0.917225 | 0.864096 | 0.810967 | 0.757838 | 0.704709 | 0.651580 | 0.598451 | 0.545322 | 0.492193 | 0.439064 | 0.385935 | 0.332806 | 0.279677 | 0.226548 | 0.173419 | 0.120290 |
| 0.072029  | 0.727862  | 1.007222 | 0.647325  | 0.502501 | 1.025461 | 1.254123 | 1.414108 | 1.511532 | 1.558956 | 1.606380 | 1.653804 | 1.701228 | 1.748652 | 1.796076 | 1.843500 | 1.890924 | 1.938348 | 1.985772 | 2.033196 | 2.080620 |
| 1.08668   | 1.028714  | 0.857519 | 1.001429  | 1.203575 | 1.022891 | 0.804804 | 0.571981 | 0.349158 | 0.126335 | 0.093512 | 0.060689 | 0.027866 | 0.005043 | 0.002220 | 0.000397 | 0.000074 | 0.000001 | 0.000000 | 0.000000 | 0.000000 |
| 0.411234  | 0.308476  | 0.623115 | 0.6179813 |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |





0.459428 0.220414 0.729400 0.407847 0.716435 1.025457 1.320233 1.227739 1.335089 1.050170 1.215234 1.207492 0.855377 0.785751 0.653024 1.080796 0.812804 0.973472 1.304943 0.823448 1.007546 0.320225 1.043327 1.150787  
 1.407324 1.345944 1.330432 1.134339 1.058449 0.854078 0.988942 0.841258 0.871329 0.843011 0.858161 1.115178 1.247509 1.115788 0.855301 0.911324 0.856929 0.859881 0.881298 0.855388 0.833876 0.949591 0.898342  
 1.408304 1.346944 1.331432 1.135339 1.059449 0.855078 0.989942 0.842258 0.872329 0.844011 0.859161 1.116178 1.248509 1.116788 0.856301 0.912324 0.857929 0.860881 0.882298 0.856388 0.834876 0.950591 0.903342

24/44

Table 30



[illegible]



1

0.8071709 1.2537666 1.143287 1.140183 1.304725 0.710228 0.8152018 0.949102 0.8712043 0.8853712 0.885319 1.300813 1.317204 1.430377 1.487288 0.880076 1.041339 0.8452943 0.945478 0.880285 0.8180107 1.002294 0.880008 1.154515  
 1.001800 0.8801802 0.7711481 0.8434311 0.781438 0.861853 1.078742 1.102828 1.082297 1.000882 0.8882208 0.940287 0.8409186 0.8082704 1.0117881 0.8382529 0.864048 1.118231 1.1820847 1.387208 1.722354 1.028583 1.885510 1.225349

2844

Total 28

[illegible]

[illegible]





0.682471 1.012781 0.808159 0.852078 1.013843  
 0.700797 1.256472 1.078159 1.247228 1.294528  
 1 0.840633 1.047162 0.863518 0.860787 0.828705  
 1.41312 1.081214 1.043055 0.80729 1.047562 0.822501 0.745091 0.800302 0.94395 0.820137 0.881150 1.12181 1.1742816  
 1.23148 1.028498 0.855044 0.903508 0.859653 1.028184 0.828398 1.081702 1.418807 0.872788 1.028128 1.009104 0.800304

32/44

Table 39



**WALL**



[illegible]

1.180272 1.200209 0.887505 0.780034 0.594137 0.809015 0.688769 0.810358 1.278223 2.068598 1.551223 1.207839 1.173699 1.1810213 0.744397 0.806677 0.748329 1.029247 1.382298 1.388115 0.7785317 1.0480489 0.8753588 0.844473  
 0.8234008 1.0233843 0.8882119 0.9136599 1.1301272 1.0725455 0.878698 0.8400049 0.8610527 0.888827 1.0181512 0.8200357 0.953625 0.776075 1.388278 1.4518284 1.0660573 1.218892 1.1847946 0.840981 1.121547 0.781541 0.0800288 0.9794013



17/185





0.006661 0.7904137 1.2965275 1.0818246 1.321374 0.9311317 0.9133398 1.104759 1.281578 1.2790304 0.8792716 1.0278417 0.8223977 0.7799337 1.0285378 0.5311053 1.1001825 0.8304606 1.143517 1.1028243 1.542209 0.8064492 1.8289816 0.8747799  
 1.0441546 1.0411309 1.2351808 1.144879 0.8331893 0.8830309 0.8723307 0.9118173 1.2011258 1.4142776 1.055982 0.8843319 0.851009 1.2014601 0.872928 1.144899 0.8901859 0.8005528 0.8795898 0.8277238 0.865318 0.7778912 -0.007161 0.4371523



| UPS | 8 | 356 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 | 526 | 527 | 528 | 529 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 538 | 539 | 540 | 541 | 542 | 543 | 544 | 545 | 546 | 547 | 548 | 549 | 550 | 551 | 552 | 553 | 554 | 555 | 556 | 557 | 558 | 559 | 560 | 561 | 562 | 563 | 564 | 565 | 566 | 567 | 568 | 569 | 570 | 571 | 572 | 573 | 574 | 575 | 576 | 577 | 578 | 579 | 580 | 581 | 582 | 583 | 584 | 585 | 586 | 587 | 588 | 589 | 590 | 591 | 592 | 593 | 594 | 595 | 596 | 597 | 598 | 599 | 600 | 601 | 602 | 603 | 604 | 605 | 606 | 607 | 608 | 609 | 610 | 611 | 612 | 613 | 614 | 615 | 616 | 617 | 618 | 619 | 620 | 621 | 622 | 623 | 624 | 625 | 626 | 627 | 628 | 629 | 630 | 631 | 632 | 633 | 634 | 635 | 636 | 637 | 638 | 639 | 640 | 641 | 642 | 643 | 644 | 645 | 646 | 647 | 648 | 649 | 650 | 651 | 652 | 653 | 654 | 655 | 656 | 657 | 658 | 659 | 660 | 661 | 662 | 663 | 664 | 665 | 666 | 667 | 668 | 669 | 670 | 671 | 672 | 673 | 674 | 675 | 676 | 677 | 678 | 679 | 680 | 681 | 682 | 683 | 684 | 685 | 686 | 687 | 688 | 689 | 690 | 691 | 692 | 693 | 694 | 695 | 696 | 697 | 698 | 699 | 700 | 701 | 702 | 703 | 704 | 705 | 706 | 707 | 708 | 709 | 710 | 711 | 712 | 713 | 714 | 715 | 716 | 717 | 718 | 719 | 720 | 721 | 722 | 723 | 724 | 725 | 726 | 727 | 728 | 729 | 730 | 731 | 732 | 733 | 734 | 735 | 736 | 737 | 738 | 739 | 740 | 741 | 742 | 743 | 744 | 745 | 746 | 747 | 748 | 749 | 750 | 751 | 752 | 753 | 754 | 755 | 756 | 757 | 758 | 759 | 760 | 761 | 762 | 763 | 764 | 765 | 766 | 767 | 768 | 769 | 770 | 771 | 772 | 773 | 774 | 775 | 776 | 777 | 778 | 779 | 780 | 781 | 782 | 783 | 784 | 785 | 786 | 787 | 788 | 789 | 790 | 791 | 792 | 793 | 794 | 795 | 796 | 797 | 798 | 799 | 800 | 801 | 802 | 803 | 804 | 805 | 806 | 807 | 808 | 809 | 810 | 811 | 812 | 813 | 814 | 815 | 816 | 817 | 818 | 819 | 820 | 821 | 822 | 823 | 824 | 825 | 826 | 827 | 828 | 829 | 830 | 831 | 832 | 833 | 834 | 835 | 836 | 837 | 838 | 839 | 840 | 841 | 842 | 843 | 844 | 845 | 846 | 847 | 848 | 849 | 850 | 851 | 852 | 853 | 854 | 855 | 856 | 857 | 858 | 859 | 860 | 861 | 862 | 863 | 864 | 865 | 866 | 867 | 868 | 869 | 870 | 871 | 872 | 873 | 874 | 875 | 876 | 877 | 878 | 879 | 880 | 881 | 882 | 883 | 884 | 885 | 886 | 887 | 888 | 889 | 890 | 891 | 892 | 893 | 894 | 895 | 896 | 897 | 898 | 899 | 900 | 901 | 902 | 903 | 904 | 905 | 906 | 907 | 908 | 909 | 910 | 911 | 912 | 913 | 914 | 915 | 916 | 917 | 918 | 919 | 920 | 921 | 922 | 923 | 924 | 925 | 926 | 927 | 928 | 929 | 930 | 931 | 932 | 933 | 934 | 935 | 936 | 937 | 938 | 939 | 940 | 941 | 942 | 943 | 944 | 945 | 946 | 947 | 948 | 949 | 950 | 951 | 952 | 953 | 954 | 955 | 956 | 957 | 958 | 959 | 960 | 961 | 962 | 963 | 964 | 965 | 966 | 967 | 968 | 969 | 970 | 971 | 972 | 973 | 974 | 975 | 976 | 977 | 978 | 979 | 980 | 981 | 982 | 983 | 984 | 985 | 986 | 987 | 988 | 989 | 990 | 991 | 992 | 993 | 994 | 995 | 996 | 997 | 998 | 999 | 1000 |
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1.6595153 0.786209 0.833254 0.760175 0.751701 0.585645 0.610712  
 0.5371837 0.6891115 0.276201 0.777377 0.6490376 0.600135 0.667597  
 1.310428 0.744882 0.787298 0.610706 0.6780023 0.785498 0.5445647  
 1.0242776 0.501606 1.224098 0.803234 0.788215 0.715180 0.622469  
 0.812881 1.168357 1.451765 1.560779 1.786051 1.507873  
 1.405923 1.274627 1.767764 1.507701 0.2303664 1.9842438  
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 2.432353 0.930397 1.249001 1.051168 1.7871486 1.448153 1.321155  
 1.626344 1.611625 1.468386 1.168631 2.036346 1.468354 1.72551  
 2.1484687 0.620009 0.732778 1.822747 0.82534 0.673759 1.11896  
 1.824234 1.419337 1.816365 0.618747 2.38755 0.317236 0.630517  
 1.72564 0.732773 0.738106 0.535361 0.516599 0.424728 0.54907  
 1.6359455 1.942324 0.576066 1.088367 1.710578 1.450223 0.852054  
 1.480386 1.422032 1.227811 1.073438 1.505046 1.150389 1.28156  
 0.672866 0.623121 0.870787 0.710548 0.658189 0.48415 0.634787  
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 0.9116381 0.757382 0.912913 0.6872181 0.422204 0.533656 0.3795407  
 1.0095402 0.940565 0.486435 0.687903 1.358316 1.212633 1.117218  
 1.024706 0.80585 0.80585 0.735656 1.11846 0.658189 0.634787  
 0.643477 0.598795 0.640987 0.675179 0.655293 0.617586 0.465713  
 1.047943 0.515159 0.755387 0.824521 1.258409 1.027054 1.3729137  
 0.5645726 1.028445 0.682095 0.632698 0.724514 0.779166 0.743864  
 1.2001963 1.2427781 1.168393 1.213382 2.03174 1.885768 2.4185815  
 1.280768 0.658144 0.6354851 0.737634 0.8310845 0.7430628 0.5946412  
 0.4273003 0.9755345 0.829384 1.0062422 0.8160377 1.127368 1.018715  
 0.6320034 0.902377 0.762077 0.800520 0.665689 0.8891309 0.7205904  
 0.786986 0.854366 0.9424797 0.821195 0.7525881 0.5547307 0.8026301  
 1.887209 1.123468 1.802805 1.084165 1.548412 1.128388 1.803748  
 0.7420718 0.871189 1.019116 0.738446 0.679184 0.679184 0.679184  
 0.742107 0.882889 1.075585 0.818713 0.308182 0.303723 0.35133  
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 0.7825236 0.6531787 0.5174894 0.8113037 0.575872 0.6474705 0.6395865  
 0.5044148 0.644854 0.5347878 0.8655432 0.1268887 0.2045717 0.1301288  
 0.618837 0.7595462 0.8708743 0.7747434 0.2903087 0.2031371 0.2281183  
 1.0181017 0.875306 0.5518612 0.8113021 0.5118419 0.7425568 0.756209  
 0.9001211 0.9711873 0.522333 0.703178 0.5604078 0.7833028 0.8897141  
 1.074013 0.830453 0.511769 0.68081 0.588181 0.588181 0.588181  
 0.804378 0.853770 0.7288126 0.889695 0.326215 1.292675 1.202478 1.2884123  
 0.7431776 1.094628 1.44283 1.060603 1.044025 1.000225 0.8741301  
 0.6152243 0.8851508 0.5550773 0.655374 0.5877089 0.340020 0.216391  
 1.0721178 1.402848 0.1768966 1.588246 1.272707 0.954325 1.0081482  
 0.6589543 1.1187 0.5377543 1.034452 0.6330068 0.9420807 0.8463647  
 1.8488682 0.688443 0.8850777 0.681440 1.4323133 0.8180237 1.3005277  
 1.700059 0.8894454 1.0315104 0.8828841 1.1883317 1.1301106 1.1004464  
 1.4827768 1.202924 0.8508003 0.9499107 0.7002848 0.6476801 0.8271102  
 0.6004568 1.1124412 0.633265 0.9732817 0.680252 0.779254 0.519171  
 1.1889574 1.02774 1.02774 1.02774 1.02774 1.02774 1.02774  
 1.646282 1.0081872 0.7286461 1.144336 1.1596833 1.484289 1.5575737  
 1.1007859 0.650381 0.821129 0.6157247 0.8824881 0.880302 0.8272149  
 1.1007134 0.5057789 0.4822691 0.3541012 0.3885153 0.3359971 0.2213891  
 0.5888704 1.048453 0.5878012 1.0182725 0.8915875 0.8804083 0.8884482  
 0.0075239 0.7383597 0.867536 0.6721481 0.6203773 0.5915491 0.400386  
 0.4607583 0.8546883 0.7540038 0.7596623 0.7711803 0.6853882 0.8118091  
 0.9895359 1.2183182 0.8302778 0.180378 1.2138481 1.001884 0.7954464  
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 0.589082 1.0044817 0.3720037 0.825428 0.534483 0.6182578  
 0.4815301 0.3512831 0.4897078 0.7314387 0.6875187 0.6303728 0.7150268



1.437456 0.753313 0.800798 0.68885 1.270808 0.823331 0.885546  
0.628801 1.287597 0.818318 1.053358 0.827048 0.828154 0.873108

4/14

Table 39

## What is claimed is:

- [c1] A method of predicting the kidney toxicity in an individual to an agent, comprising the steps of:
- obtaining a biological sample from an individual treated with the agent;
- measuring the expression of one or more kidney toxicity predictive genes in the sample, wherein the genes are selected from the group consisting of the genes corresponding to the partial gene sequences in Table 32, thereby generating a test expression profile; and
- using the test expression profile with a set of reference expression profiles in a Predictive Model to determine whether the agent will induce kidney toxicity in the individual.
- [c2] The method according to claim 1, wherein the expression of the kidney toxicity predictive gene is measured at the RNA level.
- [c3] The method according to claim 1, wherein the expression of the kidney toxicity predictive gene is measured at the protein level.
- [c4] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo All.
- [c5] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 6.
- [c6] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 5.

- [c7] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 4.
- [c8] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 3.
- [c9] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 2.
- [c10] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 1.
- [c11] The method according to claim 3, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo All.
- [c12] The method according to claim 3, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 6.
- [c13] The method according to claim 3, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 5.
- [c14] The method according to any of the preceding claims 1-13, wherein the expression of at least one gene is measured.
- [c15] The method according to any of the preceding claims 1-13, wherein the expression of at least five genes is measured.
- [c16] The method according to any of the preceding claims 1-13, wherein the expression of at least ten genes is measured.
- [c17] The method according to any of the preceding claims 1-13, wherein the expression of at least fifteen genes is measured.
- [c18] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo All.

- [c19] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo 6.
- [c20] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo 4.
- [c21] The method according to claim 3, wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo All.
- [c22] The method according to claim 3, wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo 6.
- [c23] The method according to claim 3, wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo 4.
- [c24] The method according to any of the preceding claims 18-23, wherein the expression of at least one gene is measured.
- [c25] The method according to any of the preceding claims 18-23, wherein the expression of at least five genes is measured.
- [c26] The method according to any of the preceding claims 18-23, wherein the expression of at least ten genes is measured.
- [c27] The method according to any of the preceding claims 18-23, wherein the expression of at least fifteen genes is measured.
- [c28] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo All.
- [c29] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 6.
- [c30] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 5.

- [c31] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 4.
- [c32] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 3.
- [c33] The method according to claim 2, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 1.
- [c34] The method according to claim 3, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo All.
- [c35] The method according to claim 3, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 6.
- [c36] The method according to claim 3, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 4.
- [c37] The method according to any of the preceding claims 28-36, wherein at least one gene is used.
- [c38] The method according to any of the preceding claims 28-36, wherein at least five genes are used.
- [c39] The method according to any of the preceding claims 28-36, wherein at least ten genes are used.
- [c40] The method according to any of the preceding claims 28-36, wherein at least fifteen genes are used.
- [c41] The method according to any one of claims 1-13, 18-23, or 28-36, wherein the partial gene sequences correspond to rat genes.
- [c42] The method according to any one of claims 1-13, 18-23, or 28-36, wherein the partial gene sequences correspond to dog genes.



- [c43] The method according to any one of claims 1-13, 18-23, or 28-36, wherein the partial gene sequences correspond to non-human primate genes.
- [c44] The method according to any one of claims 1-13, 18-23, or 28-36, wherein the partial gene sequences correspond to human genes.
- [c45] The method according to claim 41, wherein the agent is administered at different dose levels to determine the presence or absence of a no-observable effect level.
- [c46] The method according to claim 42, wherein the agent is administered at different dose levels to determine the presence or absence of a no-observable effect level.
- [c47] The method according to claim 43, wherein the agent is administered at different dose levels to determine the presence or absence of a no-observable effect level.
- [c48] The method according to claim 44, wherein the agent is administered at different dose levels to determine the presence or absence of a no-observable effect level.
- [c49] A method of predicting the kidney toxicity of an agent using an in vitro system, comprising the steps of:  
obtaining a biological sample from in vitro cultured cells or explants treated with the agent;  
measuring the expression of one or more kidney toxicity predictive genes in the sample, wherein the genes are selected from the group consisting of the genes corresponding to the partial gene sequences in Table 32, thereby generating a test expression profile; and  
using the test expression profile with a set of reference expression profiles in a Predictive Model to determine whether the agent will induce kidney toxicity.

- [c50] The method according to claim 49, wherein the expression of the kidney toxicity predictive gene is measured at the RNA level.
- [c51] The method according to claim 49, wherein the expression of the kidney toxicity predictive gene is measured at the protein level.
- [c52] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo All.
- [c53] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 6.
- [c54] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 5.
- [c55] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 4.
- [c56] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 3.
- [c57] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 2.
- [c58] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 1.
- [c59] The method according to claim 51, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo All.
- [c60] The method according to claim 51, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 6.
- [c61] The method according to claim 51, wherein the genes corresponding to the partial gene sequences are members of 24 hour Combo 4.

- [c62] The method according to any of the preceding claims 50-61, wherein the expression of at least one gene is measured.
- [c63] The method according to any of the preceding claims 50-61, wherein the expression of at least five genes is measured.
- [c64] The method according to any of the preceding claims 50-61, wherein the expression of at least ten genes is measured.
- [c65] The method according to any of the preceding claims 50-61, wherein the expression of at least fifteen genes is measured.
- [c66] The method according to claim 50 wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo All.
- [c67] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo 6.
- [c68] The method according to claim 50 wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo 4.
- [c69] The method according to claim 51, wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo All.
- [c70] The method according to claim 51, wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo 6.
- [c71] The method according to claim 51 wherein the genes corresponding to the partial gene sequences are members of 6 hour Combo 4.
- [c72] The method according to any of the preceding claims 66-71, wherein the expression of at least one gene is measured.
- [c73] The method according to any of the preceding claims 66-71, wherein the expression of at least five genes is measured.

- [c74] The method according to any of the preceding claims 66-71, wherein the expression of at least ten genes is measured.
- [c75] The method according to any of the preceding claims 66-71, wherein the expression of at least fifteen genes is measured.
- [c76] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo All.
- [c77] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 6.
- [c78] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 5.
- [c79] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 4.
- [c80] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 3.
- [c81] The method according to claim 50, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 1.
- [c82] The method according to claim 51, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo All.
- [c83] The method according to claim 51, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 6.
- [c84] The method according to claim 51, wherein the genes corresponding to the partial gene sequences are members of 72 hour Combo 4.
- [c85] The method according to any of the preceding claims 76-84, wherein the expression of at least one gene is measured.

- [c86] The method according to any of the preceding claims 76-84, wherein the expression of at least five genes is measured.
- [c87] The method according to any of the preceding claims 76-84, wherein the expression of at least ten genes is measured.
- [c88] The method according to any of the preceding claims 76-84, wherein the expression of at least fifteen genes is measured.
- [c89] The method according to any one of claims 50-61, 66-71, or 76-84, wherein the partial gene sequences correspond to rat genes.
- [c90] The method according to any one of claims 50-61, 66-71, or 76-84, wherein the partial gene sequences correspond to dog genes
- [c91] The method according to any one of claims 50-61, 66-71, or 76-84, wherein the partial gene sequences correspond to non-human primate genes.
- [c92] The method according to any one of claims 50-61, 66-71, or 76-84, wherein the partial gene sequences correspond to human genes.
- [c93] The method according to claim 89, wherein the agent is administered at different dose levels to determine the presence or absence of a no-observable effect level.
- [c94] The method according to claim 90, wherein the agent is administered at different dose levels to determine the presence or absence of a no-observable effect level.
- [c95] The method according to claim 91, wherein the agent is administered at different dose levels to determine the presence or absence of a no-observable effect level.
- [c96] The method according to claim 92, wherein the agent is administered at

different dose levels to determine the presence or absence of a no-observable effect level.

- [c97] A computer program product for predicting kidney toxicity from a test sample expression profile, comprising:  
an encrypted training data set;  
encrypted lists of genes selected from the group consisting of the genes corresponding to the partial gene sequences in Table 32, to be used with the training set, and  
a Predictive Model that uses said training set, said lists of genes, and said test sample expression profile to predict the kidney toxicity of the test sample.
- [c98] The computer program product of claim 97, wherein the encrypted lists of genes comprise the 24 hour Combo 6, 24 hour Combo 5, 24 hour Combo 4, 24 hour Combo3, 24 hour Combo 2, and 24 hour Combo 1 gene lists.
- [c99] The computer program product of claim 97, wherein the encrypted lists of genes comprise the 6 hour Combo 6, 6 hour Combo 5, 6 hour Combo 4, 6 hour Combo 3, 6 hour Combo 2, and 6 hour Combo 1 gene lists.
- [c100] The computer program product of claim 97, wherein the encrypted lists of genes comprise the 72 hour Combo 6, 72 hour Combo 5, 72 hour Combo 4, 72 hour Combo 3, hour Combo 2, and 72 hour Combo 1 gene lists.
- [c101] The computer program product of claim 97, wherein the prediction is made through the calculation of a certitude score.
- [c102] A method for mining genes predictive for kidney toxicity, comprising the steps of:  
collecting expression levels of a plurality of candidate toxicity predictive genes among a multiplicity of samples;  
defining a group of samples to be a training set;  
defining another group of samples to be a test set;

optionally generating additional training and test sets; and  
selecting a set of genes which are predictive of kidney toxicity based on  
evaluating the training and test sets in a Predictive Model.

[c103] The method according to claim 102, wherein the expression levels are  
stored as a database on an electronic medium.

[c104] An integrated system for predicting kidney toxicity, comprising:  
means for measuring gene expression profiles of kidney predictive genes  
from biological samples exposed to the test agent; and  
a computer system operably linked to said means that is capable of  
implementing a predictive model.

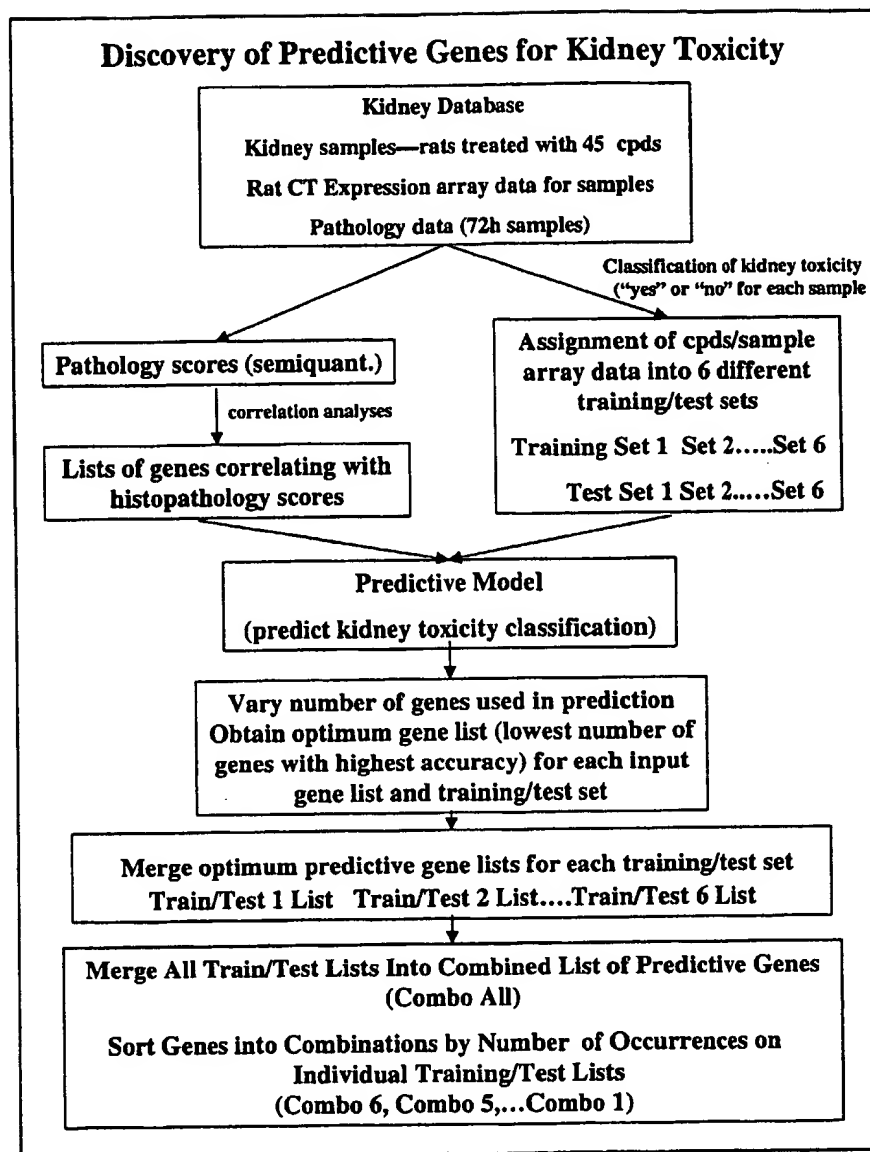


Figure 1



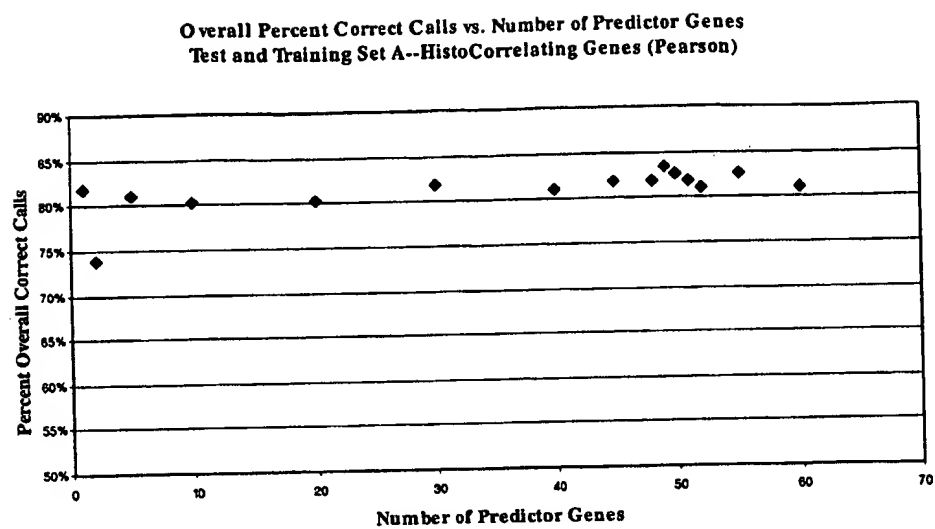


Figure 2

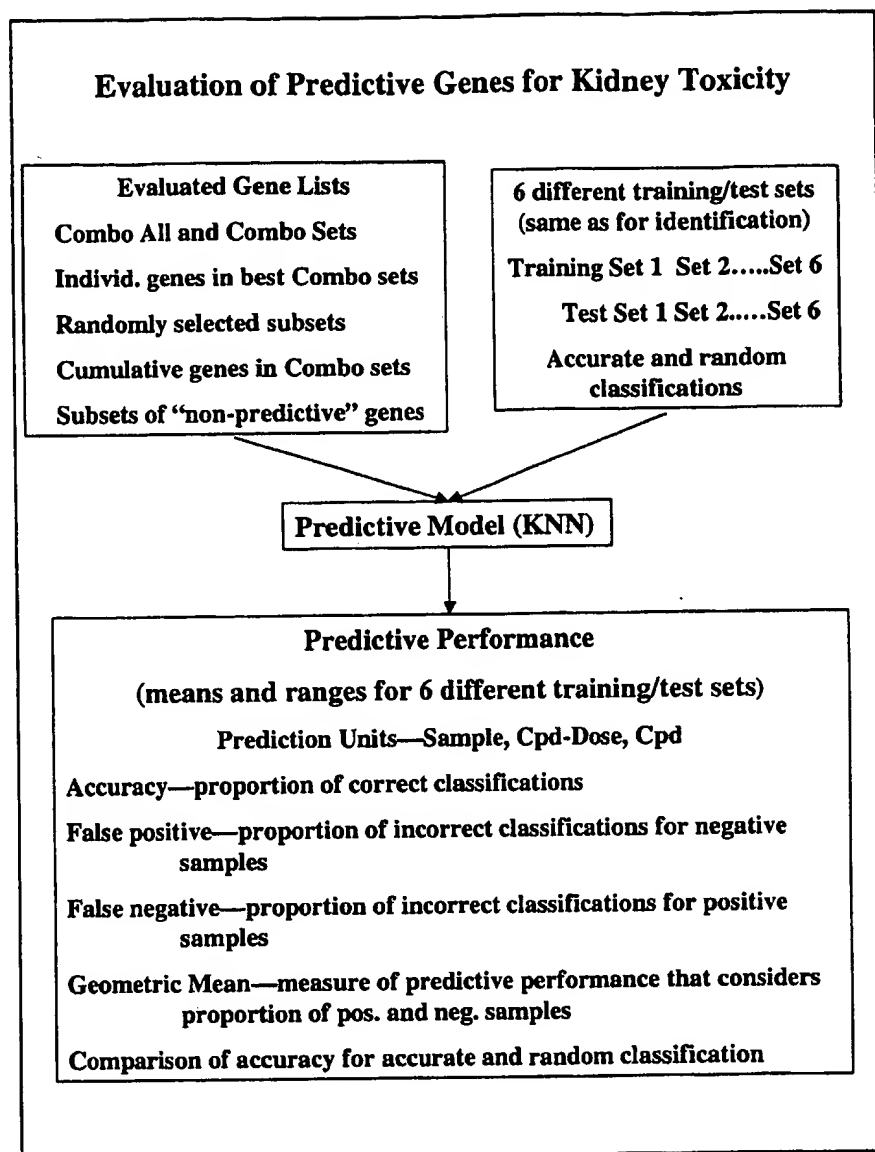


Figure 3

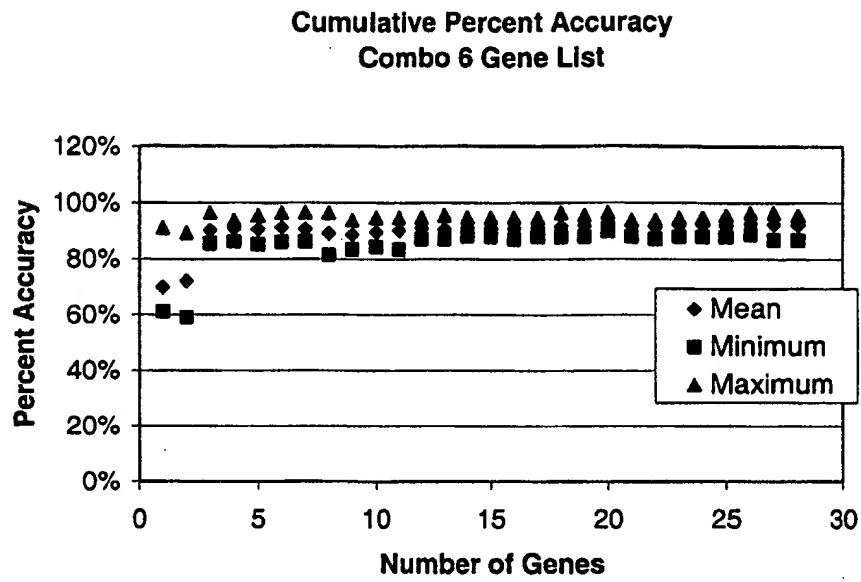


Figure 4

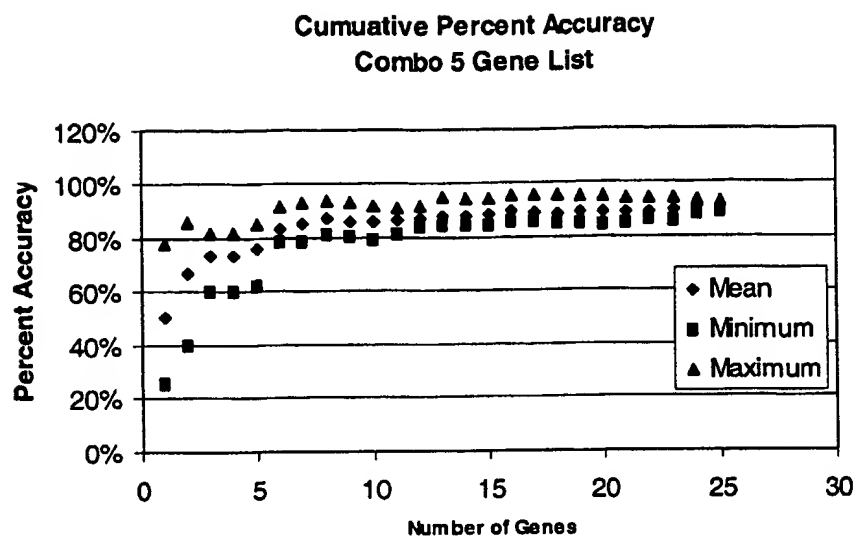


Figure 5

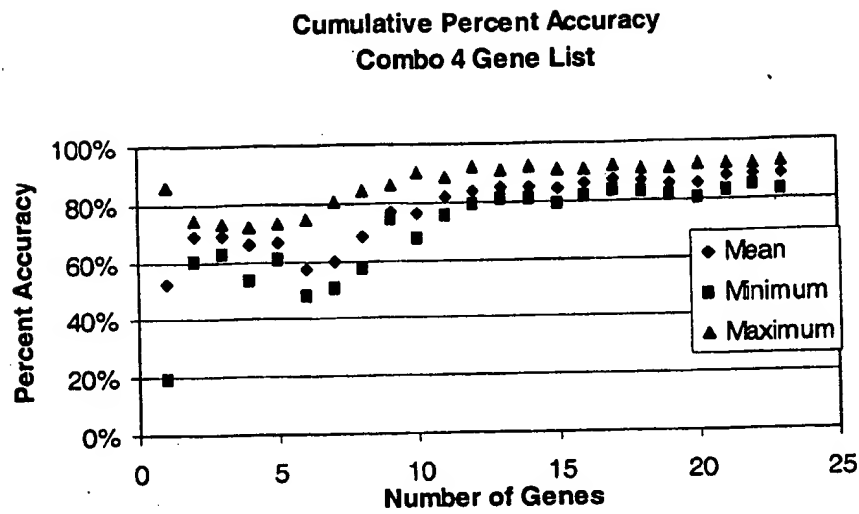


Figure 6

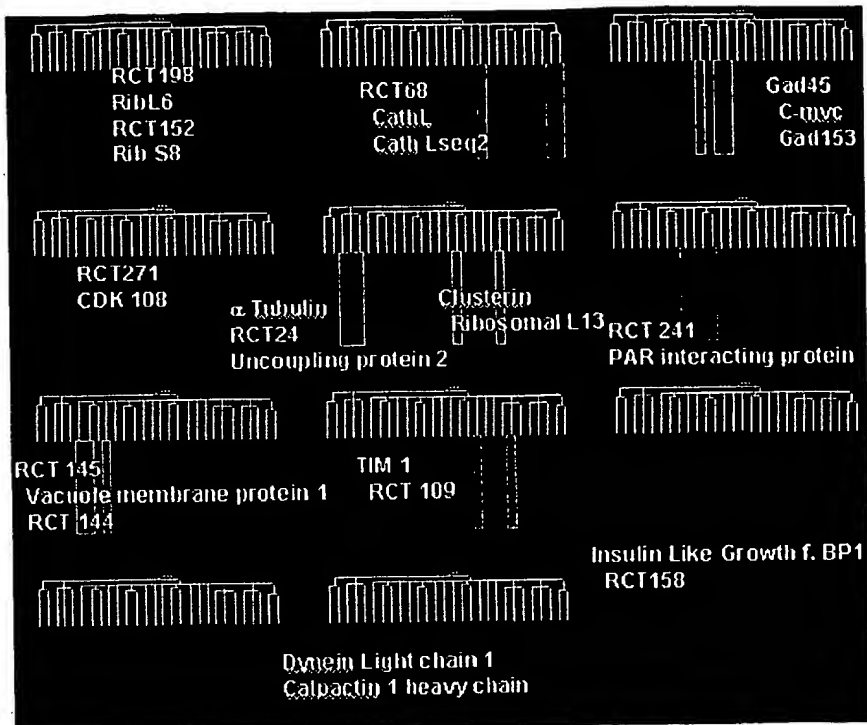


Figure 7

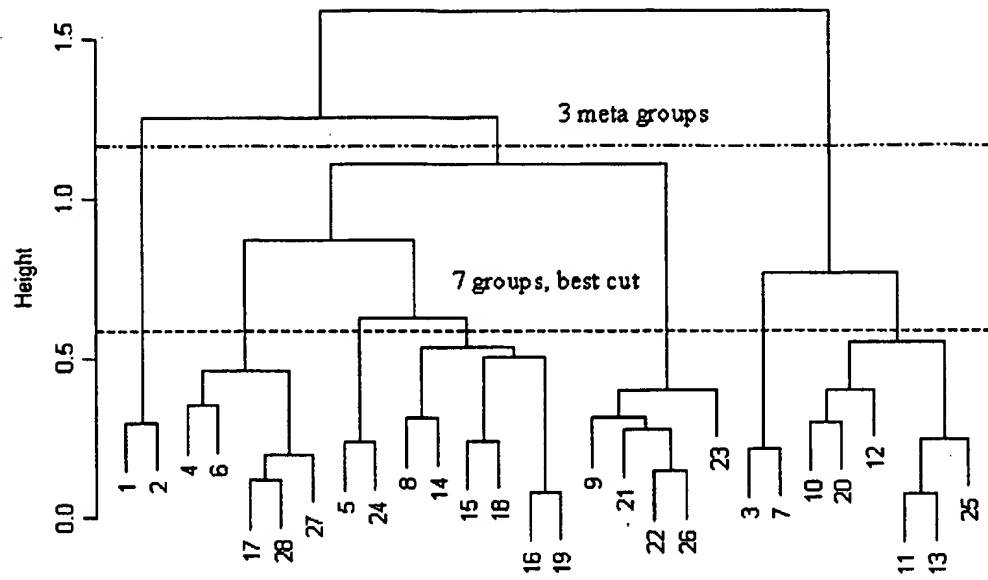
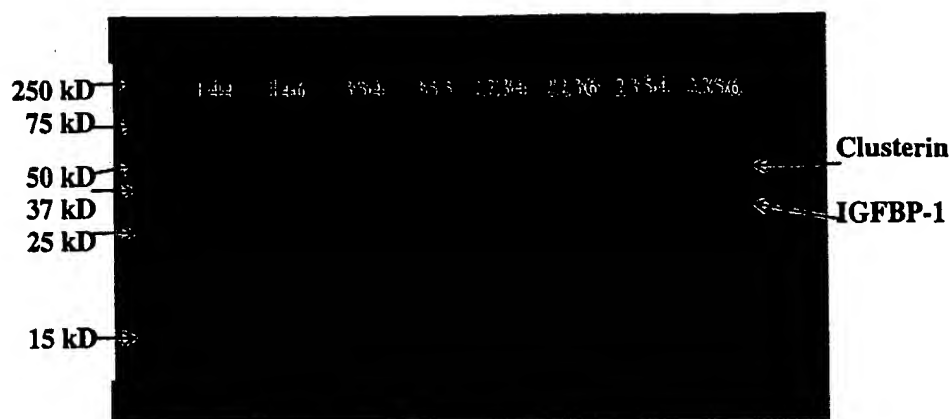


Figure 8

| Cluster Number | Clustering with 7 Groups                     |
|----------------|--|
|                | <b>Group 1</b>                               |
| 1              | Phase.1.RCT.271                              |
| 2              | CDK108                                       |
|                | <b>Group 2</b>                               |
| 4              | Phase.1.RCT.145                              |
| 6              | Phase.1.RCT.144                              |
| 17             | Ribosomal.protein.L6                         |
| 18             | Ribosomal.protein.S8                         |
| 27             | Phase.1.RCT.152                              |
|                | <b>Group 3</b>                               |
| 5              | Vacuole membrane protein 1                   |
| 24             | Phase.1.RCT.241                              |
|                | <b>Group 4</b>                               |
| 8              | Insulin.like.growth.factor.binding.protein.1 |
| 14             | Tissue.inhibitor.of.metalloproteinases.1     |
| 15             | Phase.1.RCT.68                               |
| 18             | Calpactin.I.heavy.chain                      |
| 16             | Cathepsin.L.sequence.2                       |
| 19             | Cathepsin.L                                  |
|                | <b>Group 5</b>                               |
| 9              | Phase.1.RCT.158                              |
| 21             | c.myc  |
| 22             | Gadd45                                       |
| 26             | PAR.interacting.protein                      |
| 23             | Gadd153                                      |
|                | <b>Group 6</b>                               |
| 3              | Alpha.tubulin                                |
| 7              | Phase.1.RCT.24                               |
|                | <b>Group 7</b>                               |
| 11             | Clusterin                                    |
| 20             | Ribosomal.protein.L13A                       |
| 12             | Uncoupling.protein.2                         |
| 11             | Phase.1.RCT.109                              |
| 13             | Dynein.light.chain.1                         |
| 26             | Phase.1.RCT.198                              |

Figure 8 (continued)





| Animal | Treatment                     | Kidney<br>Tox. | IGFBP-1<br>Diff. Expression |
|--------|-------------------------------|----------------|-----------------------------|
| 144    | polyethylene glycol – 5 mL/kg | No             | 1.22                        |
| 146    | polyethylene glycol – 5 mL/kg | No             | 1.16                        |
| 354    | LPS—8 mg/kg                   | Yes            | 18.13                       |
| 355    | LPS—8 mg/kg                   | Yes            | 5.14                        |
| 2234   | ketoconazole—80 mg/kg         | No             | -1.04                       |
| 2236   | ketoconazole—80 mg/kg         | No             | -1.07                       |
| 2354   | chloroform—0.5 mL/kg          | Yes            | 1.93                        |
| 2356   | chloroform—0.5 mL/kg          | Yes            | 8.86                        |

Figure 9

Table 32 Genes Predictive for Kidney Tubular Necrosis, Sequences, and Accession Numbers

| Gene Name  | Accession Number | Sequence   |
|--|------------------|--|
| 14-3-3 zeta  | D17615           | TGGNGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT<br>CGCCCTTCGCGGGATCCAAAAAGCAGCAGATGGCTCGAGAATACAGAGAGAAGATCGAGACGGAG<br>CTGAGGGACATCTGCAACGACGTACTGTCTCTTTGGAAAAGTTCTTGATCCCCAATGCTTCGCA<br>GCCAGAAAGCAAAGTCTTCTATTGAAAATGAAGGGTGACTACTACCGCTACTTGGCTGAGGTTG<br>CTGCTGGTGTGATGACAGAAAGGAATTGTGGACCAGTCACAGCAAGCATAACCAAGAAGCATTGAA<br>ATCAGCAAAAAGGAGATGCAGCCGACACACCCCATCAGACTGGGTCTGGCCCTCAACTTCTCTGT<br>GTTCTACTATGAGATCCTGAAC'TCCCCAGAGAAAGCCTGCTCTCTTGCAAAAACAGCTTTTGATG<br>AAGCCATGTCTGAAC'TTGATACATTAAGTGAAGAGTCGTACAAAGACAGCAGCTAATAATGCAG<br>TTACTGAGAGACAAC'TTGACATTGTGGACATCGGATACCCAAGGAGACGAAGCAGAAAAGCTTGG<br>CCAAGGGCGAATTCCAGCACACTGGCGGGCCGNACTAGTGGATNCGAGCTCNGTACCCAGCTTTG<br>ATGCATA   |
| 25-DX  | U6315            | TGCGATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCTG<br>CCCTTACACACACAGTGGCCCCAAATGGTCAATGTACTAAGAATGAAGAGAGAAGGTCTTAGCCA<br>TGCTATAGTCTGAAAACAAGCCCATTTTACCCAACAGACTTAACTGCATGATTTTGT'TTATCT<br>ACCTCTAAAGCAAACTGCAGTGTTCAAAGTCTGTGGTATTGATTCAAAACAGAAGTCCAGTAA<br>CAAAATGAAACTCAATATATGGGTTTAGTTGGGGCAAACACATTGCCTGTGTTCATGGACTGATT<br>TATCATCCCTGTCCCCACGTGGACACTCCCACACACAGTAAC'TCACACACCTGGTAATTGGCA<br>GTTGGAACTACAACAGAATCTGAAAATTCAGGTAGAACTTTGCAAAAAGAAAAATCTGTTGCATG<br>TAGCAGGGCAATGGTTATGTGTTATTGGCCAAATGTAAAATTTGAGAGCAATATACAGGACAGG<br>AACAGGTGTGCGCTAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGG<br>TACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTGGCACCTAAATAGCTTGGCGTAATCATGG<br>NCATAGCTGTTTCTGTGTGAAATTTGGTATTCCGCTCACAATTCACACAACATCCGAGCCGGA<br>AGCATTAAGTGT |
| 25-hydroxyvitamin<br>D3-1 alpha-<br>hydroxylase        | AB001992         | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCTG<br>CCCTTAACTAACAGCCCCAGGCAGCTTGGGCAGGGATCCCCACTGATCCTTCCATGCTTAGCAGT<br>GTTCACTGACAGCTGTCTAAGCATCCATTGCAGCACAACTAAGTGACTGTGCACCTGGTCTGCA<br>CCTGGTCTGCACCTGGTTGCGTCTCTGCGTGACCATGTGAGCTCTTTGAGAAGAGTGATGACTAC<br>TGGGCTTTTAGCTCTTTTCTTTTGGGACACAGTCTTGCTATTGTACTCCATGCTGTCTTGA<br>CCCACAAGCCCTCACCTCACCTTCCCAAGTGTGGGTACGGACATTAGCTATGGCTTCCAGCTT<br>TATTAGTCTTTCTATCTCCTGCCATGGTCTATCCCCGCTATTTGATACTATATATCTCAGATT<br>GAATCTGGACCATGTGGTAGAAGGGATGACCACTCACCAGGCTCTACCCACCACCTTATCTTAAT<br>CTTTCTCTAGGAAAGTGAATCTCTCCTTGCCTTACAGCATTTTAAAGCTCCCCTGGCTGTTCT<br>GCTCTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGNACCAACTT<br>GATGCATAAGCTTGAGTATTCTATAGGNCACCTAAATAGCT  |
| 3-beta-<br>hydroxysteroid<br>dehydrogenase<br>(HSD3B1) | AA923963         | NGCCAAGCTAAAATTAACCTCACTAAAGGGAATAAGCTNGCGNCCCGCAANGNTATTTNTTTNA<br>TANTTTTTTNNNTTAAAGCCATTACAATATTTATTGCTTTATAAATCAATGAGATATAACCAAAG<br>CAGGATGTGATTTAGGACTTGAAGAGGAACAGAAAAGTAATACTCAGCTCTAAGTGACAGGAAAT<br>TGTCATTGCTGAAGCCTTTGGTTCACAGCAGCTGAGGCACAACCTACCTGTGTGTCTCTGGACAGGG<br>GATTAGGGAAGAAAGCTTTGGACTAGCAAGGCTTCCAGTGAAGTCAATAAGACATAGAGTTAGA<br>GTCTGTGTCAAAAGAGGGCATCAGGACCTGGATTGTGCCTCTGTCTAGCTGGAGGACCTGGTAA<br>CACCCAGAACCACATCCTTGCCCCCTTTCTGTCACTGAGACTTTGTGTCCAGTGTCTCCCTGTGC<br>TGCTCCACTAGTGTCCCGATCCACTCCGAGGTTTTCTGCTTGGCTTCTCCAGCTGACAAGTGG<br>CACATAGCCCAGATCTCTCTGAGCTTTCTGTAGGAGAAAGTGAAC'TTGCTATTTGACAGTGTGA<br>CCAAGTGGCAGTTAAAGGGTGGCCTATAGTTGTAATACTCTCGTGCCGAATCTTGGCCCTCGAGG<br>GCCAAATTCCTATAGTGAGTAGTATTAAATTCGTAATCATGTCATAGAG                             |

|  |           |  |
|--|-----------|--|
| 3-hydroxyisobutyrate dehydrogenase           | J04628    | CCNNNNCTATGACATGATTACGAATTTACTACGACTCACTATAGGGAATTTGGCCCTCGAGGCCA<br>AGAATTCGGCACGAGGAGCGACACTTACAACCCCTGTACCTGGGGTTATGGATGGAGTTCCCTCAT<br>CTAATAACTACCAAGGTGGATTTGGGACAACACTCATGGCCAAGGATCTGGGATTAGCTCAAGAC<br>TCTGCCACCAGCACCAGACCCCAATTTCTCCTCGGAAGCGTGGCCCATCAGATATACAGGATGAT<br>GTGTTCAAAGGGCTACTCAAAGAAAGACTTCTCCTCTGTGTTCAGTATCTGCGGGAGGAGGAAA<br>CCTTCTGACTGCCCTGTGGTCATGGACACTGTTAGGAACCAACTCTGTCTGAGCTTCTTCTA<br>GCTCATTTCTAGAAGTCATGGGTTTAAATCAAAGGTCATCTGTCTGCTTTTGATTGTCTACATTATA<br>GCAATCCCTGGGGATTTTATCCATTTTAAATGCTGCTGCTTTCATCTGTTAGCAAACACACCC<br>AATGGTTTCCACTGACTAGCCAGTTGACCTTTTAAAGTTTGAACCTTGAGCACCTTAAACAAA<br>ATTGAGCACTCTGATCAGGATATTTTATTTTACTCTGCTTTACNAATAAAACCAAATGGTTTGT<br>TAACAAGATGGAACCATGGTAAAAAGGAAAAAATCAGTTN                             |
| 3-methyladenine DNA glycosylase              | X56420    | AATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCGCAGTGTGATGGATATCTGCAGAATTCGCCCT<br>TGACAGGTCTTGTCCGGCGACTTGTGATGGAAACAGAACTCCGTGGGCGCATTTAGAGACTGA<br>GGCATACTTGGGGCCAGAAGACGAAGCTGCCCCTCAAGGGGTGGCCGCGAGACCCCCCGTAACC<br>GTGGCATGTTTATGAACTTGAACCTGTACGTGTACCTCATCTATGGCATGTACTTCTGCTTG<br>AATGCTCTCCAGTCAAGGGGCTGGGGCTTGTGCTTGTCTAAGAGCACTAGAGCCATTGGAGGGCT<br>AGAGACCATGCGGCGAGCTTCGAAACTCCCTCCGGAAGACACTGTGCGCCGTTCCTCAAGGACC<br>GCGAGCTCTGTAATGGTCCCTCCAACTGTGCCAGGCCCTAGCCATGATAAGAGCTTTGACCAG<br>CGAGACCTGNCCTAAGATAGGCTGGGTGGCTGGAGCATGGCCCTCTGGAGTCCAGCAGCCAGC<br>TGTGGTGGCGGCGAGCCGCATAGGTATTGGCCATGCACGGGAATGGACACACAAGCCAGGGCGA<br>ATTCCAGCACACTGNCGGGCGNTACTAATGGATCCAACCTCGGNACCAANCTTGATGCATANCTTG<br>GGATTCTATATGGCACCTAAAACTTGGNGAATATGGGATACT                               |
| 60S ribosomal protein L6                     | X87107    | ANCGGGCCCTCTAGATGCATGCTCGAGCGGCCGCGCAGTGTGATGGATATCTGCAGAATTCGCCCT<br>TCGCGGGATCCGGTGAAGCTTCGAAAAATGCCTAGGTATTACCTACTGAAGACGTGCCTCGGAA<br>GCTGCTGAGCCACGGCAAGAAGCCCTTCAGCCAGCACGTGAGGAGGCTGCGCTCCAGCATCACTC<br>CCGGGACTGTCTGATCATCTCACTGGGCGCCGCGAGGGCAAGAGAGTGGTTTTCTCAAGCAG<br>CTGGGCGAGTGGCTTGTACTTGTGACTGGACCTCTTGCCCCAACAGAGTTCTCTGCGTAGGAC<br>ACACCAGAAGTTTGTCTATCGCCACCTCTACAAAAGTTGATATCAGCAAGGTAAAAATCCCAAAC<br>ACCTGACTGATGCTTACTTCAAGAAGAAGCCACTTCGCAAGCCAGGCATCAGGAGGGTGAGATC<br>TTCGACACAGAGAAGGAGAAATACGAAATTACAGAGCAGCGAAAGGCTGATCAGAAAGCTGTGGA<br>CTCGCAGATTTTGCCTAAGATCAAAGCTGTCCCCAGCTTCAGGGCTACCTGCTTGCANGGCCA<br>ANGGCGAATTCAGCACACTTGGCGGGCGGTACTAGTGGGATNCCN   |
| 60S ribosomal protein L6 (alternate clone 1) | X87107    | CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGAGCTGAGGAAGAGTAAGCCCCATTGCAGCCGGAACCCCTGTCTGTTGAGAGGAAT<br>CGGCAGGTATTACGATCTGCTATGTATTCCAGAAAGGCCCTGTACAAAAGGAAATACTCTGCTG<br>CCAAGACAAAGTTGAGAAGAAGAAGAAGAAAGGTCCTTGCTACCGTCACAAAAACAGTT<br>GGTGGGGACAAAGACGGTGGCACCCGGGTGGTGAAGCTTCGAAAAATGCCATAGGTATTACCTTAC<br>TGAAGACGTGCCTCGGAAGCTGCTGAGCCACGGCAAGAAGCCCTTCAGCCAGCACGTGAGGAGGC<br>TGCGCTCCAGCATCACTCCCGGACTGTCTGATCATCTCACTGGGCGCCACAGGGGCAAGAGA<br>GTGGTTTTTCTCAAGCAGCTGGGCACTGGCTTGTACTTGTGACTGGACCTCTTGCCCTCAACAG<br>AGTTCTCTGCGTAGGACACACCAGAAGTTTGTCTATCGCCACCTCTACAAAAGTTGATATCAGCA<br>AGGGTAAATTTCCAAACACCTGACTGATGCTTACTTCAAGAAGAAGCCACTTCGCAAGCCAGG<br>CATTAGGANGGTGAGA   |
| Acetylcholine receptor epsilon               | NM_017194 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGGGACAGAGGCATCGGCATGGAACCTTGGACCGCAGCCGCCCTCTGCCAGAACCCTGA<br>GTGCTGCAGCCCTGAAGTCCGCTGTGTGTGGATGCTGTGAACTTTGTGGCTGAGAGCACAAAG<br>GACCAGGAAGCCACTGGAGAGGAACGTCTGACTGGGTGCGTATGGGGAAGGCCCTCGACAATGT<br>CTGTTTTTGGGCGAGCGTTGGTGCTCTTTCAGCGTCCGTTCTACGCTCATCTTCTTGGAGGTTACT<br>TCAACCAAGTTCTGATCTCCCTACCCACCGTGCATCCAACCATGAGCCTGCACCAGGACCCAC<br>CTCATCCCCACCCCCAAGAAAGAGATTTGAAAACAGGCTGCTGACAATAAATCTGGTTTGTGA<br>ACTTGCAAAANNANANNANNNANNAANANANANANANNTTCTCGCGGCCGCAAGCTTATTCCT<br>TTTAGTGAGGGTTAATTTAGCTTGGCACTGGCCGTCGTTTTTACAACGTCGTGATGGGAAAACCC<br>TGGCGTTACCCAACCTAATCGCCTTGCAGCACATCCCTTTCCCACTGGNGTAAATAGCGAANAGG<br>CCCGCACCCGATCCCTTCCAACAGTTGGCANCCTGAATGGCGAATGGGACNCCCTGTACGG<br>CNCA |

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| Activating transcription factor 3           | M63282    | AGCTATGNCCATGATTACGCCAAGCTATTTAGGTGCCACTATAGAATACTCAAGTATGCATCAAG TTGGTACCGAGCTCGGATCCACTAGTAACGGCCGAGTGTGCTGGAATTCGCCCTTTGCCGGCTGA CAACATCCCTCCTAGGGAAAGATGGAGTGAGAACATTCATCATTTGAAGTTGTCCAATGGCCAGGGT ATGCTTTCTAGAAACTATGCTGTTCTGCTCTAGACTGACTGTGCATAGGGCATTCTGTTCTGAGC CTGGTGTGTGCTATTTAGATGTTTGTCTTGACACAACATTGGCGTGATTTTTTTCCGGGAGTTTC ATCAGACCTGATTTCCGAGAGTTTGGGGGTCTGCCACTGTGGACAATATCCCCCAAAAGTGTGTG GGTGGCCATGTAAACTGGCTGATGACCAGCTGTGCTACTCTGTGCTGACCGAGGACTGATGCCCTC CTCCCCCTGTACCCACTGCTGAGGAAGAACCAGGGCACAGCAGCTGCTCTGGCTACAAACTGTT ACAATGTACAGAACGAAGGCACAAAGTCCCGCTTTCAAAGGGCGTAGGACTCCACACTCAGTGA CAGGGCAGGAAGAGCCAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGGCGCTCGAGCATG CATCTAGAGGGCCCAATTTCGCA   |
| Activin receptor type II                    | S48190    | TGNNGAATTGGGCCCTCTAGATGCTCGAGCGGCCAGTGTGATGGATATCTGCAGAATT CGCCCTTCGCCGGGATCCACACGCAGGAATGGCAATGCTCTGTGAACGATAGAAGAATGCTGGGA TCATGATGCAGAAGCCAGGTATCAGCTGGATGTGTAGGTGAAAGAATTACTCAGATGCAAAAGC TAACAAATATAATTACTACAGAGGACATTGTAACAGTGGTCACAATGGTGACAAATGTTGACTTT CCTCCCAAGAATCTAGTCTATGATGGTTGCACCATCTGTCCACACTGAGAATCGGGACTCTGAA CTGGAGCTGCTAAGCTAAGGAAACTGCTTAGTTTATTTTCTGTGTGAATGAGTAGGGTGCCTCC GGGACACGTATGCAAGCAGCCCTTGTGGAAAGCATGGATTGGGAGACTTCTGCAGCGTCTGCA ACACGGATATGAAGGGGGTCTAAGGGGAACTGCGAACTGTAAAGAATCTGAAAACCTTACACG AAGAATGTGGCCCTCTCCAAATCAAGGATCTTTTGGACCTGGCTAATCAAGTAAGCTTGGCCAAG GCGCAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCAT AGCTTGAGTATCTATAGTGCACCTA  |
| Acyl-CoA dehydrogenase, medium chain        | AA925220  | TTAAGATTTTCCAGAAAGTTTGTAGTTTAAATATGGGAGAAAATGCATATAAATTTTACTC TTTTGCATAACAAGGGAATATAATCAAAATTTATGAAACAGCTCAGCACAGAAATGCTCTCTT CACAGTGTGATGGGTCCAATCCGCCACATTCTCAGTGTCTGTGTAGAACTCTGAGTCTTTTCGT GACAGCTACCTTTCTTGTCACTTGAATGAGCATTAGAATCCAGGGTATTTCTCCATCTCAAGT GATCAAGGAGCAAAATTAACACAATTCGGGGCCAAGGACTGACCACTCACTGTCCAAAACCAAAAC TATCTAGAAAGGGTCACTGTGGAACCAACAGAGGCACCCCTCCGCGTGGGACCCCATTCACAG ATCTGTGACACCGCTCTTTTATCTCATTCTGTGGGAAGACAAGTAAAGCCCTTTCCCTCTGAAG CAGCAACAGTGTCTTGAGCGTAGTTACATGAGGGTGAAGCATCGTTCGATAGTAATTTCTGTAA TTTTATACTTTTCAATGTGCTCAGGACTATGATCAGCTCTGAATTTGTGCACTACCTTCGTA AATCTGATCCTCGTCCGAATCTTGGCCTCGAGGGCCAATTCCTATAGTGAGTCGTATTAAT TCTGTAATCATGTCTATAGA  |
| ADP-ribosylation factor-like protein ARL184 | AA817697  | GGTGACAGCCCTCTCCGAGGAGCAGCAGTGGGCAGCAGTAGCAGCAGCAGGTACCGGTGGGGTT GGGAAATGTTAGTCTGGCCAGCTGGTGTCTATCCCTCCGGCTGGTGTGCGATGAGGACAGGGACCT AGACAGTGAGCTGGGACACTGAAGAAGCTCAGTCGGCAGTAAAGACACGACTGGAAATGTCATCG AGGAGCCAGTCGATGCCAGGCAGCAGGTCTCCCTGTGACGGCACTGCAGCCTTGGATGCGCCA GTGGTGGCTGCGGATGGAGTCCAGCTCTAGGGCCTCTGAATAGCATTACAGGACAGTGTCTCCAG GCAGGTCTGCTTGTGGCAAAGATGAGGAGGGTCTGCTCCAGCCAGGCGCTCTCCACCAGTAGA CTCTGCAGCTCTCGCTGACAGTCTTGCATGCGCTGGCGGTGAGCGCTGTCCACCACCCAGATGAG GCCATCTGTGCTCTCGAAGTAGTTCCTCCAGTAGGAGCGCAGAGACTTCTGGCCACCCACATCCC AGATGTTTCAGCTTGAATCCCCGGTGCTCCAGGGTCTTGCCTCGTCCGAATCTTGGCCTCGAGG GCCAAATTCCTATAGTGAGTCGTATTAAATTCGTAATCATGTCTATAG  |
| Adrenodoxin reductase                       | NM_024153 | ATTNTGNATGATTACGAATTTAATACGACTCACTATAGGGAAATTTGGCCCTCGAGGCCAAGAAT TCGGCACGAGGCCTGCGCTCAGCACTAAGGAGTCACTGTTAGCTGTTCTGCCGGCGGGTTGCTCT TCTCAGCCATGGCTCCTCGCTGCTGGCGCTGGTGAGCTGGTCCGCGTGGCTGGGGTTTGGCCG CTTCCTCCAGGAGCACTCCGACCCTGGCTTCTGCAAGAAGTTCTCCACACAGGAGACAACCCC TCAGATCTGTGTGGTCCGCAGTGGCCAGCTGGCTTCTACACAGCCCAACACTTGTGTGAAGCACA CACCCGGGCCCCACGTAGACATCTATGAGAAGCAGCTCGTCCCCCTCGGCCTGGTGGCGCTTGGTG TGGCACCTGACCATCTGAAGTAAGAATGTCAACACATTTACACAGACAGCCCGCTCAAC CCGCTGTGCTTTCGGGGCAATGTGGTGGTGGGACGGACGTGTCGGTCCAGAGCTTCCGGGAAGC CTACCATGCTGTGGTTCTGAGTTATGAGCCGAGGACCACCAACCCCTGGAAATCTTGGCGAGGA GCTGCTGGAGTGGTCTCAGCCGGGCTTGTGGGCTGTACAAATGGGCTTCTTGGAGAACCAGA ANCTGGCTNCGGATCGAGCTGGTGACACGGCTGTGATTTTGGGGCAAGGGAATGTGGCTCTGGG ATGTGGGCCCCGANC |

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| Alanine<br>aminotransferase              | D10354   | TGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTC<br>GCCCCTTCGCGGAATTCTCTAAGGGCTACATGGGCGAGTGGCGGTTTCGTGGTGGCTATGTGGAGG<br>TGGTAAACATGGATGCTGAGGTGCAGAAACAGATGGGGAAGCTGATGAGTGTGGCGCTGTGTCCA<br>CCAGTGCAGGCCAGGCCCTTGATGGACATGGTGGTCACTCCGCCAACACCCCTCCGAGCCGTCTT<br>CAAGCAGTTTCAAGCAGAGAGACAGGAGGTGCTGGCTGAACTGGCAGCCAAAGCTAAGCTACGG<br>AGCAGGTTCTCAATGAGGCTCCCGGATCCGCTGCAACCCAGTGCAGGGCGCCATGTATTCCTTC<br>CCTCAAGTGCAGCTGCCCTTGAAAGCGGTGCAGCGTGTCTAGGAACTGGGCTGGCCCTGACAT<br>GTTCTTCTGCTGTGCTCTCTGGAAGAGACTGGCATCTGCGTTGTGCCCGGAGTGGCTTTGGGC<br>AGCAGGAGGGCAGCTATCATTTCCGGATGACCATTTCTGCCCCATGGAGAACTGCGGCTTGCAA<br>GCTTGGCCAANGCGAATTCAACACACTGCGGNCNTACTAGTGGATCCGAGCTCGGTACCAAC<br>TTGATGCATAGCTTGAGTATTCTATAGNGN   |
| Alcohol<br>dehydrogenase 1               | M15327   | TAGGTGACACTATAGAATACTCAAGCTATGCATCAAGCTTGGACCGAGCTCGGATCCACTAGTAC<br>CGCCCGCCAGTGTGCTGGAATNCCCTTTCGCGGGGATCCAGTCCGCCAAGGTGACCCAGGCTCC<br>ACCTGTGCGGTGTTTGGCTGGGAGGTGTTGGTCTGTCTGTCTGTCATTGGCTGTAAACAGCAGG<br>AGCAGCCAAGATCATTGCCGTGGACATCAACAAAGACAAGTTTGGGAAGGCCAAAGAGTTAGGTG<br>CCACTGACTGTATCAACCTCAAGACTACACAAACCCATCCAGGAAGTTCTCAGGAGATGACTG<br>ATGGAGGGGTGGACTTTTCATTTGAAGTCATTGGCCGTCTTGATACCATGACTTCTGCCCTGTTA<br>AGCTGCCATTGAGCATGCGGTGTAAGCGTCATTGTCGGGGTGCCTCCCAAGTCCCAAGGCTCTC<br>CGTTAACCCTATGTGCTGCTGCTGGGACGCACCTGGAAAGGAGCAATATTCGGCGGGTTAAGA<br>GTAAAGATGCCGTCCCAAACTTGTGCTGACTTTCATGGCTAAGAAGTTTCCGTTGGAGCCGTG<br>ATTACTCATGAAGCTTGGCCAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAG<br>CATGCATCTAGAGGGCCCAATTCTCCAA     |
| Aldehyde<br>dehydrogenase 1              | M23995   | AGAATACTCAAGCTATGCATCAAGTTGGTNCNGAGCTCGGATCCACTTAGTAACGGCCCGCAGTG<br>TGTTGGAATTCGCCCTTCGCGGGATCTGTAGGAGGAGTGTGGAGCGGGCTAAGAAATACGTTT<br>TAGGAGATCCTCTGGACTCAGGAATAAGTCAAGGTCTCAGATTGACAAGGAGCAACATGCTAAA<br>ATCCTTGATCTCATTGAGAGTGGGAAGAAGAAGGCCGCAAACTGGAGTGTGGTGGAGGACGCTG<br>GGGGAACAAAGGCTTCTTTGTCCAGCCTACAGTCTTCTCCAATGTGACCGATGAGATGCGCATTG<br>CCAAAGAGGAGATATTTGGACCACTGCAACAAATCATGAAGTTTAAGTCCATAGATGTGATC<br>AAGAGAGCCCAACAATACTCCCTATGGTCTAGCAGCAGGAGTCTTCAAAAAGACCTGGACAGGGC<br>CATCACTGTGTCTTCTGCTCTGAGGCGGGGACAGTGTGGGTGAATGTATTGACTCTTTCTG<br>TCCAGTGGCCATTTGGTGGGTTCAGATGTCTGGAAATGGCGAGAAATGGGTGAACAGGGTAAG<br>CTTGGCCAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAG<br>GGCCCAATTC                           |
| Aldehyde<br>dehydrogenase 2              | X14977   | GCGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGC<br>CCTTACAAGAAGGGCGAAGCTGCTGTGCGGTGGGGGCGCCGCGCAGACCGTGGTTACTTCATC<br>CAGCCACCCGTGTTCCGAGACGTCAAAGATGGCATGACCATCGCCAAGGAGGAGATCTTCGGACC<br>AGTGATGCAGATCTTCAAATTCAGACCATTGAGGAGGCTGTGGGGCGAGCCAATAATTCGAAGT<br>ACGGGCTGGCTGCCGCTGTCTTCAAAAGGACCTGGACAAGGCCAATTACCTGTCCCAAGCTCTG<br>CAGGCTGGGACTGTGTGGATCAACTGCTACGATGTGTTTGGGGCCAGTCCCCATTGTGGCTA<br>TAAGATGTGCGGGAGCGGCAGGGAGCTGGGCGAGTATGGCTGCAGGCTACACGGAAGTGAAGA<br>CGGTACCCGTCAAAGTGCCACAGAAGAACTCGTAAAGTGGCTGTCAGGCTTCTCAGCCAGCGCC<br>CAAAAACCCCAACAAGATCTTGAGAAAAGCCACCACCAAGCACACTGCAAGGGCGAATTCCAGCAC<br>ACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTTGATGCATAGCTTGAGTATTCT<br>ATATGGCACCTAA                    |
| Aldehyde<br>dehydrogenase,<br>microsomal | AA956846 | GCCAATGANTCGTTCTTGATACNTACATAACANTTCAGACAGCTTCAACGGGTGGAACAGGT<br>TANTCAGCAAACATGGTTGTACATACGCAAGTGACATTCTCATTGAGTGGGCAGTCTTAATTTGG<br>ATCCTGGGAAGGCAATGAGACCTTGCAGCTTGGAGCTTCAAGCCTAACAGGCCCTGGCAGCAG<br>GGCCACACAGATCTCTTGCACATCCCGTGTAGCCATGTTAGGGTCTGACAGAGAATGCTGCC<br>CCGCTTGCTCAGGTGCGCTTCTGGCCATCCATCGCTTCAAGTGTGCCCCCTCAGCTCACGGTAGT<br>CTCCAACAACCCCTGCCCCATGAGTTCTGAAGCCTCATGTCTAATAACCCCCCTTCACTACAGGA<br>ACAGCTCCATGCTAAGATCTGTAGGAATCTCTTAAGATTTCAAAAGTAAATTTTGTGTGTG<br>TGCTGTGAAAATAAGCAGATTATCTCTGAAGACCTATATAACATTCAAATCGAGGGTCTCGAGGG<br>GATTGTTATGGAGGAATAATAATGAGAGGGTCCCATATGTTGCTAGGTTGGCTCAAACCTCC<br>GGGCTCCGGAATCTTCTGCCCTCGGGCTCTGGCTCGTGGCGAATCTTGGCTCGAGGGCCAAA<br>TTCCCTATAGTGAGTCGTATTAAATTCGTAATCATGTCATA |

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| Alpha-1 acid glycoprotein                      | AI029162 | ATGCNNGCCTAAGGATCCTTCTTGGTCTCCTTCTTAGTCTCCTTCTCCAGCTCCAGTCTGNTTN<br>TGATGCTCACTGCACCTATCCTTTGTCCAGTCGACAAATACGATTTCTGATTCATCCATGCCCCAC<br>ATCTTTGACAGCCTGCTGGAATATTTTCCGAGCTCTGGGGACAAGTCTGGCTTTTTAGCATAGA<br>AGGACAGCCCCCGGTTCTCATCTGTCAGGTTAAAGGCAAGCATGAAGGTCCCATGTTTCTCAGC<br>ACTATCAAATGGGCAAGATTTTCACTGCTCCTGCACACTTGGATAAAGGTCCCATTCTCTCTCTG<br>GACTCCTAGATGGGTGAAGTTATAGACACACTGGTCTGCTGTGGTCTGAACTCCCGAAGTTCAA<br>TTGTGTCGTTTATCAAGTTGGGGGTAAGGTAAAAATATTCCTGCTGTATCGTTTGAAGTGCCTGC<br>TTGAACACGGGGTCTCGGAAAGCTGCTCCCATGTAAACCATTTGTCTGAGAGCCATTTCAAGGT<br>CTCATTGGTAATAGGTATGCCTAGGGTGATGTTGGCAGGTTCTGGGTTCTGAGCTTCCAACAAGG<br>GCAGGAGGCTCAAAACGACAAGAACCATGTGCAGCGCCATGCCGAAGACCTCGTGCCGAATTCT<br>TGGCCTCGAGGGCCAAATCCCTATAGTGAGTCGTATTAAATTCGTAATCATGTCATA |
| Alpha-1 microglobulin/bikunin precursor (Ambp) | AI043784 | AGCNCNCNCNCCCTTGCACGCCATGNTTCTTCTNTCTTGGGAAGGTGGTTTACTCATGCCCTG<br>AGCTTCCNTTCTTNTCCAATACCCCTTATTGTGACAAATGAGATGCTAACACACAGAATGCTAGGAA<br>ATGACAGCTTGTTTTATTTGGGTCCAGATCATCTAAGCTGGACTGCACAGTGACGGACCGTGGCTA<br>CCCTCTGGCTTGCAGACCGGCTCCTTCAACTGCGTGTTAGCTCCTCGTACCCATCACCAGGGACT<br>CCACAGTACTCCTTGCACCTCCTTCTCAGAGTAGAAGTTGTTGCCGTTGCCCTTTCAGCCCCGATA<br>GATGAATTGGATGCACTTCCCTTGGCGTGATCAATGCCCAGAGTTCTGCAAAGGCTCGGACGG<br>GGCCTTGGACTATGGGGAGATTGCAGGCCGCTATTGTCCGGCACGCTGTCAGGCATTCTCTCTCG<br>GAGGCGAAGTTGTTACCATGCTTAGGCAGCCGCCATACTGGAAGGTCTCGCAGGCCATGGAGGC<br>GCCATTGTAGTAATCTTCTGCTGCATCCCCAGGCAGGGACCTTCTGAGTAGTTGAGCTGGCAGG<br>AGTCTTCTTTCTTGGAGGTCCCAGTTATGAGTGGTCAACCCTCGTGCCGAATTCTTGGCCTCGAG<br>GGCCAAATCCCTATAGTGAGTCGTATTAAATTCGTAATCATGTCATA        |
| alpha-1,2-fucosyltransferase                   | AB015637 | CGAATTGGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCG<br>CCTTCGCGGGATCCTTGGCCCCAGAGAACTTCAAAGACTTTTATTAGGGTGGGCTAAAAGTGG<br>GCTAGAGGAGAGAACCCTGTTGAAATGCTCCTTAAGGAGCAATGTCTAAGGTGCTCTTTAAAAA<br>AAAAAATTTAGAAACTTTTAAAAAAGAGAGCTTAAAAAGTTAAAGAATTATACAAATTAGTCC<br>TGAATTTAGGATCGAGAAGGTTTCTTCTTGAAGATGCTATAAGGGATCTGGGATCTGTGTTCT<br>GGAGGTAACCAGGCCTCCAGAAAAGAGGTTATACCCCTGGGCTCACAAAATCTTAAATCCGGCA<br>TTGAGAAGGTCAAGGTTGAAGATCAGAAGGTGTTCCAGAAGTGTGAGCTCAGCCTAAGTCCCTA<br>TAAAAACACGGGCTGGAAGCAAGATGGGACATTTGGCTGACATCAGGTATACTTGTAGCTTTTTC<br>AAGAACGGAGAAAGTTTCTCAGATAGCATTTAACCTAATTGTATTCCCTTCCAAGACCACTAA<br>GCTTGGCCAAGGGCGAATTNCAGACACTGGCGGNCGTTCTAGTGGATCCGAGCTCGGACCAAGCT<br>TGATG  |
| Alpha-2-macroglobulin                          | J02635   | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCG<br>CCCTTGGCGACTGTGCTTGGGATTACACCGTGAAGGTGACAGGAGAAGGCTGTGTCTACCTCCA<br>GACATCCTTGAAATACAGTGTCTCCCGAGAGAGGAGGATTCCCTTTCGCTGTGGTGGTGAGA<br>CTCTGCTTGGGACATGTGAGGATCCCAAAGTCAACACAGCTTCCAGATCTCACTCAACATCAGT<br>TACACTGGAAGCCGTTCTGAATCCAACATGGCAATTGCTGACGTGAAGATGGTGTCCGGCTTCAT<br>CCCCTTGAAACCAACAGTGAAATGCTTGAAGATCTGTGCATGTGAGCCGAACAGAAGTCAGCA<br>ATAACCATGTCTTGATTTACCTGGATAAGGTGTCAAATCAGACGGTGAAGTGTGCTTTCACGGTT<br>CAGCAAGATATTCCAATAAGAGACCTGAAGCCAGCCGTAGTGAAAGTCTACGATTACTATGAGAA<br>AGATGAGTTTGCAGTTGCAAAATACAGCGCTCCCTGCAAGGGCGAATTCCAGCACACTGGCGGCC<br>GTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTGTCAAC<br>TAAATAGCTTGGCGTAATCATGGGCATAGCTGGTTNCTGTGTGAATTG           |
| Alpha-fibrinogen                               | X86561   | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTGGCCCTCGAGGCCAAGAAT<br>TCGGCATGAGGCTCAAAAACCTCACTATTTGATTTTCAAAGAACAACAAGGATTCTAATTCAGTG<br>ACCAGGAATATCATGGAGTATTTGAGAGGGGACTTCGCTAACGCCAACAACTTTGATAACACTTT<br>CGGGCAAGTGTCAGAGGACCTGAGGCGCAGAATTGAGATCCTAAAGCGCAAAGTCATAGAGAAAAG<br>CGCAACAGATTAGGTTCTGCAGAAAGACGTCGGGATCAGCTGATAGACATGAAGCGCCTGGAG<br>GTGGACATTGATATCAAGATCCGCTCTTGCAAGGATCCTGCAGCAGGTCTGTAAGCCGTGAGAT<br>AAATCTAAAGGACTACGAAGGTGAGCAAAAGCACTTGAACAGGTGATTGCTAAAGAGTTGCTTC<br>CGGCAAAAGACAGGCAGTACTTGCCAGCAATAAAAATGTCTCCAGTTCCCGACTTGGTTCCCGGA<br>AGTTTTAAGAGCCAGCTTCAGGAGGGCCCCAGAGTGGAAGGCATTAACAGAAATGAGGCAGAT<br>GAGAATGGAGCTGGAGAGGCCGGGAAGGATGGGGCTTCGCGAGGAGATTTACCAGGAGATTTCGG<br>AGGAGACTCTGCNACACGT  |

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| Alpha-tubulin                         | J00798   | GGGAATTGGGCCCCCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCG<br>CCCTTTCGCGGGATCTGATGTGGTCCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAGACCA<br>AGCGCAGCATCCAGTTTGTGGACTGGTGCCCCACTGGCTTCAAGGTGGCATTAAATTACCAGCCT<br>CCCACGTGTGGTACCTGGTGGCGACCTGGCCAAAGGTCCAGAGAGCTGTGTGTATGCTGAGCAACAC<br>CACAGCCATTGCTGAGGCTTGGGCTCGCCTGGATCACAAGTTGATCTGATGTATGCCAAGCGTG<br>CCTTTGTGCACTGGTACGTGGGTGAGGGAAGCTTGGCCAAGGGCGAATTCAGCACACTGGCGGC<br>CGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTGTAC<br>CTAAATAGCTTGGCGTAATCATGGTTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAAT<br>TCCACACAACATACGAGCCGGAAGCATAAAAGTGTAAAGCTTGGGGTGCCTAATGAGTGAGCTAA<br>CTCACATTAAATTGCGTTGCGCTCACTGCCCGCTTTNCAATCGGGAAACCTGCGTGCCAACCTGCAT<br>TAATGAATCGC  |
| Annexin V                             | M21730   | GTGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCG<br>CCTTATCCGCGGATCCGGGGACGGATGAAGAGAAGTTTCATCACCATCCTTGGGACACGCAGTGT<br>GTCTCATTAAAGAAGAGTGTGTTGACAAGTACATGACAATATCAGGATTTTCAGATTGAGGAAACCA<br>TTGACCGAGAGACCTCAGGGAACCTTGAGAACCTTACTCCTGGCTGTCTGTAAGTCTATTCCGAGC<br>ATACCTGCTTACCTTGACAGAGACCTTCTATGCTATGAAGGTGCTGGGACGGACGATCACAC<br>CCTCATCAGAGTCATAGTGTGAGGAGTGAGATTGATCTGTTTAACATCAGGAAGGAGTTTAGGA<br>AGAATTCGCCACGTCCCTGTACTCTATGATCAAGGGCGACACATCTGGAGACTATAAGAAGGCC<br>CTGCTGCTCCTCTGTGGAGCGGAGGATGACTGAGGAGCTGCCTGGAGTGCCTGGGCCCGCCTGC<br>TGCCCAACATCAGCTTCCCTCAGCACACGCTACTTACGTTCAATGCCTGCCTGAAGGGCGAAT<br>TCCAGCACACTGGCGGCGGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGA<br>GTATTCTATAGTGNACCTAAATAGCTTGGCGTAAT                                   |
| Apolipoprotein CIII                   | J02596   | GCAACCCGCTTCTCCCGGGCGGTTGGCCGATTCAATATGCAGTGGCAGCAGGTTTCCCGACT<br>GAAAAGCGGGCAGTGAGCGCAACGCAATTAATGTAGTTCAGTCACTCATTAGGCACCCAGGCT<br>TTACACTTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATACCAATTTACACAG<br>GAAACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGC<br>ATCAAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCCGCAGTGTGCTGGAATTCGCCCTTG<br>CGCGGATCCTCAGGCTCAAGAGTTGGTGTGTTAGTTGGTCTCAGGGCCAGACTCCCAGAGGC<br>CAGTGAACCTATCAGTGAACCTTGCTCCAGTAGCCTTTCAGGGATTGAAGCGATTGTCCATCCAG<br>CCCCTGGCCACCACAGCTATATCAGACTCCTGCATGCTGCTTAGTGATCCTGGACCGTCTTGGA<br>GGCTTGTTCATGTAGCCCTGCATAGAGCCAGCAGCAAGGATCCCTCTCCCTCATCAGGGAAGC<br>TTGGCCAAGGCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGG<br>GCCCAATTC   |
| Apoptosis-regulating<br>basic protein | AF304429 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCACGAGGGCTTACCGCCAACAGCAGGCCATGGCTGGAGCTCTGGTGCGCAAAGCAGCGG<br>ACTATGTCCGGAGCAAGGACTTCCGGGACTATCTCATGAGTACGCACTTCTGGGGCCAGTTGCC<br>AACTGGGGTCTCCCCATTGCTGCTATCAATGACATGAAGAAATCTCCAGAGATTATCAGTGGGCG<br>GATGACTTTCGCCCTCTGTGCTATTCTCTGACATTATGAGATTTCCTACAAGGTACAACCCC<br>GAAACTGGCTTCTGTTTGGCTGCCATGTGACAAACGAAGTCGCTCAGCTCATTACGGGAGGACGA<br>CTTATCAACTACGAGATGAGTAAGCGGCCATCTGCATAGCAGTGCAAGGACCAGCTCTTGAAAGG<br>GACAGTGTCTCAGCCACTGTTGCGGGCCACAGATCACGTCAGCATGAATAGTCGTGCTGAGGGGAA<br>AACACGGAAGACTATCTTTAATGACCATGCCAACATTATGAATAGCCAAGAATCCCCAACCAA<br>CTCTCGGCTGCCCTTATCAATGCTAAACTTTATTTTGTCTTCATCAGGAGTAGTTCAAATATGCA<br>GCTAATTTTATNATT   |
| Aquaporin-3 (AQP3)                    | AI045067 | CAACTGTTGGAAAGGGGGATCGGGGNGNCCNTNTTCGTTATTACGCCAACTGGCGAAAGGGGGAT<br>GTGTGCAAGGCGATTAAAGTTGGGTAACGCCAGGGTTTTCCAGTCACGACGTTGTAAAACGACGG<br>CCAGTGCCCAAGNTAAAATTAACCTCCCTAAAGGGAATAAGCTTGGCGCCGCGAGATTTTTTNT<br>TTTTANTTTTTTTTTNTTTTTTTTTTTTTCTGTCAAATGCATACATTTTATCTTTCTTTAT<br>ATATAAAAGGCAACAGTACATTGTTGATTGGGGGATTAAAGGAAGGAAGACCTTTTAAAAAGTG<br>GAGTTTCCACCCCTATTCTTAAACTGTAAACATATATGTATGTATATATTTATATATTTAAA<br>AAAAACAAATTTGAAACTTACGACCAGGACTTTAGCCCTCCCAATGTCTATCTTATAACAGAA<br>ACATATTACATACACAGCCCCAGTTGAGGATCACAGCTCCAGATGTGAGCTACGCCCTCTTTAT<br>GCCCTCCCCGCTCCCTAAGCCTAGAAGTCCATTTGAAAACCTCAGTAGACACATACATACTTAGA<br>AACGCACTCTGGGTCCACCTCCACACTGGAGTCCCTGAAGCAAGTATACTGTGGCACTTTCCTG<br>CCTCGTGCCGAATTTCTGGCCTCGAGGGCCAAATTCCTATAGTGAGTCGTATTAAATTCGTAAT<br>CATGTCATA |

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| Argininosuccinate lyase  | D13978    | CTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCCGACAGAGGCTGGTCCACTAACCAGGGACTGTGGGACAGAGGAACAAACAAGAAAGAACT<br>CGAGGCCCTCGCTGAGTGGCGCGCTTGCTGAGTGTGCCACATCCCGCAAGCTGAGCAGGTATCCC<br>AACTCTGTTCTGCCCCGGTAGACCACCCGAGGTGGTGGTGGTCTTGCTTCCAGATTCTGTAG<br>GACAGAAGCTCCAGGAGGAGGACCCGCCAACATGGCATCGGAGAGCGGGAAGCTATGGGGTGGC<br>CGATTTGCAGGCTCGGTGACCCACCATGGACAAGTTCAACTCATCTATCGCCTATGACCGGCA<br>TCTGTGGAATGTGGACCTGCAGGGAAGCAAGGCCCTACAGCAGGGGCTGGAGAAGGCAGGGCTTC<br>TCACCAAAGCTGAGATGCAGCAGATACTGCAAGGCCCTGGACAAGGTGGCTGAAGAGTGGGCCAA<br>GGCATCTTCAAATTGTACCCTAATGATGAAGACATCCACACGGCCAACGAGCGCGCCTGAAGGA<br>ACTCATTGGTGAAGCTGCAGGGAAGTTACACACAGGCAGAAAGTCGCAA  |
| Argininosuccinate synthetase 1                                     | M36708    | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGGAGGTGACAAAGAGGCGCGGCCCTCCCGCTCTGCAGCTCTCCAGGCTCCAGCAT<br>AATGTTGTGATAAATTTGTAATTGTAGCTTGTCTCTTACCACCTGACTGGGGCTGCTGTGCC<br>CCCCCTCACTCCCCCCCCACCCACAGGCTTTGTTCCTTGGTCCCCCTATAGCCTACAAAAGTGGTCA<br>TCGAAGGGAAGGGGGGGTGGCAGGCAGCTGCAGAAAGCGCGTAAATGACAATTAAGAAGATT<br>CATTAGTCTTTTCAATTTGTCAAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAA<br>AAGCTTATTCCCTTTAGTGAGGGTTAATTTAGCTTGGCACTGGCCGTCGTTTACACGTCGTG<br>ACTGGGAAAACCTGGCGTTACCCAACCTAATCGCCTTCGAGCACATCCCCCTTCGCCAGCTGG<br>CGTAATAGCGAAGAGGCGCCGACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCNAATG<br>GGACNCGCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGGTTACGCGCANCCTGACGCTAC<br>ACTTGCCAAGCGCCCTANCC  |
| Aryl hydrocarbon receptor  | U09000    | NANNTTNAAGGTAANGGCCCTCTAGATGCTGCTCGATCGGCCGNCAGTGTNATGGATATCTGCAG<br>AATTCGCCCTTGGCCAAGCTTAGCAGCAGTCTGAAGGTGGCCAATGCTGCTCAAGTCTGCCGAGT<br>AGGCTTCATTTAAATGCTCGGACTCTGAAACTTGCTTAGGAACGCTGGGAGCCTGGAATCTCA<br>GGGCTGTACTGCATCTGGTCCACAGGGGTGTGCTGAGGCCCTGCGCTGGCACTGGTACATGGACAT<br>GGCCCCAGCGTAGTACGCTGAGGACTGACCATGGCTGACTGTGAGTTTATCCCGTGTCTTTGGT<br>TTTCANGAACTTGTAAACAAGTACAAAGTCTTCTAAATTAAGAAGCTTAGGGTGTAGGGATCGT<br>TCAAAATCCCTTCCAGGGAAGTCCAACTGTGTACCTTGGAAATGTTCTGGTAGCAATGACTGGT<br>TGCAGGGAGCAAAGTTCTGTGTGAANGCATACTGTCCACTNTGACTTGTAGGGAACTCCTGTG<br>CANTCCCCANAAACCGGAAAAAAGCTAT   |
| Aspartoacylase   | NM_024399 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACGAGGAGAGCTCTGTATTTTCACTTCTCACTTAGATCTAAACTTGGAACTTTTCTCAGA<br>AGTTAAGTGTCTTTGACCTCTCTCTCTGAATTCAGAAACAGACAGATTTTGGTATTTGG<br>TAAATGACTTCTTGTGTGCTGAAGAACCTATTAAGAAGATTGCCATCTTCGGAGGGACTCATG<br>GAAATGAAGTGAAGTGTGTTCTAGTTACTGCTTAAAGAATGGCGGTGAAGTTCACAGA<br>CAGGGCTGGAAGTGAAGCCATTCTATCAACCCAAAGAGCGGTGGAGAAGTGCACCATACAT<br>TGACTGTGACCTGAACCGTGTGTTTGAACCTTGAAATCTTAGCAAGAGATGTCTGAAGATTGCG<br>CGTATGAAGTGAAGGGCTCAAGAAATAATCACTTATTTGGTCCAAAAAATAGTGATGATGCC<br>TACGATGTGCTTTTGAACCTCATAACACTACTTCTAACATGGGTGCACTCTTATTCTTGAGGA<br>TTCCAGGAATGACTTTTAAATCCAGATGTTTCACTATATTAAGACCTGCATGGCTCCATTACCT<br>GCTCTGTTTACCTCATCGAGCCATCTTCTCAANGGGGGGGGGGGGG                         |
| ATP-stimulated glucocorticoid-receptor translocation promoter (Gy) | NM_024381 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACGAGGAGACCTTGGGACTGACCCCTGCCTCCACTCTCATGATGCCCTTACTATTCCCTT<br>AAGGTCTAGGATGAATTTGTATCTGTCCATTGAAATGTGTATCCAGTATATTCCAGATGCTGC<br>TGGCCTAAACTTGTCTGAGGAAGGGGTTGTTACTCACTCTTCAAATGAGTGGATTCTGCTTG<br>TTTGCTTTTAAAGCTCAGATGTCTTTTCTACATATTAGAAGACCACAACACCACTGGATATTT<br>AATGGAACGCTCTAAAGCATATTGGATAATAAAGTCTTCTGTTGCTTAGACATTTCTGT<br>ACAGTGTGTTGCCAAAATGAAATTTTTCAGGTGTTTACACTGTCTCACTAATGTGATGGTTCA<br>TGGCTTTCTGTCTGGATCTTACAGGGATAGATAGAATACTTTCTTTTCTGCTTTTTTTTTCATT<br>CTCCTTTTATATTTTACTCTGTATGTATAACATACATACCTATATATTTTATATGCTGAGGG<br>TAGCCCATTTTAAATTAAGAGCACATTATATTCAGTAAGTTATAAGAGGGCTGGTCTTAAGTGG<br>ACTACTATGTATATAAATTTGAGGGGGGCAAGCTGTACACATTTTGGGCAACNGTTATGCATAT |
| Bax (alpha)  | U49729    | CTCAAGTTATGCATCAAGTTTGGTACCGAGTTGGATCCACTAGTAACGGCCGAGTGTGCTGAAT<br>TCGCCCTTCGCGGAATTCGGGGCCTTTTGTACAGGGTTTCATCCAGGATCGAGCAGAGAGGAT<br>GGCTGGGGAGACACCTGAGCTGACCTTGGAGCAGCGCCCGAGGACGATCCACCAAGAAGCTGA<br>CGAGTGTCTCAGGCGAATTTGGCGATGAAGTGGACAACAACATGGAGCTGCAGAGGATGATTGCT<br>GATGTGGATACAGACTCCCCCGAGAGGCTTCTTCCGTGTGGCAGCTGACATGTTTGCAGACGG<br>CAACTTCAACTGGGGCCGGGTGGTCCCTTTTCTACTTGTCTAGCAAACTGGTGTCTCAAGGCC<br>TGTGCACTAAAGTCCCCGAGCTGATCAAGACCATCATGGGCTGGACACTGGACTTCCTCCGGGAG<br>CGGCTGCTTGTCTGGATCCAAGACAGGGTGGCTGGGATGGCCTCCTTTCTACTTCCGGACCCC<br>CACATGGCAGACAGTGACCATCTTTGTGGCTGGAGTCTCACTGCCTCGCTCACCATCTGGAAGA<br>AGCTTGGCCAAGGGCGAATTTGCAGATATCATCACACTGGCGGCCGCTCGAGCATGCATCTAG<br>AGGGCCGN   |



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| Bcl-2                     | L14680    | TTGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT<br>CGCCCTTCGCGGAATTCCAGCCTGAGAGCAACCGAACGCCGCTGTGCACCGAGACACGGCTGCC<br>AGGACGTGCGCTCTACGGCCCTTTGTGCGCAACGCTGGGCCCTGCGCTCAGCCCTGTGCCACCTGT<br>GGTCCACCTGACCTCCGCCGGGCTGGGGATGACTTCTCTCGTCGCTACCGTCGCGACTTTGCGAG<br>AGATGTCCAGTCAGCTGCACCTGACGCCCTTCACCGGAGGGGACGCTTTGCCACGGTGGTGGAG<br>GAACCTTTCAGGGATGGGGTGAACGGGGAGGATGTGGCCTTCTTTGAGTTCGGTGGGGTTCAT<br>GTGTGTGGAGAGCGTCAACAGGGAGATGTCACCCCTGGTGAGCAACATCGCTCTGTGGATGACTG<br>AGTACCTGAACCGGCATCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAA<br>CTATATGGCCCCAGCATGCGACCTCTGTTTGAATTCTCTGGCTGTCTCTGAAGACAAAGCTTGG<br>CCAAGGGCGAATTNCAACACACTGGCNGGCCGTACTAGTGGATCCAACCTCGGTACCAACTTGATG<br>CATACTTGAGT                       |
| Beta-actin,<br>sequence 2 | V01217    | TGACATGATTACGAATGTAATACGACTNCTATAGGGAATTTGGCCCTCGAGGCCCTAGAATTCGNN<br>ACGAGGCAGGATTNAAAACTGGAACCGTGAAGGCGACCGCAGTTGGTTGGAGCAACATCCCCC<br>AAAGTTCTACAATGTGGCTGAGGACTTTGATTGTACATTGTTTTTTGTTTTTTGTTTTTAATA<br>GTCACCTCCAAGTATCCACGGCATAGATGGTTACAGGAAGTCCCTCACCCTCCCAAAGCCACCCC<br>CAACTCCTAAGGGGAGGATGGCTGCATCCATGCCCTGAGTCCACACCGGGGAAGGTGACAGCAAT<br>GCTTCTGTGTAAATATGTACTGCAACATTTTTTAAATCTTCGCCCTTAATACCTTCATTTTGT<br>TTTTTAATTTCTGAATGGTCAGCCATTGTGGCCTGCCCTTTTTTTTGTCCCCCAACTTGATGT<br>ATGAAGGCTTTGGTCTCCCTGGGAGTGGTTGAGGTGTTGAGGCAGCCAGGCTGGCCTGTACAC<br>TGACGTGAGACCGTTTTAATAAAGTGCACACCTTACAAACNAAAAAAAAAAAAAAAAAAAAA  |
| Beta-tubulin,<br>class I  | AB011679  | CTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCCGGCAGGGAATTAATTACAGTAAACCGTAGCCATGAGGGAATCGTGCACATCCAGGCCGA<br>CAGTGTGGCAACAGATCGGTGCTAAGTTCTGGGAGGTGATAAGCGATGAACACGGCATCGACCC<br>CACC GGACCTACCACGGAGACAGCGACTTGCAGCTGGACCGAATCTCTGTGACTACAATGAAG<br>CTACAGGTGGCAAGTATGTCCTCTGAGCTATCTTAGTGGATCTAGAACC GGGAAGTATGGACTCC<br>GTTTCGCTCAGGTCTTTTGGCCAGATCTTCAGACCGGACAACCTTTGTTTTTGGTCACTCTGGGC<br>AGGCAACAAC TGGGCTAAGGGTCACTACACAGAGGAGCTGAGCTGGTTGACTCTGTCTTGATG<br>TGGTGGCAAGGAGGCGGAGAGCTGTGACTGCTGCAAGGCTTTCAGCTGACCCACTCGCTGGGT<br>GGAGGCACGGGCTCTGGCATGGGCACCTGCTCATCAGCAAGATTTCGAGAAGAATACCCCGACCG<br>CATCATGAACACCTTCAGCGTGGTCCCTCACCCTAAGTGTCTG   |
| Calbindin-D (9K)          | J02954    | TGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTC<br>GCCCTTATCGCGGATCCAGCGCTAAGAAATCTCCCGAAGAAATGAAGAGCATTTTTCAAAATA<br>TGCAGCCAAAGAAGGCGATCAAACCAGCTGTCCAAGGAGGAGCTGAAGCTGCTGATTCACTCAG<br>AGTTCCTCCAGCCTCTGAAGCAGGCTTCAAGTACTCTAGACAATCTCTTTAAGAGCTGGATAAG<br>AACGGTGATGGAAGCTTGGCCAAAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATC<br>CGAGCTCGGTACCAAGCTTGATGCATAGCTTGATATTCTATAGTGTCACTTAAATAGCTTGGCG<br>TAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAATTCACACAACATACG<br>AGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCATAGTGAGCTAAGTCACTAATTAATTGCGT<br>TGCGCTCACTGCCCCGCTTCCAGTCCGGGAAACCTGTGCTGCCAGCTGCATTAATGAATCGGCCAA<br>CGCGCGGGGAGAGGCGGTTTTCGCTATTGGGCGCTCTTNCGCTTNTCTCGCTCACTTGACTCGCTGC<br>GCTTCGGTCTGTTGGCTGCGCGGAGCGGTATCAGCT |
| Calcineurin-B             | L03554    | ACACTATAGAATACTCAAGCTATGCATCAAGCTTGGTNCAGCTCGGATCCACTAGTAACGGCC<br>GCCAGTGTGCTGGAATTCGCCCTTCGCGGGATCCTGAGGCGAGTTACCTTTGGAAATGTGCTCA<br>CACTTCGATGCTGATGAGATTAAAGGCTAGGAAAGAGATTCAAGAAGCTTGACTTGGACAATC<br>TGGTTCTTTGAGCGTGGAGGAGTTCATGTCTCTGCCTGAGTTACAACGGAACCTTTAGTACAGC<br>GGGTATAGATATATTTCGACACAGACGGGAATGGAGAAGTGGACTTCAAAGAATTCATTGAAGGA<br>GTCTCTCGGTTCACTGTCAAAGGCGATAAGGAACAGAGTTGAGGTTGCTTTCCGTATCTACGA<br>CATGGATAAAGACGGCTATATTTCCAATGGAGAGCTTTCAGGTGTTGAAGATGATGGTGGGCA<br>ACAACCTGAAAGATACGAGTTACAGCAGATTGTAGACAAAACATAATAGACGCAGATAAGGAC<br>GGGACGGGAGAAATATCCTTTGAGGAGTTCTGTGCTGTTGTAGGTGGCCTAGATATCCACAAAAG<br>ATGGTGGTAGATGCTGAGGGCCAAGGGCGAATCTGCAGATATCCATCACACTGGCGCCGCTC<br>GAGCATGCTATAGAGGGCCCAATTC                     |
| Calgranulin B             | NM_053587 | ATCAATGTTTTCCATCAGTACTCTAGGAAGTATGGACATCCTGACACCCTGAACAAGGGGAATT<br>CAAAGAAATGGTGAATAAGGACTTGCCAAATTTCTGAAGAGGGAGAAAAGAAATGAAATCTCC<br>TAAGAGACATCATGGAGGACCTGGACACAAACCAGGACATCAACTGTCTTTGAGGAGCGTATG<br>ATGCTGATGGGAAAGTTGATCTTTGCCTGTCTAGAGAAGCTGCATGAGAACAACCCACGTGGGCA<br>TGACCACAGCCACGGCAAAGGCTGTGGGAAGTAATTAAGAGGTGAGCCATGTAACATCTGCCCAA<br>CCAAGTCTAAAGGAATAGCTTACTAAATGACCTTGGNTCTGGGGCTGGGAAATAATTTAAATA<br>GAATAAATAAAGTCTTTATCCCTTTNNNAAGGCTACCTGNNAAAAAANACNTCTTTTTGNGGG<br>NGGCTNANTTTTTTCCCTTTTTTNGGGGGGNAATTTCTNTGGGCCCGGCNNNTTTTTTACAAN<br>TTGNCNNNTTGGGAAAACCCCGGGGTANCCAAAATAAAA   |

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| Carbonyl reductase         | X84349   | TGCGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTTCG<br>CCCTTTGACCCACCCCTTCCACATTCAAGCAGAGGTGACAATGAAAACCAACTTTTGGGTAC<br>CCAAGATGTCTGCAAGGAGCTACTCCCTATAATAAAACCCCAAGGCAGAGTGGTGAATGTATCAA<br>GCAGCGTGAGTCTCAGGGCCCTGAAAAGCTGCAGCCCGAGCTGCAGCAGAAGTTTCGAAGTGAG<br>ACCATCACTGAGGAAGAGCTGGTGGGGCTCATGAACAAGTTGTAGAGGATGCAAGAAAGGAGT<br>CCATGCGAAAGAAGGCTGGCCCAATAGTGCATATGGGGTACCAAGATAGGGGTGACAGTCCCTGT<br>CCAGAATCTATGCCAGGAACTCACTGAGGAGAGGAGAGAGGACAAGATCCTCCTGAATGCCTGC<br>TGCCCTGGGTGGGTGAGAACCACATGGCAGGACCAAAAGCCACCAAAAGCCGAGAAGGAGC<br>AGAGACCCCGTGTACTTGGCCCTTTTGCCTCCAGGTGCAGAGAAGGGCGAATTCCAGCACACTG<br>GCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGT<br>GTCACCTAAATAGCTTGGCGTAATCATGGGCATAGCTGGTTNCTGTGTGAAAT                             |
| Casein-alpha               | J00710   | TTATCACATGATTACGAATTTGAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCACAGAGGCCAGCTTCTCTCACCCTACTCTTGGGTTCAAGATCTTAGCAACCATGAACTTC<br>TTATCCTCACCTGCTCGTGGNTGCTGCTCTTGTCTTGCCCTAGAGCTCATCGTAGAAATGCAGTC<br>AGCAGTCAAACCTCAGCAAGAGAATAGCAGCAGTGAGGAACAGGAAATGTTAAACAACCAAAGTA<br>TCTCAGTCTTAATGAGGAGTTCTGTAACAACCTGAACAGACAGAGAGAGCTTCTGACAGAACAGG<br>ATAATGAAATCAAGATAACTATGGACTCATCAGCTGAGGAACAAGCAATGGCAAGTGTCTAGGAA<br>GATTCCCTCTCAAGCAGCTCATCAAGCGAGGAATCCAAGGATGCTATTCCAGTGTCTACTGAGCA<br>GAAAAACATTGCAACAAAGAAATACTCAACCGATGCACCCCTGGAACAGCTTCAGAGACAGATTA<br>AATACAGCCAACCTTCTCCAGCAAGCTTCACTGGCTCAGCAAGCTTCCCTGGCTCAGCAAGCTTCT<br>TGGCCAGCAAGCTTCTCTGGCCAGCAACCTTCTGGCACAGCAAGCTGCCCCTGGCACAGCAAGC<br>TTCCTTGGCACAGCAAGCTTCCCTGGNACAGCAAGCTTCCCTGGCACNAGAAACATCATCCAAGN<br>AC |
| Caspase 2                  | U77933   | GCCTCTTGACCGTGATGTTGATGAAGTAAGTCTTCTGTACCTCCTTAGGATGGCATCATGTTGGT<br>CCTTGTGCTTACTGCAGGTTGTAATGGCACGTTTCACTTGCTCCCTCCAAAGCTGAAGGCTCCAA<br>GAGAGCAGGACTGTACTCCTTACTTATTTGGCTATTCACTAGCGGCACTTACTAGGTCTTCAATGAA<br>TGTTTCTCTGAGTAAAGGAAGGAGACAAGCAGCTAACTTTAGTTAGAGCCTATCTTTTGGCATTTT<br>ATAATGCTTATTATAGTACTCAGTTTAAATAGTATTGTACTCTTGTGGGGGTTTTTTTCCAGGT<br>GTTTTATTTTTATCCACTGTTTTTGTGTTTTTTTACATTGTTTGAAGATGTATCACGTGTGAGAC<br>AACTTCTTTCACATCTCCATGGTGGCCCGCAAAATTTAGGGCTATGGTAGTTGAGGTGCTCAATT<br>AATGTTTGTGATGAACAGGTGGTTTGAAGACTTGCTGCCAAATTTCTGCCCTTT   |
| Caspase 7                  | AF072124 | TTGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAAT<br>TCGCCCTTCGCGGAATTCGATGCAGGATCTGCTTAGACGAGCCTTGAAGAGGACCACAGCAACT<br>CAGCCTGCTTCGCGCTGCTCCTGCTGAGCCACGGAGAAGAGAATCTGATTTATGGGAAAGACGGC<br>GTGACACCGATAAAGGATCTGACAGCTCAATTTAGGGGAGACCAGTGAACAAACCTTGCTAGAGAA<br>ACCCAAGCTTCTTCTCATCCAGGCGTGCCGAGGGACGGAGCTGGATGACGGGATCCAGGCTGACT<br>CGGGGCTTATCAACGACACCGAGCCTAATCCCGCTACAAGATCCCGGTGGAAGCTGACTTTCTC<br>TTTGCTTACTCCAGGTTCCAGGCTATTATTCTGTTGAGGAACCCAGGAAAGGACTCCTGGTTGT<br>GCAGGCCCTCTGCTCCATCTGTAATGAGCATGGCAAGGACCTGGAGATCATGCAGATCCTGACCA<br>GGGTGAACGACAGGGTGGCCAGACACTTCGAGTCCCAGTCTGATGACCCCGCTCAATGAGAAG<br>AAAAGCTTGGCCAAGGGCGAATTCAGCACACTGCGGCGNTACTAGTGGATCCGAGCTCGGTAC<br>CAACTTGATGCATAACTTGAGTATTCTATAGTGNACCT                                       |
| Cathepsin L                | Y00697   | GAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTCGCC<br>CTTATCGCGGGATCCGATCTAGGCAATCAGGGCTGTAATGGAGGCTGATGGATTTTGCTTTCCA<br>GTACATTAAGGAAATGGAGGTCTGGACTCAGAGGAGTCTTATCCCTATGAAGCAAAGGATGGAT<br>CTTGTAATACAGAGCTGAGTATGCTGTGGCTAACGACACAGGCTTGTGGATATCCCTCAGCAA<br>GAGAAAGCCCTCATGAAGGCTGTAGCGACGGTGAGGCTATTCTGTTGCCATGGATGCAAGCCA<br>TCCGTCTCTCCAGTTCTATAGTTTCAAGTATCTACTATGAACCAACTGTAGCAGCAAGGACCTCG<br>ACCATGGGGTTCTGGTGGTTGGCTATGGTTATGAAGGAACAGATTCAAATAAGGATAAATACTGG<br>CTTGTCAAAAACAGCTGGGGTAAAGAAATGGGGTATGGATGGCTACATCAAAATAGCCAAAGACCG<br>GAACAACCACTGCGGACTTGCCACCCGAGCCAGCTATCCTATCGTGAATTGATGGACAGCGATAA<br>AGCTTGGCCAAAAGGGCGAATTCAGCACACTGCGGCGNTACTAGTGGATCCGAGCTCGGTAC<br>AAGCTTGATGCATAGCTTGAGTATTCTATAGT   |
| Cathepsin L,<br>sequence 2 | S85184   | GACCTCGACCATGGGGTTCTGGTGGTTGGCTATGGTTATGAAGGAACAGATTCAAATAAGGATAA<br>ATACTGGCTTGTCAAAAACAGCTGGGGTAAAGAATGGGGTATGGATGGCTACATCAAAATAGCCA<br>AAGACCGGAACAACTGCGGACTTGCCACCGCAGCCAGCTATCCTATCGTGAATTGATGGACA<br>GCGATAATAAGGACTTACGGACACTACATCCGAAGGAGTTCATCTTAAACTGACCAACCCGTC<br>TCTGAGTGAGACCATGGTACTTGAATCGTTCAAGATCCAAGTCACGATTAAATCTGTTGACAT<br>TTTTACATGGGTTAAATGTTACCACTACTTAAAACTCCTGTTATAAACAGCTTTATAATATTGGA<br>CACTTAATGCTTAATTCTGATTCTGGAATATTGTTTTATAAAGTTGNATAAACTTTCTTTAC<br>CTTTTAAAAATAAATTTTAAGCTCAGTGCAAAAAAAAAAAAAAAAAAAAAAAAAA  |

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| Cathepsin S                     | L03201 | GAATGGGCCCCCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTGGTACATTGAGCTCCCCCTTCGGCGATGAAGAAGCTCTGAAAGAAGCAGTGGCCACTAAAGGGCCTGTCTCTGTGTGCATCGACGCCAGCCATTCCTCCTCTTCCCTCTACCAAAGTGGTGTCTATGATGACCCCTCCTGTACCGAGAATGTGAATCATGGTGTTCCTCGTGGTTGGCTATGGGACTCTTGATGGGAAAGACTACTGGCTTGTGAAAAACAGTTGGGGCCTTCACTTTGGTGTATCAAGGATATATTCGGA TGGCGAGAAATAACAAAAATCACTGCGGGATTGCTAGCTATTGCTCTTACCCAGAAATCTAAACC GTTTCTTCTTTTCTAATGGGTACAAAAGACGGAATACACTCTAATTTAATTTTGTCTGCTCCAT CCGGAGGACCCAAGTGTGTCTGTGATCAGTGTGTACATACTGTGCTAACTGGCTTACAGCTTGT TTTTATAACCTTACCTCTCTCTGAAAAGTCTGTAAGCAAGGACGCGCTGAGGAAGGGCGAATTC CAGCACACTGGCGGGCGTTACTAGTGGATCCGAGCTCGGACCAAGCTTGATGCATAGCTTGAGTA TTCTATAGTGTCCCTAAATAGCTTGGCGTAATCATGGNCATAGCTGGTTCCTGTGTGAAAT   |
| CCR-5                           | U77350 | GACCGAGCTCGGGATCCACCTAGAACCNCGCCGCCAGTGGCTGGAATTCGCCCTTCGGTCCACA GGAGACCAGGAAGTTTCTACTGGTTTATGAAGTAGGTGAGTTTGTGTATCACTTAGTTTAAAA TGTAGCTTGAGGTAGAGATGGTCTTTTGAAGAAAGAAATTAATATAGAGGGCCTAAGGTACGTG CATGTGTTTAAATATTTATTGAGATAGATTGGGTCTTTGAAAGCTGAGTAGTTTATAAACGTGA ATGAGAATGTATTGATGAGACAGTAATTTCTGGCTTCATTCTCTATTAACTACAATTTATCCCAA ACTCTTCTTTAGCCACAAAAGTTCATATTAAAAAATACTGAGCATTGGGATTTTCTTTAGAGC TCGAGTATCTGACCAAAAATAACATCATTTTTCCTTATAAAAGCAAAATTCAGGCTACTTAAA TCAGGTCTTTGTCTTGCCCTGAGAAGAAAGGATGAGACCATGACTAGTTAGGGAATAGATAACCA AGCTATATGAATTGCTTTATAGACTTGTATGATCAGTAAGTGCTCTGTGGCTGAGAAGGAAGGG CGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCCAATTCGC  |
| CD44 metastasis suppressor gene | M61875 | TGNGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTTCG CCCCTATCGCGGGATCCGGTGCATTTGGTGAACAAGGAACCAACAGAGACTCCGGACCAGTTTAT GACAGCTGATGAGACCCGGAATCTGCAGAGTGTGGATATGAAGATTGGGGTGTAGTGCCTATGCC ACTAAGCTTGAAGACACAACAATTGGAGACATGTCATTACTGGGAGCTGGGACCCCTAACAGAT GCAATGTGTACTGATATTTTATTTGGGGATTTATTTGGGCATAAAATTTCCCTTTTCTTTGTT TTTTAAAGTTTGTCTTCCAATTTATGAAAATAGCATTGCTTTCTGAAATGAGGGTCTCTTCCAG TTCCCTCTTAGAGGCCTTGCAATTACCAAGGTATGCTACCATAGGCTTCTACCAATGAATACTCT TGGTCCCGATTGAACCAAGTCCCAAGTAACATCCACCAGCTAAGGATTTCCCAAGACTTAGA GAGATTGGTCTCTGGGAGGAAATTTGAATGGGTCCATATTGCCCTCCAGCAGTCCAATCTGTAAG CTTGGCCAAAGGGCGAATTCACACACTGGCGGGCGTACTAGTGGATCCGAGCTCGGACCAAACT TGATGCATAACTTTGAGTATTCT  |
| CDK102                          | Y17321 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC GGCACGAGGCCCAACTTCCTAATGGATGCAGATAAACACAGTGTACAGATTTTGTATAATCACC GTAATAAGTATTTAGACTAGGGGTAAAGCTCTGGTTTGTAGAAATCTTAAGATCATCTGTGGTGA AAAGTAGTTATGAAGCTGGGCTTGGTGACAGACCACCATGGGATCCAGCACTCAACAGGCAGAT GTTAGTTCAAGGTCCGTCTACATAGCAAGTTCAGACCAGCCACAGTTACAAGGTGGGATGCTAC CTACTGGTTATGGGAATTTTATAATTCAGGATAACAGTGGTGTATCTTACGTACTTTTGTGACTT GCCCATATCCACCCTGGATTTTGGTCCGAGACTTCGTGTCTTCTCCTTGGAAATGCTGGGCCTG TGGGGAGGTGTTGTGCTGTGATGTCAGATGCAGGAGATTCCCGTCTTGTCTCTGTCTGTGCTGTCT CCCACGGTGAACACTGGCTTTGCAACACTGAGAAATAAATAAAACACTCATGTCTTGGTTAAAA AAAAAAAAAAAAAAAAAAACTGCGGCCGCAAGCTTTATCCCTTTAANGAGGGTTAATTTTAN CTTGGCACTGGCCGTCTTTTACAACCGCCTNGACTGGGAAAACCCCTGGCGGTACCCAACCTT AN |
| CDK108                          | Y17328 | TCTTNACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT CGGCACGAGGCAGTGTGTATGTGAGCTCCCGGGAGGCTGCCCTAAAGGAGTCAGGAGATGTTCT GTTGTGAGGGGCTGACATCTTTGCTGAGCTTGGAGAAGTGGTTTCAGGAGCGAAGCCTGCATACT GTGAGAAGACCACGGTGTCAAGTCTTTGGGGATGGCAGTGGAGGACCTGGTCCGAGCCAAATTA GTGTACGATTCGTGGTCACTCTGGCAAGTGAGCAGAGGAGCTGTGCTGTGCTGGATGGACGTCA CGGCTCAAACGCTGGCTCAGTGTCTAGATCAAAGGAGGCCTAGTCCCAAGTGAACGGGAGTGAGA GTCACCTATAAGTATTGACATCCCTATTCATGTTTGTGGTTGGATAGCTAAACCTTCTGTTAGG GGGTGTAGGCCACATTACCTACCCTTGATCTTACTAGCCTTGTGTCTCTGAAATAAATCATTT CCAGTTAAAAAAAAAACCTTTGCGGCCGCAAGCTTATCCCTTTAGTGAGGGTTAATTTAGCTT GGCAGTGGCCGTCCGTTTTACAACGCTGTGACTGGGAAAACCCCTGGCGGTTACCNACTTATCGC CTGTCAGCATATCCCCCTTTNCGCCACTGCCGTAATAAC                             |

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| Cellular nucleic acid binding protein (CNBP) | D45254 | GCTATGCCATGATTACGCCAAGCTATTTAGGTGNCCTATAGAATACTCAAGCTATGCATCAAGCT<br>TGCTCCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTATCGCGGATC<br>CCCCAGGCCAGTGAGCTTTACTTGCAGTGTAAAGGAGGAAAGGGGTGGAAAAAAACCGAATTT<br>CTGCATTTAACTACAAAAAAGTTTATGTTTAGTTTGGTAGAGGTGTATGTATAATGCTTTGT<br>TAAAGAACCCCTTTCCGTGCCACTGGTGAATAGGGATTAATGAATGGGAAGAGTTTCAGTCAGAC<br>CAGTAAGCCCTTCTGGGTTTGTAGTGTGTTCCCATGTAGGAGGTAAACCAATTCTGGATGCATCT<br>AAGCTTCCATGAATAACTTTAATTCTTAGCATAATGATGGCCTTGGATTGTCTGACCTCAGTAGC<br>TATTAATAACATCGAGTAACATCTGCATCAGGCCCTCATAGAACATTCAGTTGAGTTGGGAGTA<br>AACTGAAAAGACAAATGTGTGAAGGATATGCCAGGGAATCTGGCTAAAGCCTAATACAGGAGCA<br>TCTTCATCCCAGTGTGTGCTGGACGTACCTCAAGGGCGAATTCTGCAGATATCCATCACACTG<br>GCGGCCGCTCGAGCATGCATCTAGAGGGCCCAATTCCG                             |
| Ceruloplasmin                                | L33869 | GANAACCGTTTCGTATAAANCNTGCTCGANTCGGCCGGCAGNGTGATGGATCTNNGCAGANTTCG<br>CCCTTATNGNGGGANCCCAACCGAGGATCNAGTCAACNGATCTNTATNTTGGGCTAGGGAGGCC<br>ATTGATTGATCNTTGGAAATCTNANGTGNAAGTTTTCANTCCTAAANNGAANATGNATTTCTCCC<br>TTCTGTTNCTANNACCTTGNTTACAANGNTTCCTTGNCACCTCTNNATGAGTANCGNCAGTNCNTA<br>CATTTGGANCNCNGCTGGNNNANAGNTTTCCTCTCACACNATGGNACNCATANANNGNGNANTA<br>AACCGCACC   |
| c-fos  | X06769 | TCCAGGGAAAGGATATAGGCAAAATTCGCNCTTATCGCGGGATCCGNGTTTCTACGCNNATAAAC<br>GAGGGGTCAATCCTTCTNTTCCAAGTAGNGCNTCNCNCGGGNGGCAANCNTTCTCCTTAGN<br>ATTCCTCAAGATGACNTCCTTCTCNAGCATGGGNTTCNCCNGTCTCNCCACAGGATTTTGGC<br>GCAGATCTGCNGGTNTCTAGTGCCATTTTATCNATTGGTGCANTATTTCTANACGCCAANAC<br>TGCAATGGCTGGNGCNGCNCACCTCTGGTCTCNCNNGTGGCCCCATCGCAGACNAGAGCGCCCAT<br>CCTTCGGNCNTCCCAACCCCGTCCGCGGGNGCTTAGNCCATANNNGNAGTGGTGAANNCNATGTC<br>AGGCAGCAGAGCNCANAGCATCGGCAGAAAGGGCAAAGTAGAGCAGCTATNTCTGAAGAGGAAG<br>ANNNTGCGAGNATCCNNAGGAAAGNAATAAGATGGCTGCAGTCTAGTGCCGAAATCGGAGNAGG<br>ANANTGACAGATACGCTCCAANNNGAGNCNGATCNCNTNTNTAGTAGAAGTGTGNGTTGCAGAC<br>CGNGATTGCCNATCTNCAGAAAGAGAAGGAAATTGAGTTTNTNNCAGCCTCNACCTCTT   |
| Cholesterol 7-alpha-hydroxylase (P450 VII)   | J05509 | GAAATTGNGCCCTTAGATGCATGCTCGAGCGGCCCGCAGTGTGATGGATATCTGCAGAATTGCG<br>CCTTCATAGCTGGGGCCAGAGCTTCATCACTTTCAGAAAGCAATGTCCTTTGTATTTATTTTCAA<br>AATGAAGATATTCCAATTGGCAGGATATTTTCTAAGGAAATTGCTTTATATTTTATGAAAAC<br>TACCAATTAATTATGAAAGGGCTTGAAATTCAGTTTTAGTGAAATTACTGATTTTTACTAGTA<br>AGGTTCTTCAGGTGTGAAACTGTATTATAAAATGTTGTAAATGGGTCACACTGTGCTTTGCATAA<br>AGGTAAAGGAACTATGTTTCAGCCTTTTCTGTGCTATGAGCTTCGAAAATAATCTTACTGTTT<br>TAGAAACACTGGGGAGGCTTCGACATGCTCTCGCTATATTTTATTTTACTGGTGTAGAAATTTT<br>CATTTTCAGTTTTTCAACTACCTTATCTTTCCCCCATTTTGACATGCATGCCAATGAGAAGAGTATT<br>TTTTAGGAATTAACAAGGCACCTCCAGAACCTACCCTGAGACTAAGGGCGAATTCAGCACAC<br>TGGCGCCGTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTTATAG<br>TGTCCTTAATAGCTTGGCGTAATCATGGGCATAGCTGNTTCTGTGTGAAATTGNTATCCGCTC<br>AC |
| Cholesterol esterase                         | L46791 | AATACTCAAGCTATGCATCAAGCTTGGTCCGAGTTCCGATCCACTAGAACGGCCGCCAGTGTGTN<br>GAATTCGCCCTTCGCGGGATCTTGGAAGTCTACCCAACACTGAAAATCTCTGAGAAAATGATT<br>CCAGTGGTTGCTGAGAAGTACTTCGGAGGGACAGATGACCTGCCAAAAGGAAAGACCTGTTCCA<br>GGACTTGGTTGCAGATGTGATATTTGGTGTCCCATCAGTGATGGTGTCTCGAAGCCACAGAGATG<br>CTGGAGCCCCCACCCTTCATGTATGAATTTAGTATCGCCCAAGCTTTGTATCAGCCATGAGGCC<br>AAGACAGTGATCGGAGACCATGGTGTAGTAACCTTCTCAGTATTTGGATCTCCATTTTAAAAAGA<br>TGGTGCCTCAGAAGAGGAGACCAATCTCAGCAAAATGGTGTGAAATACTGGGCCAATTTGCTC<br>GGAATGGGAGCCCTAATGGGGGAGGCTGCCCCATTGGCCAGAATATGACCAGAAGGAAGGGTAC<br>CTGAAGATTGGTGCCTCAACTCAGGCAGCCAGAGGCTGAAGGACAAAGAAGTGGCTTTTGGTC<br>TGAGCTCACTGCAGGGCCAAGGGCAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCA<br>TGCATCTAGAGGGCCCAATTCT  |

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| c-H-ras                     | M13011 | CCTCTAGATGCTGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCGCCCTTATCCAG<br>CTGATCCAGAACCATTCTTGTGGACGAGTATGATCCCCTATAGAGGACTCCTACCGGAAACAGGT<br>AGTCATTGATGGGAGACGTGTTACTGGACATCTTAGACACAGCAGGTCAAGAAGAGTATAGTG<br>CCATGCGGGACAGTACATGCGCACAGGGGAGGGCTTCTCTGTGTATTGGCCATCAACAACACC<br>AAGTCTTTGAAGACATCCATCAGTACAGGGAGCAGATCAAGCGGGTGAAGATTTCAGATGATGT<br>GCCAATGGTGCTGGTGGGCAACAAGTGTGACCTGGCCGCTCGCACTGTGAGTCTCGGCAGGCCCC<br>AGGACCTTGCCCGCAGCTATGGCATCCCTTACATTGAAACATCAGCCAAGACCCGGCAGGGTGTG<br>GAGGATGCCTTCTACACACTAGTACGTGAGATTGCGGCAGCATAAACTGCGGAAACTGAACCCGCC<br>TGATGAGAGTGGCCCTGGCTGCATGAGCTGCAAGTGTGTGCTGTAAGGGCGAATTCCAGCACACT<br>GGCGCGCTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAG<br>TGTCACCTAAATAGCTTGGCGT              |
| c-jun                       | X17163 | GCGAATTGGCCCTCTAGATGCTGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCG<br>CCCTTATCGCGGGATCCTCGTTCTCTCCAGTCCGAGAGTGGCGCTACGGCTACAGTAACCCTAAG<br>ATTCTGAAGCAGAGCATGACCTTGACCCTGGCCGACCCGGTGGGCAATCTGAAGCCGACCTCCG<br>AGCCAGAAGCTCGGACCTTCTCAGTTCGCCGACGTCGGGTGCTCAAGTGGCGTCGCCGGAGC<br>TGGAGCGCTGATCATCCAGTCCAGCAATGGGCACATCACCCTACACCGACCCCACTCAGTTT<br>TTGTGCCCCAAGAACGTGACCGACGAGCAGGAGGGCTTCGCCGAAGGCTTCGTGCGGCCCTAGC<br>TGAATGTCATAGCCAGAATACGCTGCCCAAGTGTACCTCCGCGGCACAACCTGTGAGTGGGGCGG<br>GCATGGTTCGCTCCCGCTGTGGCTCAGTAGCTGGCGCTGGCGCGCGCGCGCTACAGCGCCAGC<br>CTGCACAGTGAAGCTCCGGTCTACGCCAACCCTCAGCAAGCTTGGCCAAGGGCGAATTCCAGCAC<br>ACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAACTTGATGCATAGCTTGAGTATTCTA<br>TAGTGTACCTAA                              |
| Clusterin                   | M64723 | GAATTGGGCCCTCTAGATGCTGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCGC<br>CTTCGCGGGATCCACAGGCTCAACAGGCCATGACGTCCAGTCCATAGCCAGCTTTACAGTT<br>CCCGGATGTGGATTCTTAAAGAAGGTGAAGATGACCGCACAGTGTGCAAGGAGATCCGCCATA<br>ACTCCACAGGATGCTTGAAGATGAAGGGCCAGTGTGAGAAGTGCCAAGAGATCTTGTCTGTGGAC<br>TGTTCCGACCAACAATCCTGCCAGGCTAACCTGCGCCAGGAGCTAAACGACTCGCTCCAGGTGGC<br>TGAGAGGCTGACCCAGCAGTACAACGAGCTGCTTCACTCCCTCCAGTCCAGATGCTCAACACCT<br>CATCCCTGCTGGAACAGCTGAACGACAGTTCAGCTGGGTGTCCAGCTGGCTAACCTCAACAG<br>GGCGATGACCACTCTTCGGGTCTCCACAGTGACAACCCATTCTTCTGACTCAGAAGTCCCTC<br>TCGTGTCACTGAGGTGGTGGTGAAGCTGTTTGTACTCTGACCCATCAAGTGGTGAAGCTTTGGCC<br>AAGGGCGAATTCCAGCACACTGGCGGCCGGTACTAGTGGATCCGACTCGGTACCAAGCTTGATGC<br>ATAGCTTGAGTATTCTATATGTC                      |
| c-myc                       | X01023 | NTNCNNANGNGCCCTNTANATGCTGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCG<br>CCCTTCGCGGGATCCTGGAGAAGAGGCAAAACCCCTGCCAAGAGGTCCGAGTCAGGGTCATCCCCA<br>TCAAGAGGCCACAGCAAACCTCCACACAGCCCACTGGTCTCAAGAGGTGCCATGTCTCTACTCA<br>CCAGCACAAATTATGCAGCACCCCTCCACAAGGAAGGACTATCCGGCTGCCAGGAGGGCCAAGT<br>TGGACAGTGGCAGGGTCTGAAACAGATCAGCAACAACCGCAAATGCTCCAGCCCCAGGTCTCTCA<br>GACACCGAGGAAAACGACAAGAGGCGGACACACAACGTCTTGGAACTGTCAGAGGAGAAACGAGCT<br>GAAGCGTAGCTTTTTTGCCCTGCGCGACAGATCCCTGAGTTGGAACAAACGAAAGGCCCCCA<br>AGGTAGTTATCCTCAAAAAGCCACCGCTACATCTGTCCGTTCAGCAGATGAGCACAACTC<br>ATCTCAGAAAAGGACTTACTGAGGAAACGACGAGAACAGTTGAAACACAAAAGCTTGGCCAAGGG<br>CGAATTCAGCACACTGGCGGGCCGGTACTAGTGGATCCGAGCTCGGTCCAACTTGATGCATTA<br>GCTTGAGTATTCTATAGTGTACCTAAATAGCTTGGGGTA |
| Colony-stimulating factor-1 | M84361 | TAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCGCCCTTATCGCGGAAT<br>TCGTCTGTGGTGACCTGGGCATGGGTGACAGGGCTCTTACTTGCTCCTTGGTCTCTTATGCTGC<br>TGCCCCCGCTCCCCCTTCTGCTGCTCCCTGGCTACTGGGTGCTAATCTTTCAGGCCATGGAT<br>CCGGAGGAGAGTGGTCTATAGGCTCCACAGCCCTGTCTGAGACAACAGAGGGGTGAGGACAC<br>TGGAGACTTTCCTGTTGGGCTTACTTACGCTTCTAGTTACAGACTATTTCCACACTAGAAAATAC<br>GTATTTTAAATAGAAGAAAAACAGAAACAAACAAAGGCATTCTCTACCCCTCCATCTTAA<br>ACATACATTATTAAGACAGAAGAACAATCCAAACCCATTGCAAGAGGCTCTTGTGGGTGCTG<br>GTTGCATAAGAACAGGAGGAGCCCCAAACCCACCTTGGAGCTTCCCTGCACAGGAACCCCTTCT<br>TCCCTCCAGAAAGCTCAGAGGGAGCACTGCCAAGCTTGGCCAAGGGCGAATTCCAGCACACTGG<br>CGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAACTTGATGCATACTTGAGTATTCTATAGTGN<br>CACCTAAATAGCTTGGCGTAATCATGGCAT                 |

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| Complement component C3   | X52477 | AATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCT<br>TATCGCGGGATCCGGACTTATCCAGCGGGGTTCGGTCAAGGTCTACTCCTACTACAATCTAGAGG<br>AGTCATGCACCCGGTTCTATCATCCGAGAGGACGATGGAATGCTGAGCAAGCTGTGCCACAAT<br>GAAATGTGCCGCTGTGCCGAGGAGAACTGCTTCATGCATCAGTCACAGGATCAGGTGAGCTGAA<br>TGAACGACTAGACAAGGCTGTGTAGCCTGGAGTGACTACGTGTACAAGACCAAGCTAACGACGA<br>TAGAGCTGTCCGATGATTTGTAGTACATCATGACCATCGAGCAGGTTCATCAAGTCAGGCTCA<br>GATGAGGTGCAGGCAGGTGAGGAACGAAGGTTTCATCAGCCACGTCAAGTGCAGAAACGCCCTAAA<br>GCTGCAGAAAGGGAAGCAGTACCTCATGTGGGGCCTCTCCTCCGACCTCTGGGGAGAAAAGCCCA<br>ATACCAGCTATATCATTGGGAAGGACACGTGGGTGGAGCAAGCTTGCCCAAAAGGGCGAATTCCA<br>GCACACTGGCGGCCGTTCTAGTGGATCCGAGCTCGTCCAAGCTTGATGCATACCTGAGTATTCT<br>ATATGGCACCTAAATAACT   |
| Connexin-32               | X04070 | TGCGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCG<br>CCCTTCAGGCCCTCTGCCCTCCTAGGATTACTCCATCAAACCTTCCCTCCCTCCTACTCCCTTC<br>CTCAGAGAGTCTTCTGTCAAAGACCTGCCGCTTGGGAGTGGGGAGCCACTTCTGCACAGGGCT<br>CAAGGTTATTGAGGGTGTGGGCAATTCTTCTGCCTATACCTTTCCCTTCTCCCTCCTCCCTGAGA<br>TGAGGGATGAGATGTTCTGAAGGTGTTTCCAATTAGGAACTAATCTTAACCCCATGCTGTCTAG<br>GTACCCCACTTTTGGGAGTCATGTCAAGTGGGGAGGGCTGTGAGCAAGCAGAGTGGAGGAGGGCT<br>CTGCACCTGTGGATGGAGAAGGGAGGGAGCTTGCCTTGTGCTGCTGTACAAGGAAAANGANGACA<br>CATCTANGGTGGGGGAAGTTCCTTGGAGGGAGAAACAGGCAGATAAATCAAATGGGGGTGGNCA<br>AGGGCTTGCCCCCATCCCCCCCCAAANTTTCCCCCAAAGGGGGCCCTTNTTTTTTTTTTTTTT<br>TGGAAAAAATGGGTNAAAGGGGGCGAAAAATTTCN   |
| CXCR4                     | U90610 | TATCAGATAGANCGTAACGTGNTNNACTGCAGNNGCGTNAANTNCAATGGCCGANNCGNCTTNCG<br>NNAGNNGANNNGNCTAACNGGNAACNNGTCNNGAANNANGTCACTCANNAATTAAANNANGAAA<br>NNTNAGNNGNAGCNNTNNGCGCNNTGATNNAGTGAANTACGNCTNGNANNCNMGACAGCNCCG<br>NCNGNACNTNNANATTGNGTNANCNNANNNGTGNNGCAATNANNTCGANCCATNNCCNCCN<br>TTCAANNNNAGTNNNNANCNNGNGTGTCAAGAGNTGNNAANANNGNAGNNNGTNGTNGAGAA<br>GTANTNTCTNNGCNGTCCAAACNAAANNATNNNGNAGNAGTNNANTANCTGCNNGAGANC<br>GGNCNTCAAGNNGCGNNGGTCCTACTCAGTNANNGCCNCCNCCNNGNNGNANCNANACGAA<br>CNTTCCAAAGNNGATGGAATATNNCANNGGATTTCCGCCCTTNNANAGNNTCCATCCATTNT<br>TCGCCCAATNTNACCCAAAGGGGCGGCGNANGANNCTTNTGGCCCGNCTTTTCCCCANNCA<br>GCCTTTTGGATGGTGGTGTTCAGTTNCGGACANCAATGGTGGGTTCATNCTGCGNNGGCATTN<br>GTACCTTNTCTGTACTGCATCATCTTCAAGCTGTACGNNTGCAAGGGCCCCNNGGAG<br>CGCAAGNCCCTCAAGNCTACGGTCATCCTATCTGCTTCTTTCCTGCTGGGTACCGTNTT<br>ACGTGGGGATCNGCATCGANTCTTATCTTTCCTTGGAGGTATCAAGCAAGGATGTGAGTTNGAN<br>AGCGTCTGTCNAGTGGATGTTCCATCAGGAGGNCCTCGCCTTGTCTTCCACTGTTGCAGTGAA<br>CCCCAGTCTTCTNCGNCTTATCGGGGCCAAATACAATAACTCCGCGCAGCATGCATGATTC<br>CNAANCAGAGNCAACAGGTTTCAANNCCCTAATTGGNNNTNNNGGNN |
| Cyclin D1                 | D14014 | GCCCTCTAGATGCATGCTCNAGCGGCCGCCAGNGTGTGATGGATATCTGCAGAATTCGCCCTTCGG<br>GAATTCCTGTGGGGACATCCTGTATGCTGGGCTTCATTTGATCTGGGACATAGCATCACAGC<br>AGTCAGGGCAACTGTGTTCTGTAGTTATCAATATTGTTACTTGTAGCGGCTGTGTGCATGCC<br>ACCATGCTGTGGACCCGGAGAGATTTGTTCTGAGTCTCTGGTGCATCTTAATCTGTTAGGTT<br>CTAGTGTCTGTCTGTGTTTGTGTTACTCACAGCATTTGTGCTAATGTAAAGCCAGCCGAATGCT<br>GTAGGCCCCAGGTTCCCTAGCAAGCTGCCAAACCAAAAGGGTCACCACCAGCTTAGCTGAGGCGT<br>CCCAACCAGGCAGGACCTTGGAGGCTGCTGTGTCATGGTGTGATGGGGTGAAGTTTGGCCAAAG<br>GGCCAAAGGCTGGTGGATCCACACAGTCTGCCCTGTGACATGAATGGCTTTGAGGGGCTCTGGCT<br>GGTGTGTCAGGTTGGCTTTTGTGTTATTCTGGTTGACACACCATGGCAAGCTTGGCCAAAGGCGAAT<br>TCCAGCACACTGGCGGGCCGNTACTAAGTGGATCCGAACCTTCGGTACCAAGCTTGATGCATAGCT<br>TTGAGTATTCTATAGTGNACCTAAATAGCTTGGCGTAATCATGGCATAACTTGT   |
| Cyclin dependent kinase 2 | D28753 | AGTTGGGTACCGAGTTGGNATCCCACTAGTANCGGCCNGCCAGTGTGTTGNAATTCGCCCTTATC<br>GCGGGATCCCNNTTGGAGTCCCTGTCCGTACTTACACTCATGAGGTGGTGACCCTCTGGTACCGA<br>GCACCGGAGATTCTTCTGGGCTGCAAGTACTACTCCACAGCCGTGGACATCTGGAGCCTGGGCTG<br>CATCTTTTGGCGAAATGGTGACCCGAGGGCCCTATTCCCTGGAGACTCTGAGATTGACCACTCT<br>TCCGGATCTTTCCGACTCTGGGGACCCAGATGAGGTGGTTTGGCCAGGAGTTACTTCTATGCCT<br>GATTATAAGCCAAGTTTCCCAAGTGGGCTCGGCAGGATTTTAGCAAGGTTGTGCTTCCCTTGA<br>TGAAGACGGACGGAGCTTGTATCTCAAATGCTGCACTATGACCCCAACAAGCGGATTTACGCCA<br>AAGCAGCCCTGGCTCACCTTTCTTCCAGGATGTGACTAAACAGTGCCCCACCTTCGACTCTGA<br>TGTCTTCCCAAGCCCTTTCACCTGTGGTCTGACCTGATCTGGGCTTTTGGACACAAGCTT<br>GGCCAAAGGGCGAATTCGAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGG<br>GCCAATTCCNCA   |



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| Cyclin dependent kinase 4 | L11007 | TTGGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTC<br>GCCCTTCGCGGGATCCAGGATCTGATGCGCCAGTTTCTAAGCGGCCCTAGATTTCCATGCAAA<br>CTGCATTGTTTCACCGGGACCTGAAGCCAGAGAATCTTAGTGACAAGTAATGGGACAGTTAAGC<br>TGGCCGACTTTGACCTAGCCAGAATCTACAGCTACCAGATGGCCCTCACGCCCTGTGGTTGTACG<br>CTCTGGTACCGGGCTCCTGAAGTTCTTCTGCAGTCTACATATGCAACGCCCTGTGGATATGTGGAG<br>TGTGTGGCTGTATCTTCGCAGAGATGTTTCGCCGAAGCCTCTCTTCTGTGGGAACCTCTGAGGCTG<br>ACCAGCTGGGCAAAATCTTTGATCTCATTGGATTGCCTCCAGAAGACGACTGGCCTCGAGAGGTC<br>TCTCTTCTCGAGGAGCCTTTTCCCCAGAGGACCTCGGCCAGTGCAGTCACTGGTGGCGAGAT<br>GGAGGAATCTGGAGCGCAGTTGCTGCTGGAATGCTGACCTTTAATCCACTTAAGCGAAGCTTGG<br>GCAAGGGCGAATCCAACACACTGGCGGGCGGTACTAATGGATCCGAGCTCGNACCAACTTGATG<br>CATAGCTTGAGTN  |
| Cyclin E                  | D14015 | TGNGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTC<br>GCCCTTCGCGGGATCCTGGAAGTGTATGATGATGAAGGCCCTTAAGTGGCGTTCAAGCCCCCTGAC<br>CATTTGTGCTCTGGCTGAATGTTTATGTCCAAGTGGCCTACGTCAACGACACGGGAGAAAGTGTGTA<br>TGCCCTCAGTACCCACAGCAGGCTTTCGTGCAATCGCAGAGCTTTAGACCTGTGCGTCTCTGGAT<br>GTTGGCTGCTTAGAATTTCTTTATGGTGTCTCGCTGCCCTGCTTTGTATCATTTTCTCTCGTT<br>GGAGTTGATGCGAGAAGGTCACAGTTATCAGTGGTGTGATATAGAGAAGTGTGTCAAGTGGATGG<br>TTCCATTGCGCATGTTATCCGGGAGATGGGAAGTTCGAAGCTCAAGCACTTCCGGGGAGTTCCC<br>ATGGAAGACTCCCAACATCCAGGCCCACACCAACAGCTTGGACTTGTGTGACAAAGCCCAAGC<br>AAAGAAAGCCATATTGTGCAACAATAAGGATTTCTCTCTCTCGAGTGGGAAACTTGGCCAAAG<br>GGCGAATTNCACACTGGCGGGCGGTACTAATGGATNCCAGCTCGGACCAAACTTGATGCATA<br>ACTTGAGTATTCTAT   |
| Cyclin G                  | X70871 | GNNTTCCNNGGGGATGGATATNTGCAGAATTCGCCNNNATCCNCGGGATCCNATGGCCTCAGGAA<br>TNACNGCAAGACTCCAGGCTCTTNTNAAAGNCAGAGATTTCCGAGNCCTAAGTCAATGATGGGC<br>TTNGACACANAAACATTTTCCCTTTGCTGTGAATTTTACTGCAGAGATTGGTTGTCTAAAATAAG<br>GACAGGNGNAGCATCTCGGATGTGTGCGCCTTGAGNNGTNTTATTTGGCTGTGGNAATNNATNA<br>AGAGGNAAGGNANTGTCCNGCTGGCENNACTTNTNTGNTCCGNATNAGNCNGTANNGGTTNCNA<br>GTTTTCAGACGTGATNAGAATGCAAAAAGATTGTGTNNANANAGTGTGNTGCANAGTCNAAGCTA<br>TTACNNCTTCCANTTTCTNCAGNTCTATCANTCCCTCATTNGGGAGCCCNATGCCATTTGAAAGG<br>AGNNACNNNTNNGAATTTNTGANAGNTACNAGCCCTNNNTNAAAGNGTGGCACNGCNGGATCATATT<br>TTCTAAGNCAAAGCCNTCTGNGATGGNNCTNGCGATCATTTNTTGGAGATCCAANCNGTNCAGT<br>ATGTGNAGNNCACNGAAGGAGNANNATGNTTCAAGCNCATTTCCAGATAAGTGGCCNGTATNTN<br>NCCTTCTGGCAAGAGCCNGNNTCTAGTGTCTTCCGAGATCTTNTATCCGAGTGGCGCGNNGNT<br>NNNNANNNNNNC |
| Cyclooxygenase 2          | U04300 | GCGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGC<br>CCTTCGCGGGATCCGTTGCTGGGGGAAGGAATGTTCCAATCGCTGTACAAGCAGTGGCAAAGGCC<br>TCCATTGACCAGAGCAGAGAGATGAAATACCAGTCACTCAATGAGTACCGCAAACGCTTCTCCCT<br>GAAACCTTACACATCGTTTGAAGAAGTTACAGGTGAGAAACGGTTGCTGAAATTTCTAAAATGAC<br>CAAGGATTAAATGAGAAAAGAGAAGGTGAGAGGGAATTTAGTGAAGGAATAAACTGTCTTCTCTCC<br>TCTTCTCTTTTTCGTCTTCTTCTGGAAACAGAAAAGGATTGAGTTTATTGAGAAAGGGGAGCAG<br>GAATGGGGTCCGCTAGTGAATGTGTACTCGTCACTCCAGGGCTATTGTGCGGCAATTTCCAGTTTG<br>ATATAGCCATATTGTCTGTACCTTCCAGGAGAGAAAGAAATGGCTGCAGAGTTTGAAGCCCTCT<br>ACCATGACATCGATGCCATGGAACGTATCCCGCCCTGCTGGTGGAAAAGCCTCGTCCAGATGCT<br>ATCTTTGGGGAGACCATGGTAGAACCTTGGAGCTTCATTCTTCTTTGAAAGGCCTTATGGGTAAT<br>CCCATCTGGTC   |
| Cystatin C                | X16957 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGAGGGCGGAACCATGGCCAGCCCGCTGCGCTCCTTGATGCTACTGCTGGCCGTCTGGCC<br>GTGGCCTGGGCCGGAACCTCCAGGCCACCCCGCGATTGTTGGGAGCTCCGAGGAGGCAGATGC<br>CAGCGAGGAGGGCGTGCAGCGAGCGTTGGACTTCGCCGTAAGCGAGTACAACAAGGGCAGCAACG<br>ATGCGTACCACAGCCGCGCCATACAGGTGGTGAAGCTCGTAAGCAGCTTGTGGCTGGAATAAAC<br>TATTATTTGGATGTGGAGATGGGCCGAACATACATGTACCAAGTCCAGACAAATTTGACTAACTG<br>TCCTTTCCACGACCAGCCCCATCTGATGAGGAAGGCACTCTGCTCCTTCCAGATCTACAGCGTGC<br>CCTGGAAGGCACACACACCCCTGACAAAATCCAGCTGCAAAAATGCCAAGAGCTGAGTCTCATA<br>GGACCATGCCAATGGTCCCTTACTTGTTCCTTACCCTGTAGTGTTTATCCCTGAAAAGGGTGC<br>TCCAGCTCTGGAGGGCATCTNCGGGGTGTTCCACCAGGAGACAGTAAAGAACTGCTGCAGGCA<br>GGTTCTGCACGTCAGAACAGCTGTCCCTGGTTCTTCTCTCTTGCAGTAN                                      |



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| Cytochrome c oxidase subunit II | M64496 | CCGGCTCGTATGTTGGGGGAATTGTGAGCGNATACCAATTTACNCAGNAACCAGCTATGNCCAT<br>GATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCAAGCTTGGTACCGA<br>GCTCGGATCCACTAGTAACGCCGCCAGTGTGCTGGAATTCGCCCTTCACACAAGCACAATAGAC<br>GCCCATGAAGTAGAAACAATTTGAACAATTCTCCAGCTGTCATTCTTATTCTAATTGCCCTTCC<br>CTCCCTACGAAATTTCTATACATAATAGACGAGATTAAATAACCCAGTTCTAACAGTAAAACTATAG<br>GACACCAATGATACTGAAGCTATGAATATACTGACTATAAGACCTATGCTTTGACTCCTACATA<br>ATCCCAACCAATGACCTAAAACCAGGTGAACCTTCGTCTATTAGAAGTTGATAATCGGGTAGTCTT<br>ACCAATAGAATTTCCAATTCGTATACTAATCTCATCCGAAGACGTCTGCACTCATGAGCATCC<br>CTTCACTAGGGTTAAAAACCGACGCAATCCCGGCCGCTAAACCAAGCTACAGTCACATCAAAC<br>CGACCAGGTCTATTCTATGGCCAATGCTCTGAAATTTGCAAGGGCGAATTCTGCAGATATCCATC<br>ACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCAATTTCG   |
| Cytochrome c oxidase subunit IV | X14209 | AACACGANTATNGNNTTNTNTAGNGTACNNNTTNANNGNNGNANNNNTNNATANAAGNATANN<br>CTNCGAANNGNACNGNANGNTANNGAAGCCNAGCANTTNACTTGAAGACNCNCGNAANTCGCGN<br>NGGTNTAAACCTTNANNGNNTAAAANNANGNTAATAANTANNAGGNNTNNGTNGTAGGANGNA<br>GNNANCNTNGAGTNANATATATTTTNGNNGNANTNNANACGTNGAANGACTNANNGNCCGTGAAAA<br>TNANNTGTGAATNATCAAANGANCANCCTTCANNGANCNANANANTGNANATTTANCTCCAAGNT<br>NNGNATNAAAGGTTGNGTCCNNNGCTCNGGATNCNTCTTAGTAAGGGCCNCCAGTGTCTNNTGGA<br>ATTNGCCCTTATCANGGGATCCANTANAATNCGGGTGTGCCCTTAGGGCCACATGGGAGTGTNTA<br>AANAGTGAAGANTATGTCTCCNCGTNATATGNTGATCGGGCNGTGNACCCCTNGCNTGATGTG<br>GCNACCGTCAANGTTNATGTCTGCCAGCCAAAAGGCCNNTAAGNAGAAGGAGAAGNCCAGTGGA<br>GCAGCCTTTCCAGGNNTNAAAAAGTCCAATTGTNCCGCATCCAGTTNANCGAGAGCTTNGCTCAG<br>ATNACAAGGGCACCAATGAGTGAAGACANTGGTGGGCCCTGGCCATGTTCTTCATCGGCTTCAC<br>TGCGCTTGTGCTGATCTGGGAGAAGAGCTACGTGTANGGCCGTCCTCATACCTTTNATCGTGN<br>TTGGGACATAAGACNGCGCANGCNGTNTNAACTTC |
| Cytochrome P450 14DM            | D55681 | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAAATTCG<br>CCCTTCAGGACATCAGGTGTGTGTTTCTCCAAGTGTCAATCAAGACTGAAAGACTCCTGGGTAG<br>AACGCTTGGACTTCAATCTTGACCGCTACCTACAGGACAACCCAGCGTCGGGAGAGAAGTTGGC<br>TATGTGCCGTTTGGAGCCGGGCGCCATCGTTGTATTGGAGAAAATTTTGCCTATGTTCAAATTA<br>GACAATTTGGTCCACTATGCTTCGTTTATATGAATTTGACCTCATCAATGGATATTTTCCAGTG<br>TGAATTATACAACAATGATTCATACCCAGAAAACCCAGTAATCCGTTACAAACGAAGATCAAAA<br>TGAAGAAAGGAACAAGGAGCCAGTGTGGAGACGGGACTGCAAGCTGCAGCTTGGCAGAGAATGAA<br>GCTTTGACACAGCTTTCATACTGTACTGTTTTTTAGGTGTGTGGTTCCGAAAGCCAGTTTGATTT<br>TAATGTTTTATTAACTCGGTGATTTTTTGTGACACCTAATGGCAAAGGGCGAATTCAGCACACTG<br>GCGGNCGTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTG<br>TCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAAATGGTATCCGCTCA<br>CAATTN  |
| Cyto-<br>chrome<br>P450 1A1     | X00469 | TCTGGTCTCAGCATCTCCAGGCTTAGACTGTCCTGGATGCTCACCAGAC   |
| Cytochrome P450 1B1             | U09540 | NGGTGACACTATAGAATACTCAAAGNTATGCATCAAGCTTGGTACCGAGCTCGGATCCACTAGTA<br>ACGGCCGCCAGTGTGCTGGAATTCGCCCTTATCGCGGGATCCAGCGGAAACCAAGTGGCCTGAAG<br>GTGAGCGGGCTTACCAATTCATGGCTCTCACCGGCCAGCAGCTGGAGATCCTGAAGTATTTTG<br>AAATTGAAGAGTAACAGGGCCCAAGGAATTTGCATACTGTTCCCCCTCACCCCATTAACACA<br>TGACACAAATCAGCATGTGTGTACAGCTATCCAACAAAATATTTAGTAACCTCTGCCTTTTTTG<br>GTCAATTTGAAAGGGAACCTTCTATGTGCAGAAATTGGCCCCATAGGAAACCACAGTAAGCAGAGG<br>CTTAGGATATATATTTTCAAGATTCAAGAAGTGATTTAAGTGTAATAATAAAGAGCAGAAATT<br>CTACCAAGAGACAAATGAGGCCACTCCCTTGTGGCCCTGGACGAGGTTTCTTTCTGCCTGTAGA<br>TGTGCCTCCCCTCTAGAACGGACATAAAGCCGTTTTTGTCTCCCCCTCAAAGCTTAAGGGCGAA<br>TTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCAA  |
| Cyto-<br>chrome<br>P450 2A3     | M33190 | ATATATATTTCAAAGGTAGAGCCAGAGAAGGGGGAATA  |

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| Cyto-<br>chrome<br>P450<br>2B1/2B2 | M19972    | CAACATACCAGATCTGCTTCTCAGCTCGGTGATCCGGCTGAGGCAGCCAT   |
| Cyto-<br>chrome<br>P450 2C11       | U33173    | ACTCTCTAAGCTCTCATCTGTAATGTCTTCTGAGGGTCTGTCTACTT  |
| Cytochrome P450 2C23               | X55446    | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGCAGGGGCCAAAGTTTCATGAGGAACCTTGACCGTGTGATTGGACGCCACCAACCCCCAGCAT<br>GAAGGACAAAGATGAAGCTGCCTTATACCGATGCTGTATGTCATGAGATTCAAAGATACATCACTC<br>TCCTTCTCTCCAGTCTGCCCCATGCTGTGGTCCAGGACACAAAATTCAGAGACTATGTCATCCCC<br>AAGGGTACTACTGTACTCCCGATGCTGTCTTCCTGTCATGCTGGATCAAAGGAGTTTGCCAACCC<br>AGAGAAGTTTGATCCAGGACACTTCTGGATAAAAAATGGCTGCTTCAAGAAGACAGACTACTTTG<br>TTCCCTTCTCCCTTGGAAGCGGGCCTGTGTTGGTGAGAGTTTGCCCGGATGGAGCTCTTCTCTG<br>TTCTTACCACCCCTTCTGCAAAAGTTTTCTTGAAGACTCTGGTGGAGCCCAAGGACCTTGACAT<br>CAAGCCTATTACTACCGGGATTATCAATTTGCCGCCACCTTACAAGCTGTGCCTTGTCTTAGAT<br>AAGGGTTTATCTTCTAATCATTCAAATCAAAGTAATGGTTTCTTTCTATAAATATTCTTTT<br>TATGCTAAGCACTGCTANGGAGAGCAATCATATGCTG      |
| D-dopachrome<br>tautomerase        | NM_024131 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGCAGGCTCCCCGTGTCTTTCTGGAACCTCAACTGGCTCCCACTGCTCTCTCGGTGC<br>AGTTACCGTTTGGCGATCCCTCTCTGCTAACATGCCGTTCGTTGAGTTGGAAACAAACTTGCCG<br>GCTAGCCCGCTACCCGACGGCTGGAGAACCAGTTGTGTGCGGCCACAGCCACCATCTGGACAA<br>ACCCGAAGACCGCTGAGCGTGACGATACGACCGGGCATGACCTTGTGTGATGAACAAATCCACAG<br>AGCCCTGCGCCACCTCTGATCTCTTCCATCCGTGTGTGGGCACCGCGGAGCAGAACCCGAGC<br>CACAGCTCCAGCTTCTTCAAGTTCTTCAACCGAGGAGCTGTCCCTGGACAGGACAGGATCATTAT<br>CCGATTCTTCCCTTGGAGCCCTGGCAGATCGGAAAGAAAGGAAGTGTATGACGTTTCTGTGAT<br>GGAGACAAGGAACGAGGGCGTTTGCTTGAGCCTGTCCAGAGCCCTTCCAGAGAGGCCCTCTGGC<br>AGATACGATACAGATCCCTCTTTTGCAATAAGTGTCTGTGATCTCACTGACCTGGTTTCTCTCC<br>CCCAGCCTCGTGGAACGAGGAGAGCAAAATTAAGAAGAGGCC          |
| Decorin                            | X59859    | ANNNCNTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCC<br>AAGAAATTCGGCAGCAGGCTCGGATACATCCGCATCTCAGACACCAACATAACTGCTATTCTCAA<br>GGTCTGCCCACCTTCTATCAGTGAAGTGCATCTGGATGGCAACAAGATCGCCAAAGTTGATGCAGC<br>CAGCCTGAAAGGAATGTCTAATTTGTCTAAGCTGGGTTTGAGCTTCAATAGCATCACCGTTGTGG<br>AAAATGGCAGTCTGGCTAATGTTCTCTCATCTGAGGGAGCTCCACTTGGACAACAACAACTCCTC<br>AGAGTGCCTGCTGGCTGGCACAGCATAAATATGTCCAGGTCGTCTACCTTCATAACAACAACAT<br>CTCCGAAGTTGGGCAGCATGACTTCTGCTTCCCTTCATACCAGACTAGGAAGACTTCTTACACTG<br>CCGTGAGTCTTTATAGCAACCCGTCCGGTATTGGCAAATTCACCCACACACCTTCAGATGTGTC<br>TTCGGGCGCTCTACCATTCAACTTGGGAACACAAAGTAACCTCCAAACAGCCTCATTTTTATAAT<br>CGGGAACAAAAAACCAATCTGTCAATATTATGCTAAAAAGAAAAAAATATTTGAAAAAGAAA<br>GAATGCTAGATTCTGGGAAATTCAGTATAGCGCGGATGCCTT |
| Defender against<br>cell death-1   | V13336    | AGAATTTGGGCCCTCTAGATGCATGCTCGAGCGGCCAGTGTGATGGATATCTGCAGAAATTCGC<br>CCTTCGGCGGATCCATGTCCGGCTCGGTAGTGTCCGTCATCTCCCGTTCTTGGAGGAGTACTTG<br>AGCTCCACTCCACAGCGGCTGAAGTTGTCTGGATGCCATCTCTTATATATTGCTGACCGGGGC<br>GCTGCAGTTCCGGTACTGTCTCTCGTGGGACCTTCCCTTCAACTCTTCTCTGCTTCA<br>TCTCTTGTGTGGGAGCCTCATCTTAGCGGTTTGTCTGAGAATACAGATCAACCCCAAGAACAG<br>GCGGATTCCAAGGCATCTCTCTGAGCGAGCCTTTGCTGATTTCTCTTTGCCAGCACTATCCT<br>GCACCTCGTCTCATAGCTTGGCCAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGA<br>TCCGAGTCCGTAACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTGTACCTAAATAGCTTGG<br>CGTAATCATGGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCACAAATCCACACAACATA<br>CGAGCCCGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAAGTGAGCTAACTACATTAAAT<br>GCGTTGCGCTCACTGCCCGCTTTTCN                                       |

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| Diacylglycerol kinase<br>zeta              | D78588    | GAAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCG<br>CCTTAAGGGGACCATGGATCAACGAGGGACACTACCAGAGGACTAGAGCTTTCCTTGCCCATCTC<br>ACTGCCCATTCCTGTTCAGATGGCTATGGGGGACCCTGTACAGGGAAGGAGCCCCGTGCCACC<br>CCCTGAGAAGCCGTTTCAGATCTAGGGCTGGACTCTAAGGAGCTGGACTCTCACCTGTCCCTGGTT<br>TCATGGGGAAACAGGAAACAAGCTGGGCTGACTGGGTCCCTCCCTTCAGGGCGGCTCCCCCTCAC<br>CACAGCTGATGGAATGGCTGGACAGCTCAGTCAGGGAGGCTGCTCTCAGCAGGACTTTCTAAAG<br>CCACCTGATCCCTTGGGCTCTTTGGAAGGTTCTGGGTGCCTAGCCCTCCTCTCTGACCCACACAC<br>CTTGGGCATCCAGAACTCAAGAGCCTGCTGTATTGCTGCTGCCGCTGCCCTGCTTGGCACCTA<br>CCCTGGTGATCCTCTCATGCACCCAGTCATTTCAATTCGACTGTATGGCCTGGGGTGAANGGC<br>GAATTCACACACTGGCGGCCGTTACTAATGGATCCGACTCGGTACCAACTTGATGCATAACTTG<br>AGTATTCTATAGTGTCCCTAAATAGCTTGGCGTAATCATGGCATAGCTGNTTNCCTGTGTGAAAT<br>TGTN |
| Dimethylarginine<br>dimethylaminohydrolase | NM_022297 | TTCTNAGAACATGATTACGAATTTAATACGACTCACTATAGGAATTTGGCCCTCGAGGCCAAGA<br>ATTTCGGCACGAGGATGATTTATTACAATCATCTCCTCAATAGACACACTATTTATTTTATTTCAA<br>TTAAAAATTTCTTCCCAAACCTTTCCTGCACCTCCCTCACCCAAAACCTATAGCCACAGAAAAAC<br>GAATAACCCCTTGAGAATCAAAATGAACGAAATCTATTTGCCTCTTTTCAATACCCCAATAAT<br>AGGTCTACCAATTTGTGTGACCATTATTATGTTCCTCAATTTCTATTCCCATCATCAGAACGCC<br>TAATCAGCAACCGACTACACTCATTTCAACACTGACTAATCAAATTTATCATCAACAAATAATG<br>TTAATCCACACACCAAAAGGACGAACCTGAGCCCTAATAATTTGTATCCCTAATTTATTTATCGG<br>CTCAACCAACCTTCTAGGGCTTCTTCCCATACATTTACCCCTACCACATCTCCTCTTACAAAGC<br>AAACGTCAACCTTACCTCACTGGAGGATAATGAATCCTAGTCATTAGAGAAAATGTTTTAGCTGAT<br>CTAAATTTACAATGGATTCTTTTATTATCACGTATGCTGTAGAAATGTAAGCGTCTCCTCTCTGGA<br>CAATGTAATGTAGAAAAAGTGCTAGATATCAGAGATTTNCAT                            |
| DNA binding<br>protein inhibitor<br>ID2    | D10863    | NACATTTTCACACAGNANCAGCTATGCCCATGATTACGCCAAGCTATTTAGGTGACACTATAGAA<br>TACTCAAGCTATGCATCAAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCGCTGTGCT<br>GGAATTCGCCCTTCGCGGGATCCATGAAAGCCTTCAGTCCGGTGAGGTCCGTTAGGAAAAACAGC<br>CTGTCCGACCAACAGCTTGGGCATCTCCCGGAGCAAAACCCCGTGACGACCCGATGAGTCTGCT<br>CTACAACATGAACGACTGCTACTCAAGCTCAAGGAAGTGGTCCCGAGCATCCCCCAGAACAAAGA<br>AGGTGACCAAGATGGAATCCTGCAGCAGCTCATCGATTATATCTTGGACCTGCAGATCGCCCTG<br>GACTCGCACCCCACTATCGTCAGCCTGCACCACAGAGACCTGGACAGAACCAACGTCACAGGAC<br>GCCGCTGACCACCCCTGAACACGGACATCAGCATCCTGTCTTGCAGGCGTCTGAATTCCTCTCTG<br>AGCTTATGTGCAATGACAGCAAAAAGCTTGGCCAGGGCGAATTCGTCAGATATCCATCACACTG<br>CGGGCCGCTCGAGCATGCATCTAGAGGGCCCAATTCGCA  |
| DNA topoisomerase I                        | AF140782  | AATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCT<br>TATCGCGGGATCCTGCAGCAGCAGTTTAAAGAGCTCACAGCCCTGTATGAGAATGTACCAGCAAA<br>GATTCATCTTATAACCGTGCCAATCGCGCTGTTGCAATTCCTTTGTAACCACAGAGGGCGCCAC<br>CAAAGACCTTTGAGAAGTCAATGATGAACCTGCAGTCTAAGATTGATGCCAAGAAAGATCAGCTA<br>GCAGATGCTCGAAAGGACCTGAAAAGCGCTAAGGCTGATGCCAAGTCTATGAAGGATGCAAGAC<br>CAAGAAGGTAGTAGAGTCAAAAAGAAGGCTGTACAGAGATTAGAAAGAGCAGCTGATGAAGCTGG<br>AGGTTCAAGCCACAGACCGAGAGGAGAACAAACAAATTGCCTTGGGGACCTCCAACTCAATTAC<br>CTGGACCCTAGGATCACAGTGGCTTGGTGCAAAAAATGGGGGGTCCCAATCGAGAAGATTACAA<br>CAAAACCCAGAGAGAGAAGTTTGCTTGGGCCATTGATAAGCTTGGCCAAAAGGGCGAATTCACAGC<br>ACACTGGCGGCCGNTCTAGTGGATCCGAACCTCGGTCCAACTTGATGCATATTGAGTATTCTAT<br>AA   |
| Dynein light chain 1                       | U66461    | AGNGAGGCTTGATCAGCGAGCTTCTAGCATTTAGGTGACACTTATAGAATAGGGCCCTCTAGATG<br>CATGCTCGAGCGGCCGCGATATCGAATTCGCCCTTCGCGGGATCCCTGTGCGCTCTGCTGCTTGA<br>GCGGCGCCAGCACCTTCCCTAGGAGCTCGCAGCAGCCGCTGGCCCTGCTCCACGGTAACCATG<br>TGCGACCGGAAGGCGGTGATCAAAAATGCAGACATGTGGAAGAGATGCAACAGGACTCGGTGGA<br>GTGCGCTACTCAGGCGTTGGAGAAGTACAACATAGAGAAGGATATCGCGGCCCATATCAAGAAGG<br>AGTTTGACAAGAAGTACAACCCACCTGGCACTGCATCGTGGGCCGGAACCTCGGTAGCTACGTG<br>ACACACGAGACCAACACTTCTACTTCTACCTGGGTGAGGTGGCCATTCTCCTGTTCAAATC<br>TGTTAATAGCATGGACTGTGCCAAACACCCAGTGTATCCATCCAAAAACAAGGACTGCATCCTAA<br>ATTCCAAATACCAGAGACTGAATCTTCAGCCTTGTCTAAGGGAACACCTCGTTTGAATCTGTTGTG<br>TTTTGTACAGGGCACAAAGCTTGGCCAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGAA<br>TCCGAGCTCGGTACCAAGCTTGGGTCTCAA   |

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| Ecto-ATPase   | Y11835    | TGTGAATTCGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT<br>CGCCCTTACATCAGCTTCTGAGCCGTGGTTACCACTTCGATGAGCGCTCCTTCAGAGAAGTGGTC<br>TTCCAAAAGAAGGCTGCAGACACGGCTGTCCGCTGGGCGCTGGGCTACATGCTGAATTTGACTAA<br>CCTGATTCTCTGCCGACCTCCCCGGACTACGCAAGGGCACCACCTTCAGCTCCTGGGTCCGCTCTC<br>CTGCTGCTCTTTCAGATCCTGTATCTTGGCGGCGCTGGTCTCTGCTCCTGCCAGGATGTCAGGTC<br>TCAGCCTGTGACTCAGGGTGAGGTCCATTCCGAGTGGGACTTTTGTTCGAAGGGCGAATTCCAG<br>CACACTGGCGGCCGTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATT<br>CTATAGTGTACCTAAATAGCTTGGCCGTAATCATGTCTAGCTGTTTCTGTGTGAATTGTT<br>ATCCCGCTCACAATTCACACACATACGAGCCCCGGAAGCATAAAAGTGTAAAAGCCTGGGGTGC<br>CTAATGAAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGGCCGCTTTTCAGTCGGGAAAC<br>CTGTCTGCGCAGCTTGCAATTAATGAATTCGGNCAACNCCCCGGGGAGAAGCGGGTTTTCGTATT<br>TGGGCCGCT |
| eIF-4E  | X83399    | NNNNNNNNNNNTTCTACATGATTACGANTTTAATACGACTCACTATAGGGGAATTTGGCCCTCGAG<br>GCCAAGAATTTCGGCAGGAGGGCCGAATGTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTAC<br>GGTCAACACAATGATTTATTAATAAATAAAACGTAAAAATGATTTTGTACATATGCTTCCAAAT<br>TTCAGGCATGGGATCCAAGTAGGTTTATAGAAAACGCTGTAGCCAGGTATCAAGTCCCTTACAAC<br>AAAGTAAACTACCCTCCACCCCAACCCACCCCGGTTTTGTACAGAATCAGCAAGTTCAGCCC<br>CCCCCCCCCNCCCCCAAAAAACACAAATTAAACGACACATCTTGNTAGTNTAAAAACNACC<br>NAGGTCCAAGTAATNATAAAAAATAGAGTCCNTCAATGACTGTAACACNAAAAATGTGTGTGG<br>GGCCGAGTCCACCTTCCGGGGGACCGGGACGGGCAAGCAANCAGGGGGTCCCCCCCCGGGT<br>GAGCGGCTCTNCCGGGGGCACCTGGGGTGGGNCNCGAAGGCCAAGGAAGCCCCCTTNCGCCCC<br>CGCCGNTTGGCATTCCGNAACCCGGCTTTTNAACNAACCTCCGNCNTTATCCGCCGNCGCCNN<br>CCGCCGNAACCCGCCNCTNGTACNGNCCACNTGTGCTTGGCGGCCNNCACTTTATTNCTTTA<br>NTGANGGTNNATTTTNNCCN |
| Elongation factor-1<br>alpha                        | X61043    | CACATATAGAATACTCAAGCTATGCATCAAGCTTGGNCCGAGCTCGGATCCACTAGTACCGGCCG<br>CAGTGTGTTGGAATTCGCCCTTTGAAGCTTTTGAGTGAAGCTCTGCTGGGGACAATGTAGGCTT<br>CAACGTAAAGAACGTGTCTGTCAAAGACGTTAGACGTGGCAATGTTGCTGGGGACAGCAAAAAATG<br>ACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCCGCCGAGATC<br>AGTGTCTGGCTATGCCCTGTTCTGGACTGCCACAGGCCACATAGCATGCAAGTTTGGCCGAGCT<br>TAAAGAGAAGATCGATCGTCTGTTCTGTAAGAAGCTGGAAGATGGCCCCAAATTTCTGAAGTCTG<br>GTGATGCTGCCATTGTTGACATGGTCCCTGGCAAGCCCATGTGTGTGAAGCTTCTCTGACTAC<br>CCTCCACTTGGTCTGTTTCTGCTGTTCTGCTGACATGAGGCAGACAGTTGCTGTGGGTGTCATCAAAGC<br>CGTGACAAAGAAGGCTGCAGGAGCTGGCAAAGTCACCAAGTCTGCCAGAAAGCTCAGAAGGCTA<br>AATGAATATTATCCCTAACACCTGCCACCCAGTCTTAATCAAGGGCGAATTCGTCAGATATCC<br>ATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCAATTTCG                           |
| Emerin  | NW_012948 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACGAGGGCTTCTCTGTAGGCTCCGAGCTGTCTGTTTCTTGGGCCCTGTGTATAGGTGCCG<br>GCCGCCCTTGGCGTTCAACACCGCTTCCAGGTGCCGGCCGTGTCTGCCATGGACGACTATGCGGT<br>TTTGTCCGATACTGAGCTGGCCGAGTGCTACGCCAGTACAACATCCCGCATGGGCTATTGTGG<br>GCTCCACTCGCAAGCTCTACGAAAAGAAAATCTTCGAGTACGAGACCCAGAGAAGGAGGCTTTTCG<br>CCCCCAGCTCGTCATCGTCTTCACTTCTCTATCGGTCTCAGACTTGGATTACGCTCCGTGGA<br>CTCAGACATGTATGATCTGCCAAAAAGGAGGACGCCCTTACTTTACCAGAGCAAGGACTATAATG<br>ATGACTACTATGAGGAGAGCTATTTGACTACCAGGACATACGGGGAGCCCCGAGTCTGTGGGCATG<br>TCCAAGAGCTTCCGCCGGCCAGGACCTCACTTGTAGATGCTGATGATACCTTCCATCACCAGGT<br>GCGTGATGACATTTCTCTTCTCAGAAGAAGAANGCAAGGATAGGGAACGCCCATCTATGGNC<br>GANACAGTGCCCTACAGANCATCGCACACTACCGCCCAT  |
| Endogenous<br>retroviral sequence,<br>5' and 3' LTR | D9005     | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGCATGACAGAAGCACTGGGTGGAGGAAAGACCTCTGCGACTGGCTGATTGATCC<br>CTGCTGAAAGCCGAGGACCTTGTCCACAGACAGGAACAGTTCTCTTATGAATGAAGGTGACAGA<br>CAAGTGGGTGCTGCCATGGTGGACAACAAATGTATCTAGAATGGCTGAACCTTACCCCCCA<br>GCACATCAGCGCCACAGATGCCCTTGGCATCTCTTGGATGCCCTGATAAAGCCAACAACTGTGAG<br>TACTATTTCATTGCCAGGAAAACAGGAGGGAAGAGATTGAGTACATGGGGCAGTGACAAAACAA<br>ATAAAGTGGCTCGGGAATGGCTATACAGGAGCCTATCTGTTTACAGCCCTGCAAGAGACAGCC<br>ACTGAGAACTAGGATTAACTAAGGGGATGGCCTCACTTAGAAAAGGCCAAGTTGTTTAAAG<br>ATAAAGAGACNATGACACACTGAGGGGAAGGCTATACTCCCCAGAAAACAAAGAAAAGACTCA<br>CTTTGCCAAATACAGAAATGGACTCATTTAGGAGATAAAAANTTTGTCCAAGTAGTTAAGGTAT<br>ATGTAATANACTTTAAAAATTTTANCCAAAGAGAGACAGTAAAAA  |

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| Epidermal growth factor   | U04842   | ATGCCATGATTACGCCAAGCTATTTAGGTGNCACCTATAGAATACTCAAGCTATGCATCAAGCTTG<br>GTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTAAGGGCCCTCAG<br>ACCTGCCCCAGCAAACAGAGCCAGTTCCTGAGAACTGGGAGCAGACAGAAGGTACCGAAGGTGA<br>AATAGCAAACAGGCTGAAGGGTGGTAGAGCGGCAGATCTGGTACTCCTGTCTCCACGGCTAATC<br>ACTGCTCAGGGTCTTGAAGATAACTGCATAGCTGCATAGCTGCATAGCCTCGACTTCTGCTTCTT<br>GCTTCAAGCAGTCCCCTTGAAGACGATCAAAAGAGAAGTGGAGAAAAATCATCAGAAACCGAAGT<br>CAAGACGTTACGCTGTTGTAAGCTGTGCTTCTTCCCTGGACTGTTGGGCTCTTTCCTTGTGT<br>CTCAGAAGAAATGGGTAAAGCAGGCGATCATATGCTTGTGATTGCACAGTAGATGATATGAT<br>CTACATAGATCTTAGCTCACTCTCACGGAAGGCTGGAACATTATAGATGCTGCTAAGATACACT<br>GCAAGTGTGGCCCTGCTCATAAGCTTAAGGGCGAATTCGAGATATCCATCACACTGGCGGC<br>CGCTCGAGCATGCATCTAGAGGGCCCAATTCCCAA  |
| Equilibrative nitrobenzylthionosi ne-sensitive nucleoside transporter | AF015304 | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGGGCGAGCACTGTGTCCCTAGCAATCAGCACCTCCAAAGGTATCCAGGCCTAGAGG<br>TTTTATCCGAGTCCCTAGGCCCAAGTGCGCCATGAGGACGGACACCCGCTGAAGCTTTGCTGGTC<br>ATTGCAAGCCTGGTCAGGACAGCCGCTGGTTGCCGCTCCTGGTCCCTGCAGGGTTGTGTTATTC<br>CCCTGCTGATGCTCTGCAATGTGAAGCAGCACCCTACCTGCCCTCCCTCTTTAAGCATGATGTC<br>TGGTTTCATCACCTTCATGGCCGCTTTGCCCTTCTCCAATGGCTACCTCGCCAGCCTCTGCATGTG<br>CTTCGGGCCCCAAGAAAGTCAAACCGGCTGAGGCAGAGACTGCCGGAACATCATGTCTTCTTTC<br>TGTGTCTGGGCTGGCTCTGGGAGCTGTGTTGCTTCTTGTGTAAGGGCACTTGTGTGAGCGACC<br>CTGTGTGACAGAGGAACCTACACTGCCTGCTTCTGCTCACTTCTTCCGCTGTAGGGACGAGCA<br>GGGCTCCAGAGGGCTGCTCTTCTGCTTCTTCCGGGCTGGGCCCAGATGTCAGGAACAAAGGAN<br>GGACCTCTGAGGATGGACTTGGGATTGGGGGTCANANTGGTANGGGGACAATGGTCTCTGA                 |
| E-selectin  | L25527   | GTTCCAGTATTGTTGTACAGGGATAAATAATATTATCAGCAGTTTTGAACAGACAAATTTCT<br>ATTTCTATCTTGGAAAAAAGGCAATTTGCCACATTCTCAGGTTATGGCTAGGGGTGTCATT<br>ATGGTTCAAATCCTGCTGAGTATTACATGGTAAGCCTTACTGGCTTTATCCCTGTGGATTGGTG<br>GCCTCTGAAGTATTCTTGAACATTGTGTTCTGTGCTTGGCATTGAGTCCAGCATAATGTCCGTT<br>ATTCTTAGTTCAGTGCAAAAGACTTAAAAAGTCAGAATCCTGTGGCCATCACAAGGCAAGGT<br>TATCCTAAATCTCTTTTGTATTAGAAAATCCAGGATTATATCTGCAATAAACCTATTTTCAAGA<br>TGAGACATTAAATCAGTGTGAAATTCAGTATTAAATGGTAGCTGGTTTTTCAGACATGGTAC<br>TATCAAAAGGATAGAAAGTAAAGAGAGTATATCTGGGGTTCCCA   |
| Fatty acyl-CoA oxidase  | J02752   | GNGAATTGGGCGCTCTAGATGCATGCTCGAGCGGCCCGCAGTGTGATGGATATCTGCAGAATTCG<br>CCCTTATCGCGGGATCCTCGTTGAAGATGGCTGAAGATAGTGCAGGCCCTGGGGAGTTTCTCCTT<br>GCTGAGAGCCGGCTCTGTGGTGAGCCCCTAGCAGCCTTACGAGGCGGTGAAACGGCCCCCTCAGA<br>TGAGGAGCAGCCTCTACAATCATTCTGAGCTTAAAGGTGAAATATGCACCTTTTGTCTATAAAT<br>GTCTATAAATGCTTGGGGGGAGGGTAATGTTTGTGTTTTTTTTTCTTGAACAGGGCCAGAA<br>TGGCCTTGAACCTGATCCTCACAACCTGGTAAATGCTGGGCCTACAGGTGTGCGCGACATGTC<br>TGGCTGATCGGAGCTCTTTATTCTTAAAGCACAGTGGGGAGATGATTGTAACATTAAGTCTGTG<br>TCTGTGGCATTGCGATTGTGAGAGCAGTTCCTTAGAACAGTCTGAGAGCACAGCATCAATGTAG<br>TGAAAACGATGTCGAGCCTGACATGAAATCACAACCTCCGGGTCTCGACACAAGCCTTAAAA<br>GCTTAAGGGCGAATTCAGCACACTGGCCGGCGTCTAGTGGATCCCACTCGGTACCAAGCTT<br>GATGCATAACTTGAGTATTCTATA  |
| Ferritin H-chain  | U58829   | GGATTGGCCNCCTAGAGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCT<br>TTTGGCCAAGCTTTACATGGCCTTGGGGACGTCAGCTTAGCTCTCATCACCCTGTCCAGGGTG<br>TGCTTTGCAAAGAGATATTCTGCCATGCCAGATTCAAGGGCTCCCATCTTGCCTAAGTTGGTCAC<br>GTGGTCACCCAGTCTTTAATGGATTTCACTGCTCATTCAAGTAATGCGTCTCAATGAAGTCAC<br>ATAAGTAGGGATCATTTCTGTGCTAGTCCAGTTTGTGAAGTCCAGTAGTGATTGATTCACACTC<br>TTTTCCAAGTGCAGTGCACACTCCATTGCATTCAAGCCGCTCTCCAGTCATCACGGTCAGTTT<br>CTTTATATTCTGCAGGAAGATTGCTCCACCTCGCTGTTCTGCAGTTTCTCAGTTTCTCAGCAT<br>GCTCCCTCTCTCATGAGATTGATGGAGAAAGTATTGGCAAAGTTCTTCAGGGCCACATCATCC<br>CGGTCAAATAACAAGACATGGACAGATAGACGTAGGAGGCATACAACCTCAGGTTGATCTGGCG<br>GTTGATGGCAGGATCCGCGATAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCC<br>GAGCTCGGTACCAAGCTTGAGCATAGCTTGAGTATTCTATAGTGTCACTAAATAGCTTGGCGTA<br>ATCATGGNCATAGCN |

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| Petuin beta (Petub)              | NM_053348 | TCTATGACATGATTACGAATTAAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGGTACCCAGTCTCAGGACAGCTGTTCACTCCAGGCCCTCCGACTCTGAGCCCCGTTGTCTTTTGCCAAAGGTTCACTGATTAAGTCCCGGGGTCCTCCTCAACGCTTTAAAAAGACTGTCACCTGTGTCGTGCGAGTTTTTCGAATCTCAGGACCAGGTCCCTGGAGGTGAGAACCCTGCTGATACCCAAGATGCTAAGAACTCCCTCAGAAAAACACAGCCCCCTACCAGCTCACCTCCATAACTGCACCAAGAGGATCTATCCAACACCTCCCTGAGCAGGAGGAGCCTGAAGACTCCAAGGGAAAGAGTCTTGAGGAACCCTTTCTGTGTCAGCTGGATCTAACCACAAACCCACAGGGTGACACACTGGATGTCTCTTCCCTCTACCTGGAGCCTGAGGAAAAGAACTGGTGGTCTGCCCTTTCCCTGGGAAGGAACAGCGCTCCCTGAGTGCCCGGGGCCGAAAAGCAAAGAACCCCTGATGCTCCCCGCTGAGACTCACTAGCAGGGTTCCACGGGGTACGGTCCCTGCAGTAGATGGGAGGTGGTGGGCATTGGGAANGCACAACAATCAAATGTAGACCGGCTAATAAAGTGTGT  |
| Fibrinogen gamma chain           | J00734    | GTATGCATCAAGCTNNGTACCGAGCTCGGATCCACTAGAACGGCCNGCCAGTGTGCTGGAATTCCGCCCTTCGCGGGATCCTTGGGCTGGGCAATGAGAAGATTCATCTGATAAGCATGCAGTCCACCATCCATACGCACTGAGAATACAGCTCAAAGACTGGAGTGGCAGGACCAGCACCGCGGACTATGCCATGTTTCAGGGTGGGTCTGAATCCGACAAATACCGCCTGACCTATGCTTACTTTCATTGGCGGAGATGCCGGGATGCCCTTCGACGGCTACGATTTTGGTGATGATCCAGTGACAAGTTTTTTCACATCCCAACGGCATGCACCTTCAGTACCTGGGACAATGACAACGACAAGTTCGAAGGCAACTGTGCTGAGCAGGATGGATCTGGCTGGTGGATGAACAAGTTCACGCTGGCCACCTCAATGGAGTTTATACCAAGGTGGCACTTACTCCAAGTCATCTACTCCTAACGGTTATGACAATGGCATTATTTGGGCCACCTGGAAAACCCGCTGGTATTTCATGAAGAAACCAACCATGAAGATAATTCCCTTCAACAGACTCTCCATGGAAAGCTTGGCCAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCACTTAGAGGGCCCAATTTCGCA  |
| Focal adhesion kinase (pp125FAK) | AF020777  | TTGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCGCCCTTATCGCGTCTAGATGCCCTTTGGGAGATCTTCTCTAGCATTCCACCAGCAGCGAGGAAGTAACCTTGTCTCGGTGCGCCGCACTCACAGCTCCAACGTATGACAGCTAGCTGAAAGTCTCTCTGTATATAAGTTTTAACTACTTATACATGGTTTGTATTCTGTTATTTTTCTAAATAGTGTTCAGAAAACTCTGGATCCAAAATGTGGCATTTTTCTGAGAATGAAGATGTACATTAAAGAGCTTTTAAATAATACTTGGTGTTCAAATTTGGGATGTATGTTCTTAGAAGTGGTAATTCATACTGACCATGACTTCGAATTGGAAGAGAAGTGTCTGAGGAGGGAGGGCTCCCAAGACACTGAGACTGGCTATCCTTCTTGCCAGAATTCCTGTCTCAGACTGAATTGCAATATGCTAATCTCATTTATAGAGAAAGTGCATAAAAGCTATATTTTGAAGAATGAGTGGTTTCAAAAGAAAACCTTCTGCCCTCCCTGTCAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGGACCAACTTGATGCATAACTTGGAGTATTCTATAAGTGNCCCTAAAATAGCTTGGCGTAATCN                                      |
| Gadd153                          | U36994    | GGGNTCCACTAGTANCGGCCNGCCAGTGTGCTGGAATTCGCCCTTATCGCGGATCCNTGAGTCTCTGCCCTTTCGCGTCTAGAGACTTTGGAGGAATTCCTCGGCCGAGAGCAGAAGATCGAAGGAGGTCTCTGCTCCTCAGATGAAATTTGGGGCACCTATATCTCATCCCAGGAAACGAAGAGGAAGAATCAAAAACCTTCACTACTCTTGACCCTGCATCCCTAGCTTGGCTGACTGAGGAGCCAGGGCCAGCAGAGGTCACAAGCACCTCCCAAAGCCCTCGCTCTCCAGATTCCAGTCAGAGTTCTATGGCTCAGGAGGAAGAAGAGGAAGATCAAGGAAGAAGTGAAGAACGGAACAGAGTGGTCAGTGCCGAGCCCGGGCTGGGAACACAGCGCATGAAGGAGAAGGAGCAGGAGAATGAGAGGAAGTGGCACAGCTTGCTGAAGAGAACGAGCGGCTCAAGCAGGAAATCGAGCGCCTGACCAGGGAGGTAGAGACCACAGCGCGGGCTCTGATCGACCGCATGGTCAGTCTGCACCAAGCATGAACGTGTGGCATCACCTCTGCTGTCTCTCCCGAGTGTACCCAGCACCATCACGCCAGTGCCAAGCATGTAATCTCCAGTGCACATGCTGAGGAGGAAGCTTGGCCAAAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCTTTAGGGGNCCTAATC |
| Gadd45                           | L32591    | TTNGGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCGCCCTTCGCGTCTAGAGACTTTGGAGGAATTCCTCGGCCGAGAGCAGAAGATCGAAAGGATGGACACGGTGGGCGATGCCCTGGAGGAAGTGCTCAGCAAGGCTCGGAGTCAGCGCACCATAACTGTGCGCGTGTACGAGGCAGCCAAGCTGCTCAACGTAGACCCGGACAACGTGGTCTGTGCCTGCTGGCTCGCGATGAAGATGACGACCGGGACGTGGCTCTGCAGATCCATTTACCCCTCATTCTGTGCTTTCTGTTGCGAGAACGACATCAACATCTTGGGGTCAGCAACCCGGGTGCGCTGGCAGAGCTGTTGCTACGAGAGAACGACAAGAGCCCGCTGAGAGCGGGGGCGCTGCGCAGACCCCGGACTTACACTGTGTGCTGGTGACGAACCCACATTTCATCAATGGAAGGATCCTGCCTTAAGTCAACTTATTTGTTTTGCGGGAAAGTCGCTACATGGATCAGTGGGTGCCAGTGATTAATCTCCCCGAACGGTGATCAAGCTTGGCCAAGGCGAATTNCAACACACTGCGGGCGGTACTATGGATCCAACCTCGGACCAACTTGATGCATACATT  |

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| Gamma-actin,<br>cytoplasmic              | X52815 | CTTTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCCGCGACGAGGGATTTGCCCTGGCAAATGTACACACCTCATGCTAGCCTCATGAACTGGAATA<br>AGCCTTTGAAAAGAAATTTGTCCTTGAAGCTTGTATCTGATATCAGCACTGGATCGTAGAATTTG<br>TTGCTGATTTTGGACCTTGTATTCAAGTTAACTGTTCCCTTGGTATTAAACCAACAGCAGACTTCC<br>AGGATTTCCCGAGGCTGGCAAGGGTTCCCTGAAGTGTACCCTTCTTTCTTGGCAGTCTAACA<br>GGGTGGGAAAGTCCGAGCCTTAGGACCCAGTTTCTGTTCTGGTTTTTCCCTCCTGACCTCCATG<br>GGTTGTTACTTGCCTTGAGTTGGGAACGTTTGCATCGACACCTGTAATGTATTATCCTTTTAA<br>TTTATGTAAGGTTTTTGTACTCAATTTTAAAGAAATGACAAATTTTGGTTTTCTACTGTTCACT<br>GAGAACATTAGGCCCCAGCAACAGTCACTTGTGTAAAGAGAAATAAAAGTGCTGCAGTAACNNCN<br>TAAAAANNCCANCNNAACNNANAAACCNATTGCGGCCGCAAGCTTATTCCTTTAGNGANGGGT<br>TAATTTTAGCTTTGGCNCCTGGCCGCCGTTTTCACACGTCNGNGACTGGNNAAAN |
| Gamma-glutamyl<br>transpeptidase         | M33821 | GATNANTTCAAGCTCGNCCAANTTCACCAACCAGTTTGGGGTAGCGCCCTCACCANCCAACCTTCA<br>TCAAGNCAGGTAAGCANCCGCTTTCATCCATGTGCCCTCAATCATCGTGGATAAGAACGGCAAG<br>GTTCCGGATGGTGGTTGGAGCCTCGGAAGGTACCCAGATCACCACGCTCTGTGCACTGGCCATCAT<br>CAACAGCCTGTGGTTTCGGGTATGATGTGAAGAGAGCTGTGGAGGAGCCCGCTTTCACAACCAGC<br>TTTTGGCCCAATACCACAACAGTAGAGAAAATATTGATCAGGTGGTGAAGTGCAGGTCTGAAGACT<br>CGGCACCACCATACAGAGGTCACACCCGACTTCATCGCTGTGGTTCAAGCTTGGCCA<br>AGGGCGAATTTGCAGATATCCATCACACTGGCGTGCCGCTCGAGCATGCATCTAGAGGGCCGCT<br>TCANAGGTAACAAA  |
| Glucose transporter<br>1                 | M13979 | TGCGAATTTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTC<br>GCCCTTATCGCGGGATCCTGGGCACCTTTCTTCAGTCAGCAATGAAGTCCAGAAGAATATTCAGG<br>ACTTTGATGGCTCCAGAATTTTAAAGCAAGACTGTTGCTCAGATCTATTAGATAAGCAG<br>CAGATTTTATAATTTTATTACTGATTTTGTATTATTTTATTTTATCAGCCACTCTCCT<br>ATCTCCACACTGTAGTCTTACCTTGATTGGCTTAGTGCCCTGAGGGTGGAGACCACGCCCTGTCC<br>AGACACATGCCTTCTTGCCTAAGCTAATCTGTAGGGCTGGACCTTTGGCCAAGGACACACTAATA<br>CTGAACAATGAGCTAGGAGGCTTTACCGCAGGAGGCGGTAGCTGCCACCCACTTCTGCAGCCCTG<br>GATCTCGACACCATAGGGGTCCAGGCTCCATTTAGGATTCGCCATTCTGTCTCTTCAACTCA<br>ACCAACCACTCGATTAATCTTCTTGCCTGAGACCAGTTGAAAGCACTGGAGTGCAGGGAGGAG<br>AGAAGCTTGGCCAAGGGCGAATTCAGCACACTGGCGGGCGGTACTAGTGGATCCGAGCTCGGA<br>CCAAACTTTGAGCATAACTTGAGTATTCTN                                     |
| Glucose-6-<br>phosphate<br>dehydrogenase | X07467 | GCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTGGCG<br>GGATCCTGGCATGTTCTTCAACCCCTGAGGAGTCTGAGCTGGACCTAACCTATGGCAACAGATACA<br>AGAATGTGAAGCTCCCTGATGCCTATGAACGCCCTCATCTGGATGTCTTCTGTGGGAGCCAAATG<br>CACTTTTGTCCGTAGTGATGAATCAGGGAAGCCTGGCGTATCTTACACCAATTGCTGCACAAGAT<br>TGATCGAGAGAAGCCCCAGCCATCCCGTATGTCTATGGCAGCCGAGGTCCACAGAGGCAGATG<br>AGCTGATGAAGAGAGTGGGCTTCCAGTATGAGGGAAGCTTGGCCAAGGGCGAATTCAGCACACT<br>GGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAATTTATATAG<br>TGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCT<br>CACAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCTAATGAGTGA<br>GCTAACTCACATTAATTGCGTTGCGCTCACTGGCCGCTTTCAGTCCGGAAACCTGCGTGCCN   |
| Glucose-regulated<br>protein 78          | M14050 | GAATNGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCC<br>TTNGCGGGANCCCTGACTGGAATCCCTCCTGCTNCCCGTGGGGTACCCANATTGNANNCACCTT<br>NGANATACATGTGAATGGNATTCNTNGAGTGGCANNTGAAGACANAGGGACAGGNAACANNACN<br>NANTCACCATCACCAATGACCAAAACCGCCTGACCCCTGAANAAATGAAAGGATGGTCAGTGAC<br>GCCGANAANTNNGCTGAGGANGACNAAANGCTCANAGAGCGCATNGACACGANGAATGAATTGGA<br>AAGCTATGCTTACTCTCTTAAAGAACANATCCGGANATNAAGAGANGCTGGGAGGTAAGCTGNCT<br>NCTGAANATAANNAGACCATGGAGAAAGCTGTAGAGGAAAGATCGAATGGCTGAAAGGCCACCA<br>GGATGCAGACATTGAACACTNTAAAGCTNNNAAGATNGAAGTACACANANATTGTTTANCCAATTA<br>TGAGCAAACCTTATNGAAGTGGACGCCCTCCCCAACTGGGGANGAAGAAGCTTGGCCCGAGGCG<br>AATTCATCACACTGGCNGGCGGTACTATTGGATCGATCTCGNTCCAACCTGANGCATAGCTTGA<br>GTNTTCTATNTG  |



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| Glutathione S-transferase Yb2 subunit    | M13590    | TTNCGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGCCAGCAGATGCCTATGACACTGGGTTACTGGGACATCCGTGGGCTGGCTCACGC<br>CATTCGCCTGTTCTTGGAGTATACAGACACAAGCTATGAGGACAAGAAGTTCAAACCTGGGCTGG<br>ACTTCCCCAATCTGCCCCACTTAATTGATGGGTCACACAAGATCACCCAGAGCAATGCCATCCCTG<br>CGCTACCTTGGCCGGAAGCACAACCTTTGTGGGGAGACAGAGGAGGAGGATTCGTGTGGACGT<br>TTTGGAGAACCAGGCTATGGACACCCGCCCTACAGTTGGCCATGGTCTGCTACAGCCCTGACTTTG<br>AGAGAAAAGAAGCCAGAGTACTTAGAGGGTCTCCCTGAGAAGATGAAGCTTTACTCCGAATTCCTG<br>GGCAAGCAGCCATGGTTTGCAGGGAACAAGATTACGTATGTGGATTTCTTGGTTACGATGCCCT<br>TGATCAACACCGTATATTTGAACCAAGTGCCCTGGACGCCCTTCCAAACCTGAAGGACTTCGTGG<br>CTCGGTTTGAAGGCCCTGAAAAAGATATCTGACTACATGGAAGACGGGCCGCAAGCTTATTTCTCT<br>TTAGTGAGGGGTTAATTTTAGCTTNGCACTGGGCCGCCGTTTACAACGTCGTG |
| Glyceraldehyde 3-phosphate dehydrogenase | M17701    | AATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCT<br>TCGCCGGGATCCATCTGCACCACCAACTGCTTAGCCCCCTGGCCAAGGTCATCCATGACAACCTT<br>TGGCATCGTGGAAAGGCTCATGACCACAGTCCATGCCATCACTGCCACTCAGAAGACTTGGGATG<br>GCCCTCTGGAAAGCTGTGGCGTGATGGCCGTGGGGCAGCCAGAATCATCCTGCATCCACT<br>GGTGCTGCCAAGGCTGTGGCAAGGTCATCCAGAGCTGAACGGGAAGCTCACTGGCATGCCCTT<br>CCGTGTTCTTACCCCAATGTATCCGTTGTGGATCTGACATGCCGCTGGAGAAACCTGCCAAGT<br>ATGATGACATCAAGAAGGTGGTGAAGCAGGCGGCCGAGGGGCCACTAAAGGGCATCCTGGGCTAC<br>ACTGAGGACCAGGTTGTCTCTGTGACTTCAACAGCAACTCCATTCTTCCACCTTTGATGCTGG<br>GGCTGGCATTTGCTCTCAATGACAACCTTTGTGAAGCTCATTTCTTGGTATGAAAAGCTTGGCCAAN<br>GGCGAATTCAGCACACTGGCGGGCGGTACTAGTGGATCCGAACCTCGGTCCAAACTTGATGCATA<br>GCTTGAGT   |
| Glycine methyltransferase                | NM_017084 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACGAGGCAGCCTTTGACAAGTGGGTCAATTGAAGAAGCCAACCTGGTTGACTCTGGACAAAGAT<br>GTGCCAGCAGGAGATGGCTTTGACGCTGTCTATCTGCCTTGGGAACAGTTTGTCTCACTTGGCGGA<br>CAGCAAAAGGTGACCAGAGTGAGCACCAGGCTGGCGCTAAAGAATCATCGCAAGCATGGTGGCGCCG<br>GGGGCCTGCTGGTCTATCGACCACCGCAACTACGACTACATCCTCAGCACGGGCTGTGCACCCCA<br>AGGAAGAATCATCTACTATAAGAGTGACCTGACCAGGACATTTACGACGTCACTGCTGACAGTAAA<br>CAACAAAGCTCACATGGTAACCTTGGACTACACAGTGCAGGTGCCAGGTGCTGGCAGAGATGGCG<br>CTCCTGGCTTCAGTAAGTTTCGGCTCTCTTACTACCCACACTGTTTGGCGTCTTTACGGAGTTG<br>GTCCAAGAAGCCTTTGGGGCAGGTGGCCAGCACAGCTCCTGGGTGACTTCAAGCCTTACAGGCC<br>CGGCCAGGCTACGTTCCCTGCTACTTCACTCACGCTGCTCAAGAAACAGGCTGANCTTGGCTNC<br>NGCTTCCACCTAANAACATCCCTACCACAGATATTGCAGANAT        |
| Heme binding protein 23                  | D30035    | CATTGAAACGGNNNCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT<br>CGCCCTTCGCGGGATCCCAAAGCCACGGCTGTTATGCCCGATGGACAATNCAAAGATATCAGCCT<br>AAGTGATTACAAAGGAAATATGTTGTTATTTTACCCTCTTGACTTTACTTTTGTGTGTC<br>CCACGGAGATCATTGCTTTCAGTGATAGAGCNGAANAATTTAAGAACTCAACTGCCAAGTGATT<br>GGAGCTTCTGTGGATNNCTACTTCTGTCATCTGGCATGGATTAACACACCCCAANAACAAGGAG<br>ATTGGNACCATGAACATTCCTTGGTATCAGATCCCAAGCGCACCATTGCTCANGATTATGGAG<br>TCTTAAAAGCTGATGAAGGTATCNTCTTTCANGGGCTNTTTATTATTGATGATAAAGGTATCCT<br>TCNCANATTAACCGATAATGATCTTTCTGTTGGG  |
| Heme oxygenase                           | NM_012580 | TTNTGACATGATTTCGAATNNAANACCGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGACCCGCTACCTGGGTGACCTCTCAGGGGGTCAGGTCTTGAAGAAGATTGCGCAGA<br>AGGCCATGGCCTTGCCAAGCTCTGGGGAAGGCTGGCTTTTTTACCTTCCCGAGCATCGACAAC<br>CCCACCAAGTTCAAACAGCTCTATCGTGTCTGCATGAACACTCTGGAGATGACCCCGAGGTCAA<br>GCACAGGGTGACAGAAGAGGCTAAGACCGCTTCTGCTCAACATTGAGCTGTTTGGAGAGCTGC<br>AGGCACTGCTGACAGAGGAACACAAGACCAGAGTCCCTCTGCAGAGACGCCCGAGGAAAATCC<br>CAGATCAGCACTAGTTTATCCAGACACCGCTCCTGCGATGGGTCTCACACTCAGTTTCTCTGTT<br>GGCGACCGTGGCAGTGGGAATTTATGCCATGTAAATGCAGTGTGGCCCCCAGAGGCTGTGAAC<br>CTGTCTCATGTAGCCTTCTCTCTCAGGGGAGAATCTTGCTTGGCTCTCTTTTCTTGGGCTCTA<br>AGAAAGCTTTTGGGGTTCTCGCCCCCTTCTGTGTCNTTCTTCTTCTTGGAAATGGGAAGG<br>AGATGCCTGGCACATTTCT   |
| Hemoglobin alpha 1 chain                 | NM_013096 | GNNNCTATNTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGC<br>CAAGAATTCGGCACGAGGCAGGAAGCAATCATGGTGTCTCTGCAGCTGACAAAACCAACATCAA<br>GAACCTGCTGGGGGAAGATTGTTGGCCATGGTGGTGAATATGGCGAGGAGGCCCTACAGAGGATGT<br>TCGCTGCCTTCCCCACCACCAAGACCTACTTCTCTCATATTGATGTAAGCCCCGGCTCTGCCAG<br>GTCAAGGCTCACGGCAAGAAGGTGTGTGATGCCCTGGCCAAAGCTGCAGACCACGTCGAAGACCT<br>GCCTGGTGGCTGTCCACTCTGAGCGACCTGCATGCCACAACTGCGTGTGGATCCTGTCAACT<br>TCAAGTTCTCTGAGCCACTGCCTGTGCTGACCTTGGCTTGGCCACCACCTGGGGATTTTACACCT<br>GCCATGCACGCCCTCTCTGGACAAATTCCTTGCTCTGTGAGCACCGTGTGACCTCCAAGTACCG<br>TTAAGCCACCTCTGTGGGCTTGCCTTCTGACCAGGCCCTTCTTCCGTCCCTGAACCAAGTCTT<br>TGAATAAAGCAGAAGTAGGAAAGAAAAAATAAAAAAAAAAAAAAAAAAATCTCGCG  |



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| Hemoglobin alpha 1 chain (alternate clone)      | NM_013096 | CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGGACTCAGGAAGCAATCATGGTGCCTCTGTCAGATGACAAAACCAACATCAAGAAC<br>TGCTGGGGGAAGATTGGTGGCCATGGTGGTGAATATGGCGAGGAGGCCCTACAGAGGATGTTCCG<br>TGCCTTCCCCACCACCAAGACCTACTTCTCTCACATTGATGTAAGCCCCGGCTCTGCCCAGGTCA<br>AGGCTCACGGCAAGAAGGTTGCTGATGCCTTGGCCAAAGCTGCAGACCACGTCGAAGACCTGCCT<br>GGTGCCTGTCCACTCTGAGCGACCTGCATGCCACAAACTGCGTGTGGATCCTGTCAACTTCAA<br>GTTCTTGAGCCACTGCCTGCTGGTGAACCTTGGCTTGCCACCACCCTGGAGATTTACACCCGCCA<br>TGCACGCCTCTCTGGACAAATTCCTTGCCCTCTGTGAGCACTGTGCTGACCTCCAAGTACCGTTAA<br>GCCGCCCTCTGCCGGGCTTGCCCTTCTGACCAGGCCCTTCTTCCCTCCCTTGACCTTATACCTCTT<br>GGTCTTTGAATAAAGCCTGAGTAGGAAGCAAAAAAAAAAAAAAAAAAAAAA   |
| Hepatocyte growth factor receptor               | X96786    | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCG<br>CCCTTATCGCGGGATCCCTTCAAGTACTAAGGGCATGAAATATCTTGCCAGCAAAAAGTTTGTCC<br>ACAGAGACTTAGCTGCAAGAACTGCATGTTGGATGAAAAATCACTGNCAAGGGTGTGATTTC<br>GGTCTTGCCAGAGACATGTACGACAAAGAGTATTATAGCGTCCCAACAAAACGGGTGCGAAACT<br>ACCGGTGAAGTGGATGGCTTTGGAGAGTCTGCAGACGCAAAAGTTCACCACCAAGTCAGACGTGT<br>GGTCTTCCGGTGTGCTTCTCTGGGAGCTCATGACGAGAGGAGCCCTCCTTATCTCTGACGTGAAC<br>ACATTTGATATCACTATATACCTGTTGCAAGGCAGAAGACTCTTGCAACCAGAGTACTGTCCAGA<br>CGCCTTGTATGAAGTGTGCTAAAATGCTGGCACCCCAAGCAGAAATGCGCCCATCGTTTCTG<br>AACTGGTCTCCAGGATATCCTCAATCTTCTCCACTTTCATTGGCGAGCACTATGTCAAGCTTGGC<br>CAAAAAGGGCAATTCCAGCACACTGGCGGGGCTACTAGTGGATCCGAGCTCCGG  |
| Hepatocyte nuclear factor 4                     | D10554    | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCCG<br>CCCTTATCGCGGGATCCCTGCGGTACAGGTGCAGGTGAGCCTGGAGGATTACATCAACGACCGC<br>CAGTATGACTCTCGGGTCTGTTTGGAGAGCTGCTGCTGCTCTGCCACTCTGCAGAGCATTAC<br>CTGGCAGATGATCGAGCAGATCCAGTTCATCAAGCTCTTTGGCATGGCCAAAGATTGACAACCTGC<br>TGCAGGAGATGCTGCTTGGAGGGTCTGCCAGTGACGCGCCCCACGCCCACCACCCCTGCACCCCT<br>CACCTGATGCAAGAACACATGGGCACCAATGTCTAGTTGCCAACACGATGCCCTCTCACCTCAG<br>CAATGGACAGATGTCCACCCTGAGACTCCACAGCCATCACCAAGTGGCTCTGGATCTGAAT<br>CCTACAAGCTCCTGCCAGGAGCCATACCACCATCGTCAAGCCTCCCTCTGCCATCCCCAGCCA<br>ACGATCAAGCTTGGCCAAAGGGCGAATTCAGCACACTGGCGGGCGTTACTAGTGGATCCGAGCT<br>CGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTGCACCTAAATAGCTTGGCGTAATCA<br>TGGCATAGCTGGTTCCTGTGTAATTTGATATCCGCTACA |
| Histidine-rich glycoprotein                     | AF194029  | CACCTTCATGGNCAGCATCCCCATGGACACACCCCATGGTCAACCATCCTCATGGTGACCATCC<br>CCATGGACACACCCCATGGACATGATTTCCTTGACTATGGACCTTGTGACCCACCTCCAATA<br>GCCAAGAACTCAAGGGTCAAGTATCATCGGGACATGGTCCACCACACGGACACTCAAGGAAAAG<br>AGGGCCAGGTAAAGGACTCTTCTCTTNCACCAACGACAAATCGGATATGTCTACCGACTCCCTC<br>CACTGAATGTAGGTGAAGTTCTCACTCTCCTCTGAAGCAATTTGCCATCTTCTCTTTGCAAAAT<br>GCAACAGACCCCAACAACAGAGATTTCNGCCCTTCCCTCANACAGCCTNAAAGTCTGTNCAGGG<br>AAATTTGAGGGTAAAGTTTCCACAAGTTCCAACCTTTTTTTGAACATACGCCTNCCAAAATAAAACC<br>TGATTTCTTGGTAGGGGAAAGAGTCAATATCTGAATAAATAAAATATGACCAGGTAGAAATGAN<br>AAANGGGGGGNGANANNTAGNGGGGNGGGGGGGGGGGNTTTTTTTTTTT   |
| HMG CoA reductase                               | X5286     | GGGGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTC<br>GCCCTTCCGGGATCCTGGTTTGTGAAGCTGTCAATCCAGCCAAGGTGGTGGAGAGATATTAA<br>GACGACTACGGAAGCTATGGTTGACGTAAACATTAACAAGAATCTTGTGGGCTCTGCCATGGCTG<br>GTAGCATAGGAGGCTACAACGCCCATGTGCGCAACATCGTCACTGCCATCTACATTGCATGTGGC<br>CAGGATGCAGCAGAAATGTGGGGAGTTCAAACCTGTATTACGTTAATGGAAGCAAGTGGTCCCAC<br>AAATGAAAGCTTATACATCAGCTGTACCATGCCGTCTATAGAGATCGGAACCGTGGTGGTGGGA<br>CCAACCTTCTACCTCAGCAAGCCTGCCCTGCAGATGCTAGGTGTTCAAGGGGCGTGCAAGACAAT<br>CCTGGAGAAAATGCACGGCAGCTTGCCCGAATGTGTGTGGCACTGTGATGGCTGGTGAAGTGTG<br>CTTGATGGCAGCATTGGCAGCAGGACATCTTGTGAGAAGTCACATGGTTCACAAAGCTTGGCCAA<br>GGCGGAATTCAGCACACTGGCGGCCGNTCTAGTGGATCCGAGCTCGGACCAACTTGATGCATAC<br>TT                                 |
| Hypoxanthine-guanine phosphoribosyltransf erase | X62085    | GAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCC<br>CTTCGCGGGATCCTGCTGAAGATTGGAAAAGGTGTTTATCTCATGGACTGATTATGGACAGG<br>ACTGAAAGACTTGCTCGAGATGTCATGAAGGAGATGGGAGGCCATCACATTGTGGCCCTCTGTGT<br>GCTGAAGGGGGCTATAAGTTCTTTGCTGACCTGCTGGATTACATTAAAGCGCTGAATAGAAAATA<br>GTGATAGGTCCATTCTATGACTGTAGATTTTATCAGACTGAAGAGCTACTGTAATGACCAAGTCA<br>ACGGGGGACATAAAAGTTATTGGTGGAGATGATCTCTCACTTTAACTGGAAAGAAGCTCTTGAT<br>CGTTGAAGATATAATTGACACTGGTAAAACAATGCAGATTTTGCTTTCCTTGGTCAAGCAGTACA<br>GCCCCAAAATGGTTAAGGTTGCAAGCTTGTGTTGTTGAAAGGACCTCTCGAAAGTGTGGATACAG<br>GCCAGACTTTGTTGGATTTGAAATTCAGACAAGTTTGTGTTGGATATGCCCTTGACGAGGCC<br>AAGGGCGAATTCAGACACTGGCGGNCGTACTAGTGGATCCGAGCTCGGACCAAGCTTGATGCAT<br>ACTT                                 |

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| Hypoxia-inducible factor 1 alpha             | AF057308  | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCGCCCTTATGCCAGATCACAGCACATTCACAGCTCCCCAGCATTTACCAATGCATTGCTGTAGTGTGCTTTAAATGCACCTTTTATTTATTTTGGTGAGGGAGTTTGCCCTTATTGAATTATTTTTAATGAAATGCCAATATAATTTTTTAAGAAGGCAGTAAATCTTCATCATGATGATAGGCAGTTGAAAATTTTTTACTCATTTTTTTCATGTTTTACATGAAAATAATGCTTGCCAGCAGTACATGGTAGTCACAATTGCACAATATATTTCTTAAATAACCAGCAGTTACTCATGCATATATTTCTGCATTATGAAACTAGTTTTTAAGAAGAACTTTTTTGGCCTATGGAATTGTTAAGCCTGGATCATGATGCTGTGTATCTTATAATGATTTAAACTGTATGGTTTCTTTATATGGGTAAAGCCATTTACATGATATAGAGAGATATGCTTATATCTGGAAGGTATATGGCATTATTTGGATAAAATTCTCAATTGAAGATTATCTGGTGTCTTTTACTTTACCGGCTCAAAGAAAACAGTCCCTATGAAGGGCGAATTCCAGCACACTGCCGG   |
| ID-1   | D10862    | GGATTTCGCCCTTATCGNNGGATCCAAAGCGTTGCCATCTCGCGCTTGCGCTTGGNACGNCGCCTGCCCCCTTGGCTGGGACGAACAGGCAGGTGAACGTTCTGCTCTACGACATGAACGGCTGCTACTCACGCCTCAAGGAGCTGGTGCCCTACCCTGCCTCAGAACCAGCAAGTGAGCAAGGTGGAGATACAGCAGCATGTTATCGACTACATCAGGACCTGCAGCTGGAGCTGAAGTCTGAGTCTGAAGTCGCGACCGCGGAGGCCGGGGCTGCCCGTCCGGCCCCGCTCAGCACCTTGAACGGCGAGATCAGTGCCTTGGCGGCCGAGGCGGCATGTGTCCAGCCGACGACCGCATCTGTGTGCTGAGGCGGCGCACTGAGGAACCAGATGGACTCCAGCCCTTCAGGAGGCAAGAGGAAAAAAGTGCTCTCGGTTCCCCAGAGCAACCCGGGAAAGACACTACCGCGGCCACGGGACTCTTGACGGATCTGTCCAGGGGGTAGAGGGTTGTATCAACGGAGTCTCGCCCTCTCCAAGCTTGGCCAAAGGCGAATTCTGCAGATATCCATCACTTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCNGTTTTCCAA   |
| IgE binding protein                          | NM_031832 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGGGAGCACTAACCAGGAAAATGGCAGACGGCTTCTCGCTTAATGATGCCCTTAGCTGGCTCCGGAAACCCAAACCTCAAGGATGGCCTGGTGCATGGGGGAACAGCCTGGGGCAGGAGGCTACCCAGGGGCTCCTATCCTGGGGCTACCCAGGACAGGCTCCTCCAGGGGGTTATCCTGGACAGGCTCCTCTAGTGCCATATCCGGGCCCAACTGGCCCTAGTGCTTATCCTGGCCCAACTGCCCTTGGAGCTTATCCTGGGCCAACTGCCCCCGAGCCTTCCAGGGCAACCTGGGGGACTGGAGCCTTACCCTAGTGCTCCTGGGGCTATCCTGCTATGGGCCCTATGGTGGCCCGACTGGACCACTGACAGTGCCCTACGATATGCCCCTGGCTGGAGGAGTCATGCCCTCGCATGCTGATCACAATCATGGGCACAGTGAAGCCCAACGCAACAGTATCACTCTGAATTTCAAGAGAGGGAACGACATCGCCTTCCACTTTAACCCCGCTTCAATGAGAACAACAGAAGAGTCATCCGTGTGCAACACGAAGCAGGACAATTAAGTGGGGAANGGAAAAAAGACAG  |
| Inositol polyphosphate multikinase (Ipk)     | AY014898  | NCNNNCGACTCCCANNTCTTATATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAATTCGGCACGAGGGAACGACTATAGCTCATTTCTCTCTCCCATTTGTGGGAGTGAGTTTCAAGTGATAATTAAGTAAACCTTTTCAAGTTTACCTTTTCTTCTTACAAATATTGACTTGTACCTGGGTGTGATTACAGGAACCTCAGGCTCATCTGGTGAACACTATTTTGAACTCTTAAGAGGCAGTTTGAGATGGTATCAACTTATATACAAGGAATTCNGAACTCGAGCTCTGGGCACACACAGCTCAGGAAAGTCTTTGCTCTACCGCTGTTTTAAACATTTCAGAAGCCAGCATCCTGCCTCCGACCACTANGNTTGTCTGAATAAAACAGGAAGTGATTCTTATCCTTGGTTCTCAGGGAAGGGATTAGCATTAGTTCTTCTTGTATTACATTTTTACTAACTGCTGCCCTCTTTGTGNTACTTTGTGCTCTTTGTGACATGATCAACTCINTATTGTGATGNAAGCAACCTGNGGGCANGCGTTTCAGGTCTGCCCTGTCTTTTAAATGATACTGAGATTTNCCNCTTTGGGTNGAAAGAGGCCATGTGTNCCCTAGCCCNAGCCNAATGTGGAACCAACNCCGANAATTTAAAGAAAATAAANNCAAATGNAGGCNGGTTN |
| Insulin-like growth factor binding protein 1 | M89791    | TTGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTTCGCCCTTCGCGGGATCCGGAGCCTCGACCTCTGCATGCCCTACCCGTTGGCCAGGGAGCCTGTGTACTAGAACCCTCCGCAACCCGCCACGAGCAGCTTGTCCGTTCTCAGCATGAAGAGGCAAAGGCTGCTGTGGCCTCTGAGGATGAGCTTGCCGAGAGCCAGAGATGACAGAGGAACAGCTGCTGGATAGCTTCCACCTCATGGCCCCATCCCGTGAGGACAGCCCATCCTGTGGAATGCCATTAGCACCTACAGCAGCATGCGGGCCCGGAGATCACTGACCTCAAGAAATGGAAGGAGCCCTGCCAACGGGAACCTATATAAAGTGTAGAGAGATTAGCTGCCGCTCAACAGAAAGCAGGAGATGAGATCTACAAATTTTATCTGCCAAACTGCAACAAGATGGATTTTATCACAGCAACAGTGCGAGACATCTCTGGATGGAGAAAGTGGGCTCTGCTGGTGTGTCTACCCATGGAGTGGGAAGAAGATCCTTGGATCAAGCTTGGCCAAGGGCGAATTCAGCACACTGGCGGCCGTACTAGTGGATCCGAGCTCGGTACCAACTTGATGATATAGCTTGAGTATTTCTATAGTGNACCTAAATAGCTTGG                             |

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| Insulin-like growth factor binding protein 3           | M33300    | TGCGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCGCCCTTCGCGGGATCCCTGAAGGCGCTGCTGAATGGCCGCGGGTTCTGCGCCAACGCCAGCGCCGCAGCAACCTGAGTGCTTACCTCCCCCTCCAGCCGCTCTCCTGGAAACACCAGTGAAGTCTGAGGAGGACCACAAATGCTGGGAGTGTGGAAAGCCAGGTTGTCCCGAGCACACATCGCGTGAAGTCTCAAGTTCCATCCACTCCATTCAAAGATGGAGGTATCATATAAAGGCCAGGCTAGGGACAGCCAGCGCTACAAAGTTGACTATGAGTCCCAGAGCACAGACACCAGAACTTCTCCTCCGAGTCTAAGCGGGAGACAGAATATGGTCCCTGCCGAGAGAAATGGAGGACACACTGAATCATCTGAAGTCTCCTCAATGTGCTGAGTCCCAGGGCGTCCACATCCCAAACTGTGACAAGAAGGGGTTCTATAAGAAGAAACAGTGTGCGCCCTTCCAAAGGCAGAAAGCGGGCTTCTGCTGGTGGTGGACAAGTACGGGCAGCCATTGAAGCTTGGCCAAGGCGAATTCAGACACTTGGCGGCCGTTCTAGTGGATCCGACTCGGTACCCAACTTGATGCATAGCTTGAGTATTCTATATGTCACCTAA      |
| Integrin beta1   | U12309    | TTGTGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCGCCCTTCGCGGATCCGCTTGTAAAGTGCACAGATCCCAAGTTCGAAGGGCCAACCTGTGAGACCTGTGAGACCTGCGCTTGGTGTCTGTGTCAGAGCATAAAGAAATGTGTTCAGTGCAGAGCCTTCAATAAAGGAGAAAAAAGACACGTGTACACAGGAGTGTCTCCATTTCACCTCACTAAAGTGGAAAGCAGGGAGAAGTTGCCCCAGCCTGTGTCAGGTGGACCTGTGACCCACTGCAAGGAGAAGGACATTGATGACTGCTGGTTCTATTTCACCTACTCAGTGAACAGCAACGGTGAAGCTACGTGCATGTTGTGGAGACTCCAGACTGTCTACTGGTCCGACATCATCCAAATGTAGCAGGCGTGGTGGCGGAATTGTTCTTATTGGCCCTTGCCTCGCTGCTGATTGGAACTTTTAAATGATAATTCATGACAGGAGGGAATTTGCTAAATTTGAAAGGAGAAAAATGAATGCCAAGTGAACACGGGTGAAATCCTAAGCTTGACCAAGGCGAATTCACACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAACTTTGATGCATCTTGAGTATTCTATANTGTACCTAAATAGCTTGGCGTAATCN |
| Integrin beta-4  | U60096    | NCCCTCTTTGAAAANCNTTCGTATACATCCATGCTCNAGCGGAACGACAGTGNGATGGATATCTGCAGAATTNTNCTTATCGCGGGATCCCGGTTCTTGGCCTCAGTGAGAACGTTCTTACAAGNTNAAGGTGCATGCCCGGACAAACAGNAGGGCTNTGNACCCANCGTNAGGGTATCATCNCCATCGANTNTCATGATGGAGNCCCTTNCACAGATNG   |
| Interferon related developmental regulator IFRD1 (PC4) | NM_019242 | AACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGGTGTATGATGTAAACATGAGAATTGCTGCTGGCGAATCTTTGGCACCTCTGTTTGAATTGGCAGAGGAATGGAGAGTGAACGGGATTTTCCAACAGAACTGTAAATTCGGTCTGAGCGCATGTATATTGATAGCTGGGTCAAAAAGCACACCTATGACACGTTAAAGAGGCTCTTGGATCAGGATGTCAGTACCCTTGCAGACAAATGAATTCCTTCGCAATGTATTGAGCTGGGACCCCTGTGATGCTCGATGCTGCAACACTTAAAACCATGAAGATTCCTGTTTGAAGGCATTTATATAACTCTGAGCTTTCAAAGCTCGAACAAAAGCCGGAAGCAATGCCGAGATAAGAGAGCAGATGTTGGAGAATCTCTTAGATGTCTGACTTTGATGTCTGTTTCTAATTTCTCTCTTATTATTATTATTGCTACTTCTAATGTATATAAGCTTTTAGAGACTTTTATCTTGGTCAACTTAGATAATTTTGTATGTANGGATGGGTATATTTAATTTAATGNACAGTGGTACAAATTAATGAGTTCTTTATCTGTAAAAATACTGATNACCACAAATNAAAGTGGTGTGGATGC                          |
| Interleukin-1 beta                                     | M98820    | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCGCCCTTATCGCGGGATCCGAGGGCTGCCTTCAGTCAAGTACCACCTGCTGCCCCGACCAAGGGTTTCAACAAGATAGAAGTCAAGACCAAGTGGAGTTTGAAGTCTGCACAGTTCCCCAACTGGTACATCAGCACCTCTCAAGCAGAGCACAGACCTGTCTTCTAGGAAACAGCAATGGTCGGGACATAGTTGACTTCACCATGGAAACCCGTGTCTTCTAAAGATGGCTGCACTATTCTAATGCCTTCCCCAGGACATGCTAGGGAGCCCCCTTGTGCGAGAATGAGCAGTCTCCAGGGGAAGCCTTTGTCTCTGCCAAGTCAAGTCTCTCAGAGCCATAAGAAAACCGTGGCAGATTCTGGTCAAAGAAAACGTGTGTTTCCCTCCCTGCTCTGACAGGCAACCCTTACCTATTATTATTATGATTTATTGATTGGTTGATCTATTAAAGTTGATTCAAGGGGGTACAGAGGCAGCATTTGTCAGACAGAAGAATCTAGTTGTCCGTGTGTATGGGATGAAAAGCTTGGCCCAAANGGCGAATTNACGCCACTGGCGGCCGTTCTAGTGGATCCGACTCGGTCCAAG                                   |
| Interleukin-10   | L02926    | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCGCCCTTATCGCGGGATCCGAGGGCTGCCTTCAGTCAAGTACCACCTGCTGCCCCGACCAAGGGTTTACCACTGCAGTCCAGTGCCTCCGGGGACGGTTGCAGCTATCTACGACGTGACTCTGAACCTTCAAGAGGGAACAAGAACCCTATCTCTCTGGGGATCCTGTATGAAAGAAGTATGAGGCAGACATGTGTGTGAGGAGGTTCCCCCTGGAAGATATCCAGCAGACGAGACCGCGCGGCCAGTGGCTTCACAAGCTGTACCAGGAGAAGGATGCCCTGCAAGAGATGTACAAGCAGAGCGGCGGCTTTTCCCCGGGGAGCAGATCAAGCCTGCGCGGAGGCGGTGACTCTTCTCAACTTCTGTGCTGGGCCACATTCCTCTCTCTCCCCCTTTCAGCTTCTGCTCTGGCGTCTTTGCCAGTGGATCCCCCTCTCTCATCTGACGTCTTGGGGTTTGTGGGAGCAACTCCTTGGAAAACAAGCTTGGCCAAAAGGGCGAATTCACACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTGATGCATAGCTTGAGTATTCTATAGTGCACCTAAATAGCTTGGCGTAATCATGGCATACTGGTTCT      |

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| Interleukin-18                                     | AJ222813  | <p>GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTG<br/> CCCTTATCGCGGGATCCTGGCTGCAATACCAGAAGAAGGCTCTTGTGTCAACTTCAAAGAAATGG<br/> TGTATTATTGACAACACACTTTACCTTATACCTGAAGATAATGGAGACTTGAATCAGACCACTTT<br/> GGCAGACTTCACTGTACAACCGCAGTAATGCGGAGCATAAATGACCAAGTTCTCTTCGTTGACAA<br/> AAGAAACCCGCCCTGTGTTTCGAGGACATGCCTGATATCGACCGAACAGCCAACGAATCCAGACCA<br/> GACTGATAATATATATGTACAAAGATAGTGAAGTAAGAGGACTGGCTGTGACCTATCTGTGAAG<br/> GATGGAAGGATGTCTACCTCTCCTGTAAAAACAAAATCATTTCCTTTGAGGAAATGAATCCACC<br/> TGAAAATATTGATGATATAAAAAGTGATCTCATATTCTTTCAGAAACGTGTGCCAGGACACAACA<br/> AAATGGAATTTGAATCTTCCCTGTATGAAGGACACTTTCTAGCTTGCCAAAGGAAGATGATGCT<br/> AAGCTTGCCCAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGACCA<br/> AGCTTGATGCATAGCTTGAGTATTCTATAGTGACCTAAATAGCTTGG</p>       |
| Intracellular<br>calcium-binding<br>protein (MRP8) | L18891    | <p>TATGAATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTG<br/> GCACGAGGCTGGTATAAAAGGGAATCACCATGCCCTCTACAGGATGACTTCAGGAAAATGGTCA<br/> CTACTGAGTGCCCTCAGTTTGTGTCAGATAAAATACCGAAAGCTTGTTCAAAGAATTGGACGTC<br/> AATAGTGACAACGCAATTAACCTTCGAAGAGTTCTTGTGTTGGTGATAAGGGTGGCGCTGGCAGC<br/> TCATAAAGACAGCCACAAGGAGTAACAGAGCTTCTGGCCTGGGCTGGGCCCTTGGATATGTCTA<br/> CAGAATAAAGTCGTATATCTTANGAAAAAATAAAAAAAAAAAAAAAAAAACATTGCGGCC<br/> GCAAGCTTATTCCCTTTAGTGAGGGTTAATTTTAGCTTGGCACTGGCCGTCGTTTACAACGTCG<br/> TGACTGGGAAAACCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTCGCGAGCT<br/> GGCGTAATAGCNAAGAGGCCCGACCGATCGCCCTTCCCAACAGTTGCGCAGCTGAATGGCGAA<br/> TGGGACNCNCCTGTAGCGCGCATTAACGCGCGCGGGTGTGGTGGTTACGCCAGCGTGACCGCT<br/> ACACTTGCNCGCCCTAAGCGCCCGCTCCTTTCCTTGGGGGGGGNGGGTTG</p>                |
| Iron-responsive<br>element-binding<br>protein      | NK_017321 | <p>TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br/> GGCAGGAGGGGAAGACCTTCCAGGCCGTGATGAGGTTTCGACACCGATGTGGAGCTCACTTACTT<br/> CCACAATGGAGGCATCCTGAACATACATGATCCGAAAGATGGCCAGTAGGTGCTGGCCCTCTCAGG<br/> AGACCCGCGCTTGGTGCTAGACCCAATGAGGTACCAGGCCTCCGCTGGTGGAGGCTGGCGAGCA<br/> GCCACCTTACTTCTCGTGAGGGTGCCTAGCAAGATGAGCAAGTGGGCCCTGCCATTCTCTGGAGGC<br/> TCAGCGGCAGGAGTCTCTAGTTCGGTGATTTGTTAATCTTTTTATCCTTTTCTGTAATCCGGAAT<br/> CTAGAATCATGGGAAGGTCCATAGTCCCAAAGAGAGCTACCTTCTCTTAAAGTCACTCATCACC<br/> GGTCATTGATTTTTTTTCACTCTGACTAATCTTCAGCAGAACTAGCCAGTATCTCAGAAGTGTCTC<br/> CTACCCCTTTCTGTTACTCTGTCTGTCTGTCTGCTCAGTGACACCTTCCCTGGAGAGCCCATTCCTC<br/> CGTGATCACACCAATGGTAACGACATAGCTTCAGACTCTGTACACTTCAATTCATAGTAATCG<br/> NGTGATCCCTTNCCTTCCAAGTGAGCGAAAAACCTTGTGGCTAAGGCG</p> |
| Jagged 1   | L38483    | <p>TGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTC<br/> GCCCTTATCGCGGGATCCATAGGCTTCTTCCCCTGGGAATACTGATGGATTTTTTTTTTTTTTT<br/> TTTTTTTTGTACGACGTCAAGGTGTTCAAACACTTCCCTTGATAGCATCACTTTAAGACACATTCTA<br/> AGGACTGACTGAGGCAGATTGAGAATTCGTCTAGAACAGGTTTTTGTTTTTTCTCTTTCTCTT<br/> TTTATTTTTTCTGCTTTAGACTTGAAAAGAGACAGGCAGCGATCTGTGACAGAGTAGTTTAAAG<br/> GGAACAAACTGAGCTATGTAGTCAGAATGTGACTGGTTGGATCTCATTAAAAGTATCAGATTGTG<br/> TGAAGTTGGAAGCTTACCAATCTTACTTTGTAAATTCGATTTCTTTTACCATTCTGATGTAAT<br/> GCTGAACCACTTGTAGATTGATTTCAITGTTGGTGTCTACTGCATTTAGGGAGTATTCTAATAA<br/> GCTAGATGAATACTTGAACCATAAAATGTCCAGTTAGAGCACTGTTTAGATTGGCCATAGAGTAC<br/> ACTGCCCTGCTCGAGGGCCAAAAGGGCGAATTCAGCACACTGGCGGGCGGTACTAGTGGATCCGA<br/> GCTCGGTACCAAGCTTGATGCTAGCTTGAGTATTCTAT</p>                 |
| Keratinocyte growth<br>factor                      | X56551    | <p>GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCG<br/> CCCTTATCGCGGGATCCTGCTTCCACCTCGTCTGTCTTGTGGCACCATATCTTTAGCTTGCAAT<br/> GACATGAGTCCAGAGCAGACGGCCACGAGCGTGAACGTCTTAGCCCCGAGCGACACAGAGAAG<br/> TTATGACTACATGGAAGGAGGGGATATAAGGGTGAGGAGACTGTTCTGTGCGACCCAGTGGTACC<br/> TGAGGATTGACAAACGAGGCAAGTGAAAGGGACCCAGGAGATGAGGAACAGCTACAACATCATG<br/> GAAATCAGGACTGTGGCAGTTGGAATTTGGCAATCAAAGGGGTGGAAAGTGAATACTATCTTGC<br/> CATGAACAAAGAGGGAACTCTATGCAAGAAAGATGCAATGAGGATTGCAACTTCAAAGAAC<br/> TGATTTCTGGAAAACCATTAACACCTATGCATCAGCTAAATGGACACACAGCGGAGGGGAAATG<br/> TTCTGTGGCCTTAAATCAAAGGGGCTTCTGTCAAAGGAAGCTTGGCCAAAGGCGAATTTCANCA<br/> CACTGGNGGGCGTTCTATNGGATCCNGCTCTGNCCCNCTNGATGCATATCTNGAGNATCTATA<br/> TGGN</p>   |

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| Liver fatty acid binding protein        | V01235 | TNGNNATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTAGTACCAAGTGCAGAGCCAAGAGAACTTTGAGCCCTTCATGAAGGCGATGGGTCTGCCTGAGGACCTCATCCAGAAAGGGAAGGACATCAAGGGGGTGTGAGAAATCGTGCATGAAGGGAAGAAAGTCAAACTCACCATCACCTATGGGTCCAAGGTGATCCACAATGAGTTCACCTTGGGGGAGGAGTGCGAACTGGAGACCATGACTGGGGAAGGTCAGGCGAGTGGTTAAGATGGAGGGTGACAATAAAATGGTGACAACCTTCAAAGGCATAAAGTCCGTGACTGAATTCAAATGGAGACACAATCACCATAACCATGACACTGGGTGAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAACCTTGATGCATAGCTTGAGTATTCTATAGTGTACCTAAATAGCTTGGCTGATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAATCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTACTCCATTAATTGCGTTGCGCTCCTTGCCCTTTTCAGTCNGGAAACCTG  |
| Low density lipoprotein receptor        | X13722 | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTATCGCGGAATTCGACATGGCTGGCAGAGGGGACGAGGTGCAGCGGCACGGTGTGGGGTTCCTTGCTCCATCTTCCTCCCCATTGCACCTGGTGGCCCCCTTGTCTTCGGGGCCATCCTCCTGTGGAGGAACCTGGCGGCTGAGGAACATTAACAGCATAAACTTTGACAACCCAGTCTACCAGAAGAACACGGAGGACGAGATCCACATTTGCCGAGCCAGGATGGCTATACCTACCCTCGAGACAGATGGTCAGCCTGGAGGATGATGTGGCATGAACAGCTGAGGGGAGCCATCTCTTCCGGGATCCGCTGCCACCCTTAGGCGAGGAAGGACGCTTTCTCACACCTCCCCGCCCTGCACCTGGTCTTCCACCTCAGTGGTCTCTGTGTGTCTCAAAGCAAGATAAGAGCAAACTGGGCTGGGGCCAAAGCTCAGCGGCTGTCTGCCCTGGGTCTGTCTTATATATTTATTGTCTGGGGACAGAAAAGGCTATTGGCCATGCTCCAGATGGGAAAGCTTGGCCAAAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAATGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTGNACCTAAAT               |
| Macrophage inflammatory protein-1 alpha | U22414 | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTATCGCGGATCCTGGCGCTCTGGAACGAAGTCTTCTCAGCGCCATATGGAGCTGACACCCCGACTGCCTGCTGCTTCTCCTATGACGCGCAATTCACGAAAATTCATTGCTGACTATTTTGAGACCAGCAGCCTCTGCTCCCAGCCGGGTGTCATTTTCTTGACCAAGAGAAAACCGGCAGATCTGCCGTGACCCCAAGAGACCTGGGTCCAAGAATACATCACTGAGCTGGAACATAATGCCCTGAGATTAGAGGCAGCAAGGAACCCCCAACCTCCGTGGGCCCGGTGAGAGCAGGGGCTTGAAGCCCAAGACATTCCTGCCACCTGCAAAATCTCCCCCTCCTATAAGCTGTTTGCTGCCAAGTAGCCACATCCAGGGACTTTCACCTGAATTTTATTTAATTTAATCCTATTGATTAAATACATTTAATTTTAAATTTATTTATTGNCACATTTGTGTTTGTAGCTATTATTCTGAAAGACCTCAGGGCACATTCCTCAGCCC TCCCCCAAGCTTGGCCAACAANGGCGAATTCAGCACACTGGCGGGCGGTACTAGTGGATCCCCACTCGG  |
| Macrophage inflammatory protein-2 alpha | U45965 | CCGCCAGTGTGTGGAATTCGCCCTTTGNCGGATCCGCCAGCTCCTCAATGCTGTACTGGTCCTTGC TCCTCTGCTTGCCCAACCAACCATCAGGGACAGGTGAGACTCGAGGCTGACATTCCTGGAGGAGCCTCAGGTGGGCGCAGCCATGCCAGGCCCTCTGACCCACTCTCTTCTCTACAGGGGTGTGTGTGCCAGTGAGCTGCGCTGTCAATGCCTTGACGACCCTACCAAGGGTTGACTTTCAAGAACATCCAGAGCTTGACGGTGACCCCTCCAGGACCCCACTGCGCCAGACAGAAAGTCATAGCCACTCTCAAGGATGGTCATGAAGTTTGTCTCAACCTGAAGCCCCCTTGGTTCAGAGGATCGTCCAAAAGATACTGAACAAAGGCAAGGCTAACTGACCTGGAAAGGAAGAATGGGCTCCTGTACCTCAACGGGCAGAATCAAAGAGAAAAGAAACAACTGCACCCAGGAAGCCTGGATCGTACCTGATGTGCCCTCGCTGTCTGAGTTTATCTATTTATTTATATATGTATTTATTTATTTATTTTCAAGTGCCTAGATGTTGTTACATTACTATGATATTTAAAGATATGCATTGGCCAGCTCACTGTAAAGCTTGGCCAAGGGCGAATTCCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCAGCATTNAGNGATCTAANGGCCATNCAA |
| Macrophage metalloelastase              | X98517 | CCAGCTTGGGACCGAGCTGGGATCCACTAGAACCGGCCGCCAGTGTGCTGGAATTCGCCCTTTTGGAGTCCAGCCACCAACATTACTTCAATTTCTTCATGTGGCCAACATCCCATCTGGTATTCAAGCTGCTTATGAAATGGAGGCAGAAATCAACTTTTCTTTTAAAGATGAGAAGTACTGGTTAAATAACAACCTGGTACCAGAGCCACACTATCCAGAAGCATACATTCTCTGGGCTTCCCTGCATCTGTAAAGAAGATTGATGCAGCTGCTTTGATCCACTTCGCCAAAAGGTCATTTCTTTGTGGATAACAATATTGGAGGTACGATGTGAGGCAGGAACATCATGGACGCTGCTTACCCCAAGCTGATTTCTACACTTCCAGGAATCAGGCCAAAAATTGATGCAGTCTCTATTTCAAAGGCACTACTACATCTTCCAAGGAGCCTACCAATTGGAATATGACCCTTACTGCATCGTGTACCAAAAACATTGAGCAGTACGAGCTGGTTCCGTTGTTAGGAAGAAAAGGCGAATTCGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCAATTCG  |

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| Major acute phase protein alpha-1 | M11661    | GTTGGTACCGAGCTCGGATCCACTAGTAGCGNCGCCAGTGTGCTGNAATTCGCCCTATCGCGGGA<br>TCCACACAATTGCTGGCTTCTCACAGAGCTGTGACCTTTATCCAGGAGATGGTTTGTGTTGAAC<br>CTTCCCAAGAAATGGCGTGGCTGCCCCAGGGAGATACCTGTAGACAGCCCCGAGTTGAAGGAGGC<br>ACTTGGTTCATTCCATTGCACAGCTTAATGCACAGCATAACCATATTTCTATTTCAAGATTGACA<br>CCGTGAAAAAGGCAACATCACAGGTGGTTGCTGGAGTAATATATGTGATTGAGTTCATAGCCAGA<br>GAAACTAACTGTTCCAAGCAAAGTAAACAGAACTGACAGCGGATGTGAGACCAAAACACCTCGG<br>TCAAAGCCTCAACTGCAATGCTAACGTGTACATGAGACCTTGGGAGAACAAAGTCGTCGCCAGT<br>TCAGATGCCAAGCACTAGATATGATGATTTCTAGGCCTCCAGGATTTTCACCTTTCCGGCTGGTG<br>CGAGTACAAGAACTAAAGAAGGAACAAGTGGCTCTAACTCATGTGAGTACAAGGGCAGACT<br>CTCAAAGGCAGGCCTAGGAAGCTTGGCCAAAAGGGCGAATTCTGCAGATATCCATCACACTGGCG<br>GCCGCTCGAGCATGCATCTAGAGGGCCAAATTCGC      |
| Major basic protein 1             | D50568    | GCGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCAGTGTGATGGATATCTGCAGAATTCCG<br>CCTTATCGCGGGATCCTGTCCCTGGAGGAGGAGGAGGAGGAAGAGGAGGAAGAAGTTCTGGAAG<br>TGAAGGTGCTCTTGGAAATGAAGGAGCTGTCTCAGGTCAGGATGTGACAGATGAGAACCTTCAGT<br>GCCCAAGGAGGAAGACACACAGAGTCTGATGGGTGACTCTGGATTCAAGACTGGTCGCTACCTC<br>CTAGTCAGGAGGCCCTGAGTGTCTTAAACAAAGCTCAGTTGGTCTGCCGGAGCTGCTACCGGGCAC<br>CCTTGCCCTCCATCCACAGTTTCAGTGTAACTTCCGAATCCAGTCTTTGTGTCAGGGGAATCAACC<br>AGGTCAGTCTGGATTGGAGGCAGGATTGTGGGCTGGGGTCCGCTGCAAAACGCTTCCGATGGATT<br>GATGGAAGCTCTTGGAAATTTGTCATATGGGCTGCTGGGCAGCCTCGTCGCGCGGTGGCAGATG<br>TGTGACCTGTGTACCCGAGGAGGCCACTGGCGCCGATCTGGCTGTGGCAAAGAGACCAAACTTG<br>GCCNAAAAGGGCGAAATTCACCACACTGGCGGGCCGTTTNCCTAGTNGATCCCCAANTTCGGT<br>ACCCAAC                                  |
| Malate dehydrogenase, cytosolic   | AF093773  | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCACAGAGCCCTCGTGCCGCTCGTGCCCCAAGGAGAACTTCAGTTGCCTGACTCGATTGGAC<br>CACAAACCGAGCAAAATCTCAAAATGCTCTTAACTCGGTGTAACCGCTGATGATGTAAGAAATGT<br>CATTATCTGGGGAAATCATTCATCAACCCAGTATCCAGATGTCAATCATGCCAAGGTGAAATTCG<br>AAGGAAAAGAAGTTGGTGTGTATGAAGCCCTCAAAGACGACAGCTGGCTCAAGGGAGAGTTTCATC<br>ACGACTGTGTCAGCAGCGTGGTGTCTGCTGTCTCAAGGCTCGGAAGCTGTCCAGTGCCATGTCTGC<br>TGCGAAGGCCATCTCGGACCACATCAGAGACATCTGGTTTGAACCCCGAGGGCGAGTTTCGTGT<br>CGATGGGCGTAATCTCTGATGGCAACTCTATGGTGTCCCTGATGACCTGCTCTACTCGTTCCCT<br>GTCGTGATCAAGAATAAGACCTGGAAGTTTGTGAAGGCTCCCCATTAAACGACTTCTCCCGTGA<br>GAAGATGGACCTGACAGCAAAGGACTGACCGAGGAAAAGGAAACGGCTTTTGAGTTTCTCTCCTC<br>CGCATGACTACACAGTCTGTGACGTCAGCAACAN |
| Matrix metalloproteinase-1        | X91785    | TTGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCAGTGTGATGGATATCTGCAGAATT<br>CGCCCTTATCGCGGGATCCGGTACTGGCAGTGGGCTTGTGTCTTCTTCTTTAGACGCCATGGG<br>ACACCCAAGCGACTGCTTTACTGCCAGCGTTCACTGTGGACAAGGTCTGACCCCCACCACTGGC<br>CCACCCGCTTCTACCACAAGGACTTTGCTCTCCGAAGGCAGTGGCAGCCGGTGGTGGCAGGTG<br>GGCTGTCTCACCCATCCTGGGCTCCCTCCCTCCAGCCTCCCTTCTCAGTCCCTAATTGGCTTCT<br>CCCACCTCACCCAGCCTTGTTCATCCATAGGTGGGTCCCTTGAGGGCTGAGCAGAAGATGGT<br>CTGGCTGTGCGCCCTCAAGGGACCTCATAGCTTGGTGTGTGTCCAACCTATTTGAATGTTGTC<br>AAGGCTGTGCATTGAAGGCAGGACCTCTGACCTTACAGGCAAAGGCCAAATGGGGTCTATCTGC<br>TTCTCTTCCATCCCCCTAACTACATATCTTAAATCTCTGAATATGACCTCAGGAGGCTTTGGGA<br>AGCTTGGCCAAAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTAC<br>CAAC   |
| Methylacyl-CoA racemase alpha     | NM_012816 | CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGATAAAAATGGCTGTCTCTGAGGCATTCTAGAGCTCACTTAAAGGGGTGTTCAA<br>TTTGCTGTCTTGGTGCAGGTGTCTGTCAAAGATTGGCAGGAGCGGTGAGAACCCATACCTCC<br>CCTGAACCTCCTGGCCGACTTTGGTGGCGGTGGCCTCATGTGCACATTGGGCATTTTGCTGGCTC<br>TCTTCGAACGCACGCGTCTGGCTAGGGCAGGTCAATTGATGCTAACATGGTGAAGGAACGGCA<br>TACTTAAGTACTTTCTGTGAAAACCTCAGGCCATGGGTCTGTGGCACAGCCTCGAGGGCAAAA<br>CCTGTTTAGATGGCGGGCACCTTTCTACACAACCTACAAGACCCGAGATGGGGAGTTTATGGCTG<br>TAGGTGCAATAGAACCCAGTTCTACACACTGCTGCTTAAAGGACTTGGACTTGAGTCTGAGGAA<br>CTCCCCAGCCAGATGAGCATAGAAGATTGGCCAGAAATGAAGAAGAAATTTGCAGATGTGTTGTC<br>AAGGAAGACTAAGGCAGAGTGGTGGCAGATCTTTGACGGGACAGA  |

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| MHC class I antigen<br>RT1.A1(f) alpha-<br>chain      | X99767 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGCAGGCATAAATGACATAGGTTTCCATGTTGGAGTCGGTGGATAGAGAAGGCTCCCATC<br>TCTGGGTAAGCGGCTCAGGCAGCCCCCTCATGCTCCACACGGCATGTGTAATCTGCTCCTTCCCA<br>AGTGGCACCACCACAGATGCCCCACTTCTGGAAGGTTCATCCCTGCAGGCCCTGGTCTCCACAAG<br>CTCCATGTCTGGGTGAGGTCTCTCCCATTCACCTGCCAGCTCAGGGAGATGTCAGCAGGGTAGA<br>AGCCCAGGGCCAGCACCTCAGGGTGACATCACCTTCAGGTCTGGGGTGAAGGTCACATGTGCC<br>TTTGGGGGATCTAAGCGCAGCAGCGTCTCCTTCCCGTGCTCCAGGTATCTGCGGAGCCACTCCAC<br>GCACGTGCCCTCAGGTAGGCCCTGAGTCTCTCTGCAACACCAGCCGATCCCACTTGTTCGGG<br>TGATCTGTGCGCAAAGTCCGCGCGCTCCACGTCTTCAGGTCTTCGTTTANGGCGATGTAATCG<br>CGGCCGTCGTAAGCGTCTGCTTATTACCCGCGGAGGAGGNTTCCCGTTCGGTTCACGCTCAC<br>AAGCCATACATTCTCTGGATGGGGGTGAAANNCCGCCCTCGCTCTTGG |
| Mitogen activated<br>protein kinase<br>(P38)          | U73142 | CCCAGTGTGCTGGAATTCGCCCTTCGCGGGATCCTTAAATTTACGGCACTTTGTGCTATATGAGG<br>ACCCATATATTTAAAGCTTTTGTGTCAGTAAGAAAGTGTAAAGCCAATTCCAGTGTGGACGAAA<br>CAGGTCTCGGTATTTAGGTCAAGGTGTCTCCATTCTCTATCAGTGCAGAGACATGCAGTCTCTGTG<br>GGCAGGGTAGGACCTGCATCATCTGGAGCCAGAAAGGAGGCCGACTGGCCAGGCCCTCACCGCT<br>CAGTATGCAGTCCAGCTTCAGTCTACCTCACAATGGTTAGTAGCAACGTCCTGGGTTTGAACG<br>CCAGGCGTGGTTATTTTATTGAGGATGCTTTGCACATGTGGCCATGCTGTGTTAGGACTGTGCC<br>CCAGGGCCCGACTTGAAGCTAGAGCTGGCAGAAAGACTCCTGGCATCCATGGTGCATGTGCTGCC<br>GCCACCCAGTTTCTCCATTGGAAGACAAGGGAATGAGAAGACTGCTGTGTATGTGTTATTTGTGAA<br>CTTGGTTGTGATCTGGCTGCAGGGCCAAAGGGCGAATTCGAGATATCCATNACACTGNCGGCCG<br>CTCGAGCATGCATNTAGAGNCCCCG  |
| Monoamine oxidase A                                   | D00688 | TGGTGAATTTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCAGTGTGATGGATATCTGCAGAATT<br>CGCCCTTCGCGGGATCCGAGAAGAACTGGTGTGAGGAGCAGTACTCCGGGGCTGCTACACAGCC<br>TACTTCCCTCCTGGTATCATGACCCAGTATGGAAGGGTATTCCGCCAGCCAGTAGGTAGGATTTA<br>CTTTCAGGCACAGAGACAGCAACACAGTGGAGTGGCTACATGGAAGGAGCAGTTGAAGCTGGAG<br>AACGAGCAGCTAGAGAGGTGTGAATGCTCTAGGAAAAGTCGCGAAGAGGATATATGGGTTGAA<br>GAACCCGAGTCCAAGGATGTTCCAGCCATTGAAATTACCCACACCTTCTTAGAGAGGAACCTGCC<br>TTCCGTGCCCTGGTCTGCTCAAGATCACTGGTGTTCCTACTTCTGTGGCTCTTCTCTGCTTTGTAT<br>TGTACAAGATTAAAGAGCTCCCATGCTGAAGTTTACCCTCAGGCCTCTGACAGTATCATCGCAT<br>GTGAAAGAAAGTGTGGATAAATTACAGCCTATGGTTTGGGCCATTTAAAGCTTGGCCAAGGGCGA<br>ATTCCAGCACACTGGCGGGCGTTACTAGTGGATCCAACTCGGACCAAGCTTGATGCATACTTGAG<br>TATTCTAT                                 |
| Monoamine oxidase B                                   | M23601 | GTGATCAAGCGAGCTNTAGCATTAGGTGNCACATATAGAATAGGGCCNTNTAGATGCATGTTCGA<br>GCGCCCGCGATATCGAATTCGCCCTTCGCGGGATCCATTGGCAGCCAGAACAGAACTGTGTGA<br>TGTCACAGCAAGACCCATTACCAACACCTTCTGGAAGAGACACTTTGCCCTTCTGTACCAAGGTCTA<br>CTAAAGCTGCTTGGATTGACCACCATTTGTCAGCAACAGCTCTTGGTTTCTTGGCCCAAAAA<br>GGGTCTGTTTGTACGTTTCTAAAGATGGGCTTTAGGACCATATCCACAGGTTTCTCATTCAAGTGT<br>GTCACAAAAGCTTTTGAAGGAGTTGGGATAAAAAATCTGACAAAGGTGCAGAGATTATGGAGTGA<br>GAAAGCACAGTAACCTGGTCTCCATTTTGGCTATCTTTTAGCATCGCTGTGGTCCACTCATTTTC<br>AACTTTCCTGCACTCTGAATATTGAGAACAGATACACAGGCTCTCTCACAACCTACCTGCCCTAT<br>GCACATAGTTGTTTTCAAAACCTATGCCCTTGTGCTTGTCTTCTTCTGCTGTGTTAGGTCTCT<br>CACCTGACAGGGCCAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGG<br>TACCAAGCTTGGNCTCAA                         |
| Monocyte<br>chemotactic<br>protein receptor<br>(CCR2) | U77349 | GCGAATTTGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTCCG<br>CCTTATCGCGGGATCCTGATCAGCATACTTGTGGCCCTTATTTTCCAACAATCTGGAAGAATTTTC<br>CAAACAATAATGAGGAATATCTTGAGTTTGATCCTGCCCTACTTGTATGTCATCTGCTACTC<br>AGGAATCTTCCACACCTGTTTTCGCTGTAGGAATGAGAAAAAGAGGCATAGGGCTGTGAGGCTCA<br>TCTTTGCCATCATGATTGTCTACTTTCTCTTCTGACTCCATACAATATTGTCTCTTCTCCTGACC<br>ACCTTCCAGGAATCTTGGGAATGAGTAAGTGTGTTGACATGCACCTTAGACCAGGCCATGCA<br>GGTGACAGAGGCTCTTGAATGACACACTGCTGCGTTAATCCTATCATTTACGCCCTTTGTTGGTG<br>AGAAGTCCCGAAGGTATCTCTCCATATTTTTCAGAAAGCACATTGCCAAAAATCTCTGCAACAA<br>TGCCAGTTTCTATAGGGAGACAGCAGACCCAGTGAGAAGCTTGGCCAAGGGCGAATTCAGC<br>ACACTGGCNGGCCGNTACTAGTGGATCCGAGCTCGGNNCCANCTTTGAN  |



31/73



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| Myelin basic protein  | M25889   | TTTGAGAATCGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAAT<br>TCGCCCTTATCGCGGAATTCCTTCACAGCGACACGGATCCAAGTACTTGGCCACAGCAAGTACCA<br>TGGACCATGCCCCGGCATGGCTTCCCTCCAAGGCACAGAGACACGGGCATCCTTGACTCCATCGGG<br>CGCTTCTTTAGCGGTGACAGGGGTGCGCCCAAGCGGGCTCTGGCAAGGACTCACACACAAGAAC<br>TACCCACTACGGCTCCCTGCCCCAGAAGTTCGAGAGGACCCAAGATGAAAACCCAGTAGTCCACT<br>TCTTCAAGAACATTGTGACACCTCGTACACCCCTCCATCCCAAGGAAAGGGGAGAGGCCCTGTCC<br>CTCAGCAGATTTAGCTGGGGAGGAAGAGACAGCCGCTCTGGATCTCCCATGGCAAGACGCTGAGA<br>GCCTCCCTGCTCAGCCTTCCGAATCTGCGCTCGGCTTCTTAATATAACTGCCTTAAACGTTTA<br>ATTCTACTTGACCAAATAGCTAGTTAGAGCAGACCTCTCTTAATCCCGTGGGGCAAGCTTGGC<br>CAAAAGGGCGAATTCAGCACACTGGCGGGCGGTACTAGTGGATCCGAGCTCGGGACCAAGCTTG<br>ATGCATAGCTTGAGTATTCTATAGTGTACCTAAATAGCTTGGCGTAATCATGGGCATAGCTGGT  |
| Na/H antiporter<br>(APNH1)                                  | AA998340 | CNAANGGGNATTAATTTGGNAACCCCAAGGTTTTTCCNACCCCCCNNTTTTAAANCCNCCNN<br>GGCCNAAATNAAANTNANCCCCCNAAAAANGNAAANNCNTTCNNCCCCANTTTTTTTTTTTTT<br>TTTTTTTTTTTAAAACTCACATTGATTTATTAGAATATGAAAAAGGTTCAAGTTTCTCTGTACA<br>GGCGGCAGAGAGGCAGCGGCTGCGGTGGCTTTGTACATGGTTGTGATGTCACCTTGATGGCAA<br>CTCTGCCTAAAAACAGCACTTGCATGGAGAGAGACAGCTGGGCCAAGCACCCATAGCCCCATCC<br>CCTGGGAGGGGACCCCTCTGACTATTGCACGATCTGGGGAGGGAGTGTCTAGGGGTGGACAGAC<br>ACCCACGGGCTGGCCAGCCATGGCGGTAGGAGTACATGCTGTGAGCAAAGGCCGCTAGGGGTG<br>CACTGTCTGTCTACTCTACAGGATGCAGGTAAGAGAGTGGTCTAGACGAGGGGTGGTGGCCCTGTG<br>CCGAATTCCTTGGCCTCGAGGGCCAAATTCCTATAGTGAAGTTCGTATTAAATTCGTAATCATGTCA<br>TANCCNNNC  |
| Na/K ATPase alpha-1   | M14511   | ANNGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCT<br>TCGGTTTCTGTCCTTTCACCTGTGGGCATCCGAGAGACCTGGGATGACCGCTGGATCAATGAT<br>GTGGAGGACAGCTACGGGCAGCAGTGGACCTACGAGCAGAGGAAGATTGTGGAGTTCACCTGCCA<br>CACGGCCTTCTTTGTCAATCTCGTGGTAGTGCAGTGGCTGACTTGGTCACTCTGCAAGACCAGAA<br>GGAATTCGTCTTCCAGCAGGGAATGAAGAACAAAGATCTTAATATTTGGCCTCTTTGAAGAGACA<br>GCTCTGTCTGCTTCTCTGTCTTACTGCCCTGGGATGGGTGCAGCCCTTAGGATGTATCCCTCAA<br>ACCTACTTGGTGGTCTGTGCTTCCCTTACTTCTCATCTTCTGTGTATGACGAGGTGGCGA<br>AGCTCATCATCAGGCGACGCTTGGCGGCTGGGTGGAGAAGGAAACCTACTACTAGCCCACTGCC<br>CTGCAGCCCGTGGACATTTGTGCCACACACTGCACCTACCCCTAAGGGCGAATTCAGGCACATG<br>CGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTG<br>NCACCTAAATAGCTGGCGTAATCATGGGCATAGCTGTTCCTGTGTGAA   |
| NADP-dependent<br>isocitrate<br>dehydrogenase,<br>cytosolic | L35317   | TCTCNTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAG<br>AATTCGGCAGCAGGGGAAGGTTTTTTAATTGTATTTACTGTGTAATAGCAGTCTAGGAATGT<br>GTTAGTATCTGTTTACAATTAACGTGCTACTTTTCTTTGCTCTAATGTAATGACCAAAATCAGA<br>AATGCTCAAGGGTGAACAATCACTACACTATGTTTCCCGTAAAGGTGAAGGAGAGGCTCACCT<br>CCCCACTGTCCATGAGTGTGAACACAGGGAGCTTTTGTGTGCAAAATGTTGCACTGTGTGTGAA<br>GAGACTGGAACAAATAGAATGTGTGTAGCTGAATGCATGGCAGCCATGTTTGTAAAGAGCACTT<br>ATGTGTCCAATATACTAATTATACGTTAAGACCCTGGAGAATTCGAAGTCTAGAATAAATACAG<br>ACTGGAGGTTTCTGCTCTTTGATTCTCTCTGTGGCCGAGCCCAAGTATGATCTTACCCACAGACAG<br>CACAGCATTTCACCCATGTGCAATAATGGGAGCTGCATCGTTTTTCGGATTTCTGCTGGCCTACTA<br>CATTTCTTTTATATAAATGTGATTGTTTTTCAGAAGTTGATATTAAACACTATNCCAGTCTAGTC<br>CTTCTAAACTGGTAATTT  |
| NADPH cytochrome P450<br>oxidoreductase                     | M10068   | NGNGNGNNTGGCGGNANGNNGTNNCCNTNGNGANCNANGATGANAAAAAAGNNGTNNNGAGG<br>NGGNNNTNNGAGAGACNNACGGCCTCNCATNCGGCCNNNNNCNANNAGNNGAGAGCCGN<br>NNGGNAGACNNNGNNGNCCNACACNAANNAAGNGTCCGTGCGCAGCNCNCGCCCAAGTNNNGC<br>CNCCGGAACNNNGGAGCGCNCNNGGTANGACNCGNCTCGNNGCAGGCCGCGCCNNGGTGGNAGG<br>AAANCTCCANAATTTGNCNCNAGTCNCGGANANNGNNGGGGNCNCGACCNACNNGGNTCA<br>NTNTTAGAAAGAAGAAAANAAGANATNCCGANGTTNAGNAAGATTTCAAACAACGGGCCCCACN<br>CGTCAAAGNAGAAGCAGCTTNGTGGAAAAGAATNAANAAAAACGGGAAGGGANNCNTATNGTANT<br>NTATGGCTCCAGACGGGAACCGNTGAGGAGTTTTTNCACCGGCTGTNCAAGGAATGNCNCC<br>CGCTACGGGATGNGGGGCAAGNCCGAGACCCTGAAGAGTATGACTGTNCCGNCCTGAGCAGCCT<br>GGCAATGCGCAGGACTTCTATGACTGGCTGCAGGAGACTGACGTGGACCTCACTGGGGTCAAGT<br>TTGCTGTATTTGGTCTTGGGAACAAGACCTATGAGCACTTCAATGCCATGGGCAAGTATGTGGAC<br>CAGCGGCTGGAGNAGCTTGGCGCCAGCGCATCTTTGAGTTGGGCCCTGGTGATGATGACGGGAA<br>CTTGGAAAGAGGATTTATCAGCTGGAGGGAGCAGTTCTGGCCAGCTGTGTGCGAGTTCTTTGGG<br>TAGAAGCCACTGGGGAGGAGTCGAGCATTCGCCAGTATAGCTC |

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| NADPH cytochrome<br>P450 reductase                                 | M12516   | GGCAANTAGAAGGCACAGTCGAGGCTGATCAGCGAGCTCTAGCATTAGGTGACACTATAGAATA<br>GGGCCCTCTAGATGCATGCTCGAGCGGCCGCGATATCGAATTCGCCCTTCGCGGGATCCAGGAAC<br>CAGCAGGCGAGAATGGCGGCCGCGCCCTGGTACCCATGTTTCGTGCGCAAATCTCAGTTCCGCTTG<br>CCTTTCAAGTCCACCACACCTGTCTATCATGGTGGGCCCCGGCAAGGCAAGGAGGTGGGAGAGACGCTGCTATACT<br>ATGGCTGCCGGCGCTCGGATGAGGACTATCTGTACCGTGAAGAGCTAGCCCCGTTCCACAAGGAC<br>GGTGCCCTCACGCAGCTTAATGTGGCTTTTCCCGGAGCAGGCCNACAAGGTCTATGTCCAGCA<br>CCTTCTGAAGAGAGACAGGGAACACCTGTGGAAGCTGATCCACGAGGCGGTGCCACATCTATG<br>TGTGCGGGGATGCTCGAAATATGGCCAAAGATGTGCAAAACACATTCTATGACATTGTGGCTGAG<br>TTCCGGGCCATGGAGCACACCAGGCTGTAAGCTTGCCCAAGGGCGAATTCAGCACACTGGCGG<br>CCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGGNCTCAA  |
| N-cadherin   | AF097593 | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCGAGTGTGATGGATATCTGCAGAATTTCG<br>CCCTTGGAGCCTGATGCCATCAAACCTGTGGGAATCAGACGGCTAGACGAGAGGCCATCCACGC<br>TGAGCCACAGTATCCAGTCCGATCCGACGCCACACCTGGGGATATGGGGACTTCATTAATG<br>AGGGCCTTAAAGCTGTGACAAATGACCCACGGCGCCACCATATGACTCCCTTTTGTCTTCGAC<br>TATGAGGGCAGCGGCTCCACGGCTGGCTCCTTGAGCTCTCTCAACTCCTCCAGCAGCGGCGGGGA<br>CCAGGACTATGACTACCTGAATGACTGGGGACCCCGCTTCAAGAAGCTGGCCGACATGTATGGTG<br>GTGGTGATGACTGAACGGCAGGACGGACTTGGCTTTTGGACACGTATGAACAGTTTACCTGATA<br>TTCCCAAAAAGCATACAGAAGCTAGGCTTTTAACTCTGTAGTCCACTAGCACCGTGTGCTGGAG<br>GCTTTGGCGTAGGCTGCGAACCAGTTTGGGCTCCAGGGAAGGGCGAATTCAGCACACTGGCGG<br>CCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTGTCA<br>CCTAAATAGCTTGGCGTAATCATGG  |
| Nerve growth factor<br>receptor                                    | X05137   | GCGATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCGCAGTGTGATGGATATCTGCAGAATTTCG<br>CCTTGAAGCTGCCCCAGAACTACAGTGCAGTGCAGGAGCAGACTGGTGTGAGAACACAAGAAAA<br>GCAGATGCTGGCCCTGCAGTCTGTGGCAGCTTTCTCCTCAGCTTCAAGGCCCTGCAAGGACCG<br>ATTTCTCTGAGCACGGCCAGGAAGGGGCAAGAGGGTTCGGTTTCACTGGCGCTTTCTCCCGCTCCT<br>TGGCCTGTTCTGTTTGTCTTGTGTTGGAATGAGTGGGACCCCTCTATTAGCATGAAGGAGC<br>CCCAGGCAGGGTATGCACAGACTGACCCACCATCCCTCCCCACCCAGGGTCCACCCAACCCGGTGA<br>AGAGACCAGGAGCATGTACGCATACGCGGTGGTATTTTATGGACCCCAATCTGCAATTTCCCA<br>GACACCTGGGAAGTGGGACATTTCTGTATATTTATTTCTCCCCAGGAGCTGGGGAGTGGTG<br>GGGGCTGCAGGTACGGTTTACATGTGTTTGGTCTGGGGGTCTCTAAGGGCGAATTNCAACACA<br>CTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTAT<br>AGTGTACCTAAATAGCTTGGCGTAATCATGNCATNAGCTGNTTCTGGTGTGAAAATTGTTAT<br>NCCCTTCACA |
| NGF-inducible anti-<br>proliferative<br>protein secreted<br>(PC3)  | M60921   | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGCTAGAGCCAGCCAGTACCCCTTAGTGAGGATCCCTTCCCCATGTCTCTCCACT<br>GCCGTGGCATCCCATGTCTGGATTTCTCAATTCCTCAGTTTCTACTCAAAGGTGCTACTTACCA<br>AACACTCTGCCCGTCCCGCTCTCCCCAGCTTCGCACAGCCGTCCAGGTGGCTTCGTCTCTCCTG<br>CTTTAAAGTTAACTTTGGGCCACAGACCCGAGAGCTGTGGGTTGAAGCAAAGCTGTGAATCGCT<br>CCAGATGGTCCCTGTGTTCTGTCCACACACAGGTCCCCGCCTTTTGAAGCAGCTCCTGGTCT<br>CATGCTTAAATCTGTTCTCTCACTGCCCCGTGTTCACTTTAGAAATGGCAGAACACAGAGCTGGAC<br>TGTTGAGCAGGCTGTCTCTCTCATTAATAAAAAAAGTAAGTTTGAAGCTATTCGACAGAA<br>GAGACAAAGGTTACTGATTGTACAATAGCGCTTTTATATGGAAGACTGTACAGCTTTATGGACAA<br>ATGTAAAACCTTTTGTGTTTAAATAAAATGTAGCAGACCAAAAAAAAAAAAAAAAAACATGC<br>GGGCCGCAAGCTTATTCCCTTTTAGTGAGGGTTAATTTTACC                                      |
| N-hydroxy-2-<br>acetylaminofluorene<br>sulfotransferase<br>(St1c1) | AI030692 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>GGCAGGAGCTTACTATTACTTCTCAAGAATGAATAAAATGCTGCCGTGACCCTGGTACCCCTGGGA<br>GAATACATTGAACAGTTCAAAGCTGGAAAAGTGCTGTGGGGCTCCTGGTATGACCATGTAAAGGG<br>ATGGTGGGATGTGAAGACCAACACCGTATCTGTATCTCTCTATGAAGACATGAAGAGGACC<br>CTAAAAGAGAAATTAAGAAGATAGCAAAATTCCTGGAAAAAGACATATCAGAGGAAGTTCTTAAT<br>AAAATCATCTACCACACCTCCTTTGATGTAAATGAAGGAAAACCAATGGCCAACTATACCACTCT<br>ACCCCTCCAGTATCATGGACCACTCTATATCTCTTTCATGAGGAAAGGGATGCCTGGAGACTGGA<br>AGAATACTTTACTGTGGCACAAAGTGAGGATTTTGTATGAAGACTACCGGAGGAAGATGGCAGGG<br>AGCAATATTACCTTCCGCACAGAGATCTGAGAGCAGTGAAGGAAGAGGGAAGCCCTAGATTTCCCTG<br>ACTATATGCTTTAGCTATTGTAGCTTCCATTCTGAGTTTGTATGTCTGNGATACTATTTCAT<br>CAAATGNAATCAGACCTTCCACACTAGGTGATTATTCTTATTGATACC                      |

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| Notch 1                                  | X57405   | ACTCAAGTATGCATCAAGGTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTCTGGA<br>ATTCGCCCTTATCGCGGGATCCCTTGGGTCCGAGCTTCTGAGCGGGAGCCAGCCAGGCAGAC<br>GTACAGCCGCTGGGCCCCAGCAGTCTGCCGTGTGCACACCATTCTGCCCCAGGAAAGCCAGGCTCT<br>GCCGACATCACTGCCATCCTCCATGGTCCCACCCATGACCACTACCCAGTTCCCTGACCCCTCCTT<br>CTCAGCACAGCTACTCATCCTCACCTGTGGACAACACCCCCAGCCACCAGCTGCAGGTGCCAGAG<br>CACCCCTTCCCTACCCCATCCCTGAGTCCCTGACCAGTGGTCCAGTCTCTCCCGCATTCCAA<br>CATCTCTGATTGGTCCGAGGGCATCTCTAGCCCGCCACGAGCATGCCGTCCAGATCACCACA<br>TTCAGAGGCATTAAAGTAAACAGAGATGTGGGATGAAGACCCAGCTTCCGTTCCCAAGCTCT<br>GTTGGGAGTCCCTTCCAGTGTCTCCAGGATGCTGGGGCGACCAAGGAGCCTTAAGCTAAGGGCGA<br>ATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCGATTTCGCCAA                                |
| Organic anion transporter 3              | AF041105 | TTGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAAT<br>TCGCCCTTCGCGGGATCCGCATCCGGTTCATCAGGAAATTCATCTGCAGTCTCGGGTTATGTAAA<br>AAAGGCCCTGAGTGTGCTAATAAATACTACAGTACTTTTTAATCATGTCTAGTAATTGGCAGTTTCAT<br>CTACTCGATCACAGCCATACCTGGGTATATGGTCTTCTGAGGTGTATCAAGCCTGAAGAGAAGT<br>CGCTTGGGATTGGATTACATGCATTTTGACAAAGAGTATTCGCTGGCATTCCGGCACCATTAC<br>TTTGGCGCTTTGATAGACAGAACCCTGTTTACATTTGGGGAACCCTGAAATGTGGTGAGCCGGGGC<br>ATGCAGGATGTACAAATATAAATACTTCAGGCGCATTTACCTAGTGTTCCTGCAGCTCTTAGAG<br>GATCAGGCTATCTCCCTGCACCTCTTCATTCTGATACTTATGAGGAAATTCAGTTCCCTGGGGAA<br>ATCGACTCTTCAGAACTGAACCTGCAGAGATGAAGATCACAGTGAAGAAAGTGAGTGCACAGA<br>TGTGCAAGCTTGGCCAAGGGCGAATTCCAGCACACTGGCGGNCGTTACTAGTGGATCCGAGCTCG<br>GACCAAC              |
| Organic anion transporter K1             | D79981   | TGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTC<br>GCCCTTGTCCAGGAAACTCGTCCGAGTCTCGGGCTGTGTAATAAAGGCCCGAGTGCACCA<br>ACAAGCTGCAGTACCTTTTAATACTATCAGGATTTCTCAGTATCCTCTACTCATTCGAGCCATA<br>CCTGGATACATGGTTTTCTGAGGTGTATCAAGTCTGAAGAGAAGTCACTTGGGATTGGAATACA<br>TGCGTTTTGCATAAGAGTATTTGCTGGCATTCCAGCACCTATTACTTTGGAGCTTTGATAGACA<br>GAACCTGTTTACACTGGGGAACCTCAGAAATGTGGTGCGCCAGGGGCGTGCAGGATGTATGATATA<br>AATAGCTTCAGGCGCATTTACCTTGGGATGTCTGCAGCTCTAAGAGGATCAAGCTATCTCCCTGC<br>ATTTGTTATTGTAATACTTACAAGGAAGTTCTCTCTTCTTGGGAAAATCAACTCTTCAGAAATGG<br>AAATTGCAGAGATGAAGCTCACAGAGAAGGAAAGCCAGTGCACAGATGTGCAAGCTTGGCCAAGG<br>CGCAATTCACACACTGCGGCCGTTACTAGTGGATCCGAGCTCGGACCAAGCTTGATGCATAGCT<br>TGAGTATTCTATAGGNCACCTAAN   |
| Organic anion transporting polypeptide 1 | L19031   | ATAGAATACTCAAGCTATGCATCAAGTTGGTCCGAGCTCGGATCCACTAGTACCGCCGCGAGTGT<br>GCTGGAATTGCGCCCTTCGCGGGATCCAACTCGTCTGCAGTCTCGGGTCTGTGTAAAAAAGTCCCT<br>GAGTGTGCCAACAGGCTGCAGTACTTTTTAATCTTAACAATAATTATCAGTTTTCATCTACTCACT<br>TACAGCCATACCTGGGTACATGGTTTTTTGAGGTGTGTCAAGTCTGAAGAGAAGTCACTTGGAG<br>TTGGATTACATACATTTTGCATAAGAGTATTTGCTGGTATTCGCCACCTGTTTACTTCCGGCGCT<br>TTGATAGACAGAACCCTGTTTACATTGGGGAACCCCTGAAATGTGGTCAGCGAGGGGCATGCAGGAT<br>GTATGACATAAACAGTTTCAGGCACATTTACCTGGGGTTGCCTATAGCACTAAGAGGATCAAGCT<br>ATCTGCCCTGCCCTTCTTCATTCTGATACTTGTGAGGAAATTCAGTTTCCCGGGGACATTGACTCT<br>TCAGCAACTGATCATAACAGAGATGATGCTCGGAGAGAAGGCAAGCGAGCACACAGATGTGCAAGC<br>TTGGCCAAGGGCGAATTCGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGG<br>GCCCAATTCCGNAA |
| Organic cation transporter 2             | D83044   | GAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCC<br>CTTATCGCGGGATCCTTGGTGTCTTGTCTGCTCCTCCATGTGTGACATTGGCGGCATCATCACG<br>CCTTTCCTCGTCTACCGTCTCACGGACATCTGGATGGAGTTCCACTGGTGTATTTGCTGTGGT<br>TGGCCTTGTGCTGGGGCACTTGTGCTGTGTGCTACCTGAGACCAAAGGGAAGGCTCTGCCTGAGA<br>CCATCGAGGATGCCGAGAATATGCAGAGGCCAAGAAAAAAGAAAGAAAAGAGAATTTACCTCCA<br>AGTCAAGCAAGCAGACCGTCCGCTAAGCTAAAAAGAAAGGGCATCATTTGCTGCTGGAGCTGACTT<br>TGCTCTCTCTGAGGCCAGAGATGGAGCTTCTCTCTCCCTCCCCCAACCCACACAAACCAACC<br>TCACTTACCCCTGAACCTCCATCAGCAAGAGCTGTAGCTTGCACGGTCTGTTGCACTGATGTGTCA<br>AGCTCTTCTCTCCAGCCAGGATTTTCCGCTCACTCTGCTCTAAGCTTGGCCAAAAGGGCGAATT<br>CCAGCACACTGGCGGNCGNTCTAAGNGGATCCAG  |

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| Organic cation transporter 3 | AF055286 | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCG<br>CCCTTATCGCGGGATCCCCCTAGGTGGCGCCGTTCCAAGGAACCGTAAAGATTCCAGAGTATTT<br>TATATGGAATAAGATAAAGATTTATCATGCTACCCAAGCTTCTGGGAACACATAACCTTTGACCT<br>CTTTAGCAAGATCCAGTAGGTACACAGATTCTGCCTAGGTTCTCTTCATTGGGACCAATGTCT<br>CTGACCCAC TGGGGAGGAGATATGAGAAGGTCCCAACCAGTTCTCCAGTTCTCAGGACAGTCCCA<br>TCCAGGAAGCAGGATGAACATATCAAGGCTTGGCAGTGAACGGAAGTGACTCAGCTGATCTGAT<br>CAAGACTGAGCAGTGAGGAGTGTCTGAAGAGTCTGAGAAGTGCATTCTGATTCTGCTTAAGCT<br>CCGAATACATGCCTTCAGAGAGCCGACATGCCTGGTGGCCCTCCCTTCTGTCCCAAGCCACT<br>GAGGTTCCAGGCCCCAGGTTAGGCACCTCGAGGGCAAGGGCGAATTCAGCACACTGGCGGCCGT<br>TACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTGTACACCTA<br>AATAGCTTGGCGTAATCATGNCATAGCTGTTCTCTGNGTGAAATTGTN             |
| Ornithine aminotransferase   | M11842   | NTTTCACNCAGGAACCAGCTATGNCCATGATTACGCCAAGCTATTTAGGTGNCACTATAGAATAC<br>TCCAAGCTATGTCATCAAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGG<br>AATTTCGCCCTTCTGCTGTGAGAGGGAAAGGGTTGCTAAATGCCATCGTCATCCGAGAAACCAAG<br>ATTGTGACGCCTTGAAGGTGTGCTTGGCAGCTCCGAGATAATGGGCTTCTGGCCAAGCCAACCAT<br>GGTGATATCATCCGGCTTGGCCCTCCACTTGTGATCAAAGAGGATGAGATCCGGGAGTCACTGGGA<br>GATCATCAACAAGACCATCTTGTCTTCTGAGAGTAGGAAGTCTGGGGAGCCATCTTCAGATGGG<br>GCTCTTGTGAACTCTGCTTGGGATGGGCAGATTCCGGCTTGTCTGTCTCTTAAAGACAATTTTT<br>TGAATATGTATTATATATTTCAGTTGATGCATAGTGGAGTGACACCTAGGAACCTGCAGGTGGCT<br>CGGTGACACAAGAGTGAGAGCGAGAGGCATCTCTTTGTTAAAGTTTGACTGTGTGGGAGCTTTCT<br>AAGGAGAAACAGATCTATCTGCATACAGCTGCAGAGTCTGCCGTAATAAGGGCGAATTCGCA<br>GATATCCATCACACTGGCGGCCCTCGAGCATGCATCTAGAGGGCCAATT       |
| Ornithine decarboxylase      | J04792   | TTTGAGAATTGGNCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAAT<br>TCGCCCTTATCGCGGGATCCCATCGAGAACCACCATGGGCAGCTTTACTAAGGAAGAGTTTGAC<br>TGCCATATCCTCGATGAAGGTTTCACTGCTAAGGACATTCTGGACCAAAAATCAATGAAGTTTC<br>TTCTCTGATGATAAGGATGCTTTCTATGTTGCGGACCTCGGAGACGTTCTAAAGAAGCATCTGA<br>ATGTGGCTGAAAGCTCTTCCCCGTGTTACTCCCTCCTATGCTGTCAAGTGTAAATGACAGCAGAGCC<br>AGATGAGCACCCCTGGCTGCCATTGGGACAGGATTGATTGTGCAAGCAAGACTGAAATACAGTT<br>GGTGACAGGACTTGGGGTGCCTCCAGAGAGGATTATCTATGCAAATCCTTGTAAGCAAGTGTCTC<br>AGATCAAGTATGCTGCCAGTAATGGAGTCCAGATGATGACTTTTGACAGTGAAATTGAGTTGATG<br>AAAGTTGCCAGAGCACATCCAAAGGCAAAGTTGGTTTTCGCGATTGCCACTGATGATTCCAAAG<br>CAGTTTGTCCGCTCAGTGTTAAGTTGGTGCCACACTGAAACCANCAGGCTTCTCTTGAACGG<br>GCAAAAAGAGCTAAA  |
| Osteopontin                  | M9252    | TTGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTTCG<br>GCACGAGGCAGGACAGCAACGGGAAGACCAGCCATGAGTCAAGTCAGCTGGATGAACCAAGCGTG<br>GAAACACACAGCCTGGAGCAGTCCAAGGAGTATAAGCAGAGGGCCAGCCACGAGAGCACTGAGCA<br>GTCGGATGCGATCGATAGTGGCGAGAAGCCGGATGCAATCGATAGTGGGAGCGGTTCGGATGCTA<br>TCGACAGTCAGGCGAGTTCCAAAGCCAGCCTGGAACATCAGAGCCACGAGTTTCACAGCCATGAG<br>GACAAGCTAGTCTTAGACCCTAAGAGTAAGGAAGATGATAGGTATCTGAAATTCGCAATTCTCA<br>TGAATTAGAGAGTTTATCTTCTGAGGTCAATTAAGAAGAGGCAAAACCACAGTTCTTACTTTG<br>CTTTAAATAAAAACAAAAAGTAAATTTCAACAAGCAGGAATACTAACTGCTTGTCTCAGTTCA<br>GTGGATACATGTATGTGGAGAAAGAAATAGATAGTGTTTTGGGCCCTGAGCTTAGTTCTGTTGTTT<br>CATGCAGACACCAGTGAACCTAGAAGTTTCAGCATTTTGGCTTCTGGTCTTCTGTGCAAGAAAT<br>GCAAAATGGNCACTGCATTTTAAATGATTGCTATTCTTTTATGAATAAAATGTATG |
| p53                          | X13058   | TTGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAAT<br>TCGCCCTTTCGCGGGATCCAGGCAGACTTTTCGGCACAGCGTGGTGGTACCGTATGAGCCACCTGA<br>GGTGGCTCCGACTATACCACTATCCACTACAAGTACATGTGCAACAGCTCCTGCATGGGGGCA<br>TGAACCGCCGCCCCATCCTTACCATCATCAGCTGGAAGACTCCAGTGGGAATCTTCTGGGACGG<br>GACAGCTTTGAGGTTCTGTGTTGTGCTGTCTCTGGGAGAGACCGTCGGACAGAGGAAGAAAATTT<br>CCGCAAAAAAAGAGCATTGCCCGGAGCTGCCCCAGGGAGTGCAAGAGAGCACTGCCACCA<br>GCACAAGCTCTCTCCCCAGCAAAAGAAAAAACCCTCGATGGAGAATATTTACCCCTTAAGATC<br>CGTGGGCGTGAGCGCTTCGAGATGTTCCGAGAGCTGAATGAGGCCTTGAATTAAGGATGCCCG<br>TGCTGCCGAGGAGTCAGGAGACAGCAGGGCTCACTCCAGCTACCCGAAGACCAAAAGCTTGGCCA<br>AGGGCGAATTCAGCACACTTGGCGGCCGGTACTAGTGGATCCGACTCGGTACCAAACTTGATGC<br>ATAGCTTG   |

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| Pancreatic secretory trypsin inhibitor type II (PSTI-II)                   | M27883    | GNNNNCTNCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGC<br>CAAGAATTCGGCAGGAGGCGATGAGAAGACCCAGTGAGCGAGAAGGTCACCAAGTGTGTAGTG<br>GGTCCCTGGTGGAAAGACGGCCATGTTTCTCTGCTCTGACAGTTGACGAGACATATGTCCCAAA<br>GAGTTTAAAGCTGAGACCTTACCTTCCACTCTGATATCTGCACACTCCAGACAAGGAGAAGCA<br>GATAAAGAAGCAAAACGGCTCTCGCTGAGCTGGTGAACACAGCCCAAGGCCACAGAAGATCAGC<br>TGAAGACGGTGATGGGTGACTTCGCACAATTCTGTGGACAAGTGTGCAAGGCTGCCGACAGGAT<br>AACTGCTTCGCCACTGAGGGGGCCAAACCTTGTGTCTAGAAGCAAAGAAGCCTTAGCCTAAACACA<br>TCACAACCATCTCAGGCTACCTTGAGAAAAAAGACATGAAGACTCAGGACTCATCTCTTCTGT<br>GGTGTAACCAACACCCTAAGGAACACAAATTTCTTTGAACATTTGACTTCTTTTCTCTGTGCC<br>GCAATTAATAAAAAATAGAAAGAATTNGNNCAAAAAAAAAAANANAAAAAGNGNGGGG  |
| Pancreatic secretory trypsin inhibitor type II (PSTI-II) (alternate clone) | M27883    | GNNNNNTCTATGACATGATTACGAATTTGAATACGACTCACTATAGGGAATTTGGCCCTCGAGGC<br>CAAGAATTCGGCAGGAGGCTGAAGAGAAGCACCCCTGCACAGTTCTTCTGAGTTTGGACCTAGGT<br>CTACAACCATGAAGGTAGCAATTTATCTTCTTCTCAGTGCTTTGGCCCTGCTCAATTTAGCAGGT<br>AACACTACAGCTAAGGTGATTGGGAAAAAGGCTAATTGCCCTAATACACTTGTGGATGCCCCAG<br>GGATTATGATCCTGTGTGTGGTACTGACGGAAAACTTACGCCAATGAATGCATTCTATGCTTTG<br>AAAAACAGGAAATTTGGAACATCTATCCGCTTACAGAGGAGAGGGCTTTGCTGAATAAATGCATCTGAACAT<br>CGAAATCTTTTAGGGCTACCATAATGTTTAGCAAGAAGGTTTGTGTAATAATGCATCTGAACAT<br>AAAAAAAAAAAAAAAAAATCTCGCGCGCGCAAGCTTATTCCCTTTAGTGAGGGTTAATTTTAGC<br>TTGGCACTGGCCGCTCGTTTACACGCTCGTGACTGGGAAAACCTGGCGTTACCAACTTAATCG<br>CCTTGACGACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGA   |
| PAR interacting protein  | U83590    | CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>CGGCACGAGGGCTTTCTTGGGCATGCTTCAAGGCAAGCAGCAGAAGCTGCAGCAAAACCTGCAGC<br>AAGGGAATCACTCGTCTGGCTCCAGTCCGCTCTACGATCTCTACTGGCAGGCCATGAACCTTGCTT<br>GGAGTGACGCGTCCAAAGTCAGAAAAGAAGGATTTCTTGCCAGAGACCAAGAAGCGAAAGAACTTAAAT<br>CATTAGCACAAAGCGGAAGAAAAAGGATTCTTGCCAGAGACCAAGAAGCGAAAGAACTTAAAT<br>CTGAGGGTACCACATCAGAAAAGAAGGCTGCATCACAGCAGGATGCAGTGACAGAGGGTGCCATG<br>CCTGCTGCCACTGGTAAAGACCAGCCCCCAGCACAGGCAAGAAAAGAAGAAAGAGAGTGAAGGC<br>TAACACCCCATCCAGGTGAATGGAGTAACCTGTGGCCAAAGAGTCCGGCTCCCAATAACCCCAACC<br>TGAGTCCCAGCACCCCCCTGCCAAGACCCCAAAAGTGCAGAAGAAAAGAGAAGCTGTACAG<br>GTGAATGGATCCACTCCTGTGTCCCCCGTAGAGCCTGAAGCAAAAAGCATCAGAANGCTCTCA<br>GCACAAAGGAGGTCAAAAAGAAAGTCTCCAGTCTGGCCTGNCAAAAAANA |
| Peroxisomal 3-ketoacyl-CoA thiolase 2                                      | M32801    | GAACCAGCTATGCCATATTACGCCAAGCTATTAGGTGCACTATAGAATACTCAAGCTATGCATC<br>AAGTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTCGCGG<br>GATCCCCGTGTCTCAGGATGAGGGTGTCCGCCCCAGCACCCATGGAGGGCTGGCCAAGCTGA<br>AGCCTGCCCTCAAGGATGGAGGCTCTACCAGGCTGGAACCTCCAGTCAAGTGAGTGATGGAGCA<br>GCCGCCGTCTGTGTCGCCCGGAGGTCCAAGGCTGAAGAAGTGGGCTCCCATCTTGGCGTCTT<br>GAGGTCTATGCAGTGGTTCGGGTCCCTCCTGACATCATGGGCATCGGACCTGCCTGTGCCATCC<br>CTGGCGCTTGCAGAAAGCAGGGCTGACTGTGAATGACATAGACATCTTTGAGATCAATGAGGCC<br>TTTGCAAGTCAGGCCCTCTACTGTGTGGAGAAGCTGGGAATTCCTGCAGAGAAGGTGAACCCCT<br>GGGGGGTGCAATAGCCCTGGGCCACCCCTGGGCTGCACCGGAGCAAGGCAGGTGGTCACGCTGC<br>TCAATGAGCTGAAGCGCCGAGGCAGACGGCTTATGGCGTGGTGTCCATAAGTTGGCCAAGGGCG<br>AATTCGACATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCAATTC |
| Peroxisomal multifunctional enzyme type II                                 | NM_024392 | TACATGATTACTACTTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGC<br>ACGAGGCCCTCGTGCCGAGAGACCTGGGAGCCATTGTGAGGAAGCGGAATCAGCCCATGACTCC<br>CGAGGCAGTGAGGACAACCTGGGTGAAGATCTGTGACTTCAGCAATGCCAGCAAGCCGAAGAGCA<br>TTCAAGAGTCCACAGGTGGTATAATCGAAGTTTACATAAAATAGATTCAAGGAATCTCACAA<br>AATCACACCGGTCAAGTGGCATCTGCAGATGCATCAGGATTTGCTGGCGTCTGTGGCCACAACT<br>TCCTTCATTTTCTTCTCATATACGGAAGTGCAGTGCATTATGTATGCCCTCGGAGTAGGAGCTT<br>CAGTCAAAAATCCAAAGGACTTGAAGTTGTTTATGAAGGGAGTGCTGACTTCTCTGTTTGCTT<br>ACATTTGGAGTCATTGTGCTCAGAGTCTTGTATGAGTGGAGGCTTAGCAGAGGTTCTGGGCT<br>GTCAATCAACTTTGCAAGGTTCTTATGCGGGAGCAGTACTTGGAGTTGTATAAGCCACTTCCCC<br>GATCAGGGGAATTTAAATGTGAAGCAGTTATTGCTGACATCTGGATAAAGGCTCTGGCATAGT<br>GATTGTTATGGACGTCTATCTTATTCTGGCAAGGACTTATATGCTATNATCAGTTC     |

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| Peroxisome assembly factor 2                     | D63673 | TTNGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGACGGAGTTGTGTC<br>TCAGCTCTTAGCTGAGCTGGACGGGCTTCACAGCACTCAGGATGTGTTTGTGATCGGAGGCCACCA<br>ACAGACCAGACCTCCTGGATCCTGCCCTTCTGCGGCTGGCAGATTTGACAAGCTGGTGTGTTGTA<br>GGAGCAAGTGAGGACCGGGCTCCAGCTGCGCGTTCTGAGCGCCATCACAGGAAAGTTCAAGCT<br>GGAGGCTCTGTGAGCTGATGAATGTGCTGGATTGCTGCGCGCTCAGCTGACCGGCGCAGACC<br>TCTATCTCTCTGCTCTGACGCCATGATGACCGCCCTCAAACGCAGGGTCCGAGACCTAGAGGAA<br>GGGCTGGAGCCTCGAGCTCAGCACTGTTGCTCACCATGGAGGACCTGTTGCAGGCGCAGCCCG<br>GCTGCAGCCCTCAGTCAGCGAAAGCTTGCCCAAGGGCGAATTCAGCACACTGGCGGCGCTTACT<br>AGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTATAGTGTACCTAAATA<br>GCTTGGCGTAATCATGTCATAAGCTTGTTCCTGTGTGAAATTGGTATCCGCTACAATTNCACA<br>CAACATACGAGCCGGAACATAAAGTGTAACCTGGG        |
| Peroxisome proliferator activated receptor alpha | M88592 | TTNGATTGCGCCCTCTAGAGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCG<br>CCCTTGCGCGGATCCTACGGCAATGGCTTCATACCCGAGAGTINCTAAAGAACCTGAGGAAGCC<br>ATTCTGCGACATCATGGAACCAAGTTTGACTTCGCTATGAANTTCAATGCCCTNNAAGTGGATG<br>ACAGTGACATTTGCCCTTNTGNGGCTGCTNTNATNGCTGTGGANATCANGCCTGGCCTTTAAAC<br>ATAGGATACATTNNNAAGTTNCA  |
| RCT-10   |        | TCTCTANNACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGA<br>ATTTCGGCAGGAGGAGGATAACACCAAGCCAGGCTTCACTTGTCTCCATACTTCTCTACGGT<br>TTTTGAGGTTAACTGTTGTTAAGTGTGAAGTGTTCCTTAGAATAAGAGCTTAGAACTGTCTTCT<br>AACAATTTCTTTCTGATGACTTGGAGGGACAACGTAGGGGCAGATCTTGCAATCACTGAACTGT<br>TCATCTCTGAGCCTCAATTATAGCCCTCCACAGTCCCCACACTATCAAACATGTAACCTAGTT<br>TTAATTATCCAGCATGGTGATGACTGCTTTTCTGCTCAATACCACTTTCTTCATGGCCACTATT<br>TAATCTATCCATTTCTTGCTTCTTAAAATACTTCTCAAGGTACCTCAGGATGAAGTGATAAGTT<br>AGCTTTTGTGTACATGTGCCATTCTTCATGGTTTGCCCTCAACAAATCATTAAACCAATACTCTAGC<br>CATTAATTCAGATACAAATAAATCCTTAGACAAAATATTTACAAAATGGTTTTTGACCCAGAAAT<br>CAAAGGATCTCCAATCTGAAAGTGAATAGACTCTTGCCCTAAGTAGCCTTACCTATTATTGCA<br>AAATATGTTATTCTTTCTTTTGACAGCATTTCTC       |
| RCT-101  |        | CTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCGGCACGAGGACCCTGCCCCATAACCTTTCCTCTGGTCTCTTCTCCTCTGCTTCTCCTTCCCC<br>ATCTTTGTACCTGTTCTCTCTGCTGCTGCCCCATCCTCAGTAGCATCCCCGGTGCTGCTGGCC<br>CCTGCCCTCAGCAGTCAAATTCAGAGAGCAGTCCAGGCGGCTGGGCTGACTCCTGAGACCCCCGC<br>AGAGATCTTGGCCCTGGAGCACAAGGAGACACGCTGTACCCCAATGCGGAGAGGAGATGACTGGA<br>CACAGATGCTGCGGGACACGATTGAGGCCCTGTCCCTGCGCTGGAAAGGCTGTGTAGAGAACACC<br>GCAGAATAGCCAGGCTGGAATGGGTTTGAAGACTTTTGTCCAGGGACGGCTGGGACAAGATGGC<br>TCAGTAGTTAAGAACTTTTGTGCTCTTCCAGGAGACCCAGTGCCCATGTGAGAAGACTCACACT<br>ATCTATAACTTCAGCTGTAGGTTTTTTGACACCTCTGACCTCTGTAGGCAATGCACTCATACACA<br>GATACACATACCTATATGTAATTAATAAATAAAGATAAGCCTTCTTTTCAAAAAAAAAAAAAA<br>AAAAAAAAAAAAAAAAATGNGGGNGGNCNAGCTTN   |
| RCT-102  |        | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGTGAAGATGAAAAGCAAAACAACCTTTTGTATAAGCAAGGTATAGATTTTACATTT<br>TTGTCTTGTCTCCCAATGAAATGGATAAAACAAAATAAAATCTGACAATGCCGTCTCTTCACGGA<br>ATGTTGTGTGTTAGCCGGACTGAAAGCCCACTTAATTTTTATATAACGTCTTTAGCTCTTCCT<br>TTGACAGGGCAGGCCCTTGTCTGAACTGTTTGCCTCTGACTGTTAGACACCAATGACGCATGC<br>ACTGTCCCTCTCATTCTCTTGTCTTCCCTCTGGCCTGAGTTCTTGTGCATCTCTCCCTACCCC<br>CACCTCTGTTAGGTTAGATATACAGCTATGTAATAGAGCAAGGAAACGGTATGTGCAATTTGT<br>GGCATTTACGNAGAGTTGCAGTTGTACGCTGCTGAAAACGCANGCTTTTGTAAACATGTGGTCTT<br>TCCATAAGTACCCNATGTATTTTAGNCTATTTTAGTCGTATTGNTCNATAAAATATGCAAGCTA<br>TANGGTAACANANAACAAANAAAAANACCNNTGCGGCCGCCAAGCTTATTCCCTTTAATGAG<br>GGGTTAAATTTAGCTTGGGCTGGCCGCGGTTTAAACAANGNCC |

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| RCT-103 | TTATNACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGCTCCGCTTCCCGCTTCTCTCGGGTCCCTCGTTTTGAGACAATGTTTCATTATT<br>TAGTGCTAACTGGACCAGAATCCTGGTGTGGAACAGTCTGGCTTCCAGTTACAGATCTTCCGA<br>TCTCTGCCTCTCCAGGGCTGGGATTTCTTTAAAAAAGAGATGTGTGGGT<br>GTCTGGCATCTTAGGAAACCAAGCAGACAGGCGCGCAGACATATACAGACAAAACACCCATA<br>GAAAGCCAAGTGGAGGGGTGGGGATTTAGCTCAGTGGTAGAGCGCTTGCTTAAGAAGCGCAAGG<br>CCCTGGGTTCGGTCCCGAGCTCCGAAAAAAGAACAAAAAAGAGAAAGGAAAGCC<br>AAGTGGAGTGTGATGATGGCCACCTGCAATTCAGTGCACAGGAAACAACTAAGGAAATTCCTCG<br>GAGCAAACTGTCTAGCCAGACTACTGAAATGGNGAGTCTATCTANAACCTGATTAGTGAAGAA<br>TGTGGANAGTCATGGAGGAAAACAACTATGTCACCTCGGNAATTNCATATACCCGTGNGCAT<br>ACCTGNGNAATTTTCANAACATTCATTACATTGCATTGCC   |
| RCT-108 | TTTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCACGAGGGAGCGGCCAAAGGTTTTTTTTTTTTTTTGTCTTAAGTATACTATTAAATGAA<br>TTACATTTGTAAAGTTATCTCTAGTTTTTCTTTTCTTATTCATCACTTTTGTGGCAATTCATAC<br>ATTTTATTTGTAATATATTAAGTATTAGGGGTAGGGAATGAACCACTGTACTATTCCAATGTTT<br>ATATTTAATCTAATTGTGAGAATTGAACCTTCTGAAAATTCATGGTAAACAAATGTCTAAAGG<br>TTTATTTCTTAAACAGGAGCTTCATGAGTAACTGATGTTTTAATGTAATGGTCAGTAAACAC<br>AAAAATGATTATCTAAAGAACACATGAAAAGCCACATCTCGGGGCTGGGGATTTAGCTCAGTGGT<br>AGAGCGCTTACCTAGGAAGCGCAAGGCCCTGGGATCGGTCCCGAGCTCCGGAAGAAAGAACCC<br>NNNNAAAAAAGAGAAACCTTTGCGGCCGCAAGCTNATTCCTTTAGGGAGGGTTAATTT<br>TANCTTGGCACTGGCCGTCGTTTTACACCGTCGTGACTGGGAAAACCTGGCGTTCCCCANCTT<br>AATCC   |
| RCT-109 | TCTCAAAGTGATTTTCCCAAGNATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCACGAGGGAGAAGCTACTAGGCATGTCAAGCAGTCAGCAGGATTTGTCTTCATGGTCTTCT<br>GCAGATGAGGTGGACACGTCCGGGTGCTAGTGTCTTACATCAGGAAGAAGTACCCCAACAGACA<br>GAAATCGGTCCACAAAGGTGGCTCCGATTCCTCCCTTTCTAAACAGGCCAGCACGGGCGGTC<br>GAGATTTCTTGTTCGGGTCTCAGGGCAGCTCTTCCGATTCAGTGTCTCTACTACTCTTATC<br>GGACTCACCTCCCGTGTACCATATACGGAAGAAGACTACAGCTGTGCCCTCTCCAACAACTTTGC<br>CAGATCGTTCCATCCCATGCTCAGATATACCAACGGTCTCTCTCCCTCTGAAGCAAGCACAGT<br>GCAGGCAGCAAGAGGGGAAGCAGGTCCAAGCAACCCAGGCTGTGAGAGAAGGTGTGATCTTGG<br>CAGAGGTATCATATGGCAGCTTCGGTTCTCCCTAACCCGTGTATAAAGAAAGGAAAAAAGC<br>CTTTGGGACATGGGACAGTAAACAAACAGGAGGCAACAACTTGTAAATGGTACAGTGNCTAT<br>TTGANACTCTGAGCCCTTAATACTAAAAGAAATTAAGGACATATANGGTTCCCTANAACCCATG<br>AAGTCTTGGGCCC |
| RCT-111 | AATCCCAANCCCGGAAGGTAAGTTTAAACCAATCCTTTTGTGTNACATTCAAGGAATGNA<br>GGGCACAAGAGCAGTTAAGTAACTTTGCCCAAGGCACACAGCCAGGGAAGGGTGGGCCAAGGCA<br>AGAGTGGACCAAGGTGTACCTTGAGAGTCCATGCCCAACCAAGGACCCCTTGTCTCTCTGGC<br>TCCCTCATTTGAGAAGCAGGCCCGCCATTCCACCCGACTCTGCAGCCTACCTAGTCTGAAAGAA<br>GAGCTAGTTAAATGGGAACATATTAAGTCAAAAGTCAAGAGTCCAGCAGGAAGGAGACTCAGGCAG<br>GGAACCCCTGAAGAGCCTATTGTGTGCTAAGGCTGCAGCTCATATTGGCCCTCCGTGGCTGTGTAG<br>AAGTCTCCAGCACTGACTGCAGGAACTCAAAGGTAGGCCGCTCCTCAGGTCCGCCCTCGCCAGCA<br>CTCAGTGATGACGTATGGTACAACCTCAGGCGGACATGTCTCTGGGCATGGCATTCCGGTAGCCAT<br>GCTCCAGGCTACGGATGACCTCAGGGTTGCTCATTCCTGGGTAGGGAACACGCCCATATGTGAC   |
| RCT-12  | CNTTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCCGGCACGAGGCTGAATTCAGGTCACTCAATGATAAGTCTTCGACTTGCCCAATGTTAGTCC<br>TGCATTCTTAGCTCTTAAGAGATGCAATGACACTTACTGGCTATTCTTGTCAAGTTGGATGCGG<br>TAGCGGGAGATGAAGGTGGGTTTTCTGTCTGTCCACCATCAGTAGAAGGCCATTGAAGCCCCA<br>GAAGCACAGCCCCGGCACGAGGACAACCTGAGGCAGAGAGCAAGGGACTTAGAGCAGCCCCA<br>GGTACCACAGTGGCTCACCAGGAAGGAAATGAACAGGCACATGGATCTGTCTCTGTCTGGTGA<br>CTCAGTGTTCAGTCTTAGCTATGGAACCTGAACAAGTCACTAAGTGTCTGTATTGTCTGTCT<br>TGCTCTGTCTGTCTCCCTTTGCACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  |
| RCT-126 | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>CGGCACGAGGCGACTGACTATGTGGATGAGATCAAAAGATCTCCCCAAAGGAGTAGACATCGT<br>CATGGACCTCTGGGTGGTTCGGACACTGCGAAGGGTACCACCTTCTCAAACCATGGGCAAG<br>TTGTCACTTACGGAATGGCAACCTGTGACGGGCCCAAGCGGAACCTGATGGCCATGGCCCCG<br>ACCTGGTGGAAATCAGTTCACTGTGACAGCTCTGCAGTGTCTGCAGGCCAACCGAGCTGTGTGCGG<br>CTTCCACCTGGGCTACCTGGACGGTGTGGTGGAGCTCGTCAGTAGAATGGTTACCCACCTCTGG<br>CTCTGTACAATCAGGGCCACATCAAAACCCGAATCGACTCAGTCTGGCCCTTCGAGAAAGTGGCT<br>GATGGCATGAGGCAGATGCAGGAGAGAAAACATAGGCAAGTCTCTTGGTTCTTGGGCTGTAG<br>AAGGAGACCTAGGGCCAGCGGCTGAGGGCCCTGGAACAGGAAAGGGGAANATGGGAANTCTGT<br>TTGTGTTGCCACCAACCTCTCACATTTCTCTGTCTATGATGCTCTACCTCCCTCCCCAAAAA<br>GGTCTCTGTCTGTATGACTGCTTCCTGCTCTGANCTTGTCTCN                                     |



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| RCT-127 | NTNNNTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCC<br>AAGAATTCGGCAGCAGGCTGTTTGTGGTGTAGGGACAATGGCGCCATTGTTCTTCGCGCTTCAA<br>AGCAGTTTCAGAGGAAACAAAGATGGCGGGAGCTCAAAGCATCCGAGAGAATTCGTGAAGGGA<br>GGAAAGTTGCTTAAACTTGACCATGTTAAAGTTCTTACTCCTGGCAGTCATGATACCTTCTGC<br>CAGCAGTGAATGCCAGCCATTGAGATGCCCGTCTCTGGGAAGCTCCTGGAGCAGAAATGCATG<br>GCCAGTGAGAGGAGACTTCTTGCGAAGGAAAACCTGGATGTGGTGTATGTTAGAAAAAGCAGACAC<br>AAGAAGCAAATACAGAGTATTAGTACTGGGATGTTTGTAGATGGGGTCTGCATGGCCCTTGCTGTG<br>TCCCTCTTAAACTGTCTAGTGGATGGGACAGCATCTGGTATGGCCTGCAGAGTTGAGCCTTGTGT<br>ATACCTTTTGAAGGCTCTATGTTAATGTATGACAGAGTGTCTATTCTGGGAAGGTTATGGGTGA<br>GCTGAGGATACAACCTTACAGACTAGCACAAATGAGTGACAAATTAAGTAAAAAAGGCAGTTTAC<br>ATTTTATTGTTATGAATTGNTTCCTTATTCATCCAACAGTGATCACTTGGGAGTGCTGCAATA<br>AACT   |
| RCT-128 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGACAAGAATTC<br>GGCAGCAGGATACTATTAGACCAAGCAGCTCTCAAGTGTTTAATGTCTACTGTGACACCCAATCA<br>GGCAGCTCCACGGACATTAATCAACACCGGAAAGATGGCTCTCAAAACCTCAACCAACCTGGGA<br>AAACTACGAAAAGGTTTGGGAGGCTTGATGGAGAATTCGGTTGGGCTAGAGAAGATCTACG<br>CTATAGTCAAACAGTCTAACTACATCTTACGACTGGAGCTACAAGACTGGAAGGACAGCAAGCAC<br>TATGCTGAATATTCCTTTCATCTGGGCAATCATGAAACCACTACACGCTACATGTGGCTGAGAT<br>TGCTGCCAATATCCTTGAGGCCCTACAGAACACAGAGACCTGATGTTTCTACATGGGATCACA<br>GAGCAAAGGGACAGCTCTACTGTCCAGAAAGTTATTCAGGTGGCTGGTGGTTCAAGTACATGTGT<br>GGAGAAAACAACCTTAAATGGTAAATACAACAAACCCAGAGCCAAATCCAAACAGAGCGGAGAAG<br>AGGAATCTCCTGGAGGCCCTCGGGCGGAAAGCTCTACTCTATCAAATCATCTAAATGATGCTCC<br>AGCAGACCACCTAAGGAACGTGAGTGAACCTGAGACAAATTTAAAGACCAACACATTCAATATTA<br>AAATCC |
| RCT-129 | TTATGACATGATTATGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGGTGATGGTGGTGTATGATCAGTGCCTGCTGAGCCACTAGAAGCTGTGACCCGCT<br>CCTTTCATCAGCCGACACAGCCAGGCCGAGGAGAGACGACGAGGACTGTCTCGGAAGGATGC<br>CTCTGGCCGTGCGAGAGCAGCGTGTGAGCGGAATGCCGAGCCACAGGTCTATGCCCCACCTCG<br>GCCCCACTGACCGCCTCGCTGTGCCCCCTTCGTCCAGCGGAGCCGTTTCCAGCCACCTACCCCT<br>ACCTGACGACGAAATTCGCCCTGCCACCCACCATCTCGCTGTCTGATGGGGAGGAGCCCCACCC<br>TACCAGGGCCCCCTGCACCCCTCCAGTTACGGGACCCGAGCAACAGCTGGAGCTGAACCCGAGCTC<br>TGTGCGCGCCCCCAACCGGACCATCTTCGACAGTGACCTCATAGACAGCAGCATGTGGGGG<br>GCCCCCTGCCCCCAGCAGTAACCTCGGCATCAGCGCTACCTGCTATACAGCGNGGGCGCATGG<br>AGGGGCTCTCCACCTACAGTGAGGTGATGGTCACTACCGGGCTCTCCTTCAGCAGACCA<br>GCAAAGTNAANGGCACTCCTCT  |
| RCT-137 | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGGTGATCTCGGTTCTGCGCCACCATGGGGAAGCGACAGCACCAGAAGGACAGATG<br>TACATCACCTGTGCAGAGTACATCATTTCTATGGTGGCAGGAAGCCAGATATCACACAGACAAG<br>TTTTCGCCGCTTACCTTTTGACCATTCAGTCTCTCTCTCCAGCCTTTTGTCTACCCAGTCTGCA<br>CCCCGGAAGGTGCTGCTTTCGACTTGTGTAACATGTCCCATGGCTTAAGAAGTATGGGACCGAT<br>CCGAGCACTGGAGAGAACTTGATGGGAAGTCCCTGATTAAAGCTGAACTTTGCAAAGAACAGTGA<br>AGGGCAGTACCACGTGTCAGTGTGTAAGTCCGTTTCACTGACAACACCCACATCGTGGCCATCA<br>GGACAACCTGGCAATGTCTACACCTATGAGGCAGTGGAGCAGCTAAACATCAAGGCCAAGAAGTTG<br>AGGGACCTGTAACTGATGAGCCCTTTTTCAGGCAAGACATCATCACCTGCGAGGACCCACCAA<br>TCTGGACAAATTTTAACTGACGAGCTTCTTCCATGTAAAGAATAACATGCGAATGATAGATCCA<br>GATGAGGAAAAGGCCAAACAGACCCATCTTTNTATTG                                     |
| RCT-138 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGGAGGTCTGGCCACCATGGGGGCCAGAGCCCTCTGGTGTCTTCTGTTCTCTCTG<br>TCCTCTGACTGTGGGAGGATTAAGTCCCGTACAGGCCAGAGTGGTAAGCCATAACACCCCTGG<br>TCTTTCTCTCTCTCTCAAGATTTCTCAGGCTACCCCTTTTCTCTCTAGCTCTCTCTCTG<br>TAACGCCGAGCCCTGATTGTTAACCCTGTGTCTCCCTCTTCATCCTCTGAGACAATTACCCAGGA<br>TGCGAATGTTCTCTGTGAGCCCGGTGTACTGGCTGGGATGTGCTGGGCGACTTGGTGTGAC<br>TCTGCTCATCGCCCTGGCGGTGTACTCTTGGGCCGCTGGTCTCTGAGGCCGAGGACTGCAG<br>ACGGGACCCGAAACAGCACATGGCTGAGACTGAGTCACTTATCAGGAGCTTCAGGGTCAGAGG<br>CCAGAAGTATACAGTGACCTCAACACACAGAGGCAGTATTACAGATGAACCCACCTATGCCAC<br>CAACAACCTGATGCCCGGATCCACTCATTCCAGACGCTTACTCAACAACCCCTCCCTGGGATCAG<br>GACTCCCGCTGGAATAAATATCCACAGAATGGCCTCTGGGAGATAT  |



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| RCT-139 | <p>GNGCTAAGNNTATGACATGATTACGAATTTAATACGACTCACTATANNGAATTTGGCCCTCGAGG<br/>         CCAAGAATTCGGCACGAGGAAAGGTTTTTTTTTTTTTTTTTAAATGATTCTTAAACAGGCCA<br/>         TCTGAGTAGGAACTGTAGGTTTATAAAATACATGGNAACTGAAGTTTCTGAGATGGGACTTGCTC<br/>         TGTTAGCCAGGCTGATGTGGCTGGTGCCTTGCCANCCTAGGGAGGAGAGAGATGTGTANATTT<br/>         CCTAGGACATGTGGCCAGCCAGCCAGCCTGCTCAGGGACCCACCTGCCCTCCATCGTCCAGGCGC<br/>         TGATTACCCATATGTCATGGTAGGTTCTAAATTTGAATTCAGGCCCTCAGGCTTGCAAGTTAAACA<br/>         TGACATGAGCAGTCTCCCTGGCCCACTGGTTTCATGTGATCCCTAAANGCATTTCCTTTGGCAT<br/>         ANTAATCATGTTTGGACAATGCTACCATCCTTTGGGTATAAACTTACATGGTTTCCCGGATATT<br/>         TTGTTTAAAAATGTGAATATTCTAAAAATGTTTAGAGACTCNTTCNTACAATTTTCTATGATCAA<br/>         ATATTTTNCATAAGTAGAAAATAAACTTTTCNGANTAAAACCTCTGTAACCTTGGGGGNNNNNTNNNC<br/>         NNNCCCNNNNNCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCCCTTTGGNCCCCAAGGNTTTT<br/>         TNCNTTT</p> |
| RCT-14  | <p>CNNCTNNNTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAG<br/>         GCCAAGAATTCGGCACGAGGATTAGGCACGCCCCGGAGTGGGCAAAGACTGGCACGAAGGCACT<br/>         CTTGCACATGCGCACACAGTTAACTTCTGAAAGGAAGTCGGCTGGCGCGGCGGAGGCCAGCGCC<br/>         ATCTTGTAATGGCAAAGCTATCCCGCTTTCCACGTGGGGCACAGTGGAGGCAAGCCGCATCTT<br/>         GTGGTGGTGAATGTTATTGGCGCTCTCCACAGGTCCTTACTTGGGTTTAAAAATCATTATGTAT<br/>         GTGCTGGTGTGTATGTGTATATGCCACAGCCCAAGTGTAAAAAGAAGAGAAAAATTTGTAGGAA<br/>         TAAGATGGGCATTTCAAGGATTGAACCTCAGATTATTAGGTTTAGCAACAACCACTTTACTCAG<br/>         GAGATAATTTCTCTGGCATTCAATTGTAGTTCTGAGAAAGTGTATGAGCAAATGTTTACTCAGAA<br/>         TAAATTAACAAATTAACAAAAAACAGTAGTCTGGGTTCGGTCCCGAGCTCAAAAAAAGAAAAA<br/>         AAAAAAAGCAATTCGCGCCGCAAGCTTATCCCTTTAAGGGAGGGTTAATTTTAGCTTGGCAC<br/>         TGGCCGTCGTTTTACAACGTCGTGACTGGGAAACCTGGCGTTACCCAACCTAATCCCTTGCAG<br/>         CACATC</p>              |
| RCT-140 | <p>TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br/>         GGCACGAGGACCGGGAAGCCCCAGCCTGTGATGGTAACCTGGGTGAGAGTCGATGACGAATGCC<br/>         TCAACATGCCGTTCTGTCTGGGCCGAATCTGTTTCATCAATAACCTAAACAAAACAGACAATGGTA<br/>         CTTACCGCTGTGAGGCTTCCACACAGTGGGGAAAGCTCATTCAGACTATATGCTGTATGTATAC<br/>         GATCCCCCACAATATCCCTCCTCCACAACAACCACCACCACCTACCACCACCACCACCAC<br/>         CACCACCATCCTTACCATCATCAGACACACCAGGCGACGACAGAACCAGCAGTTCACGATTCTC<br/>         GAGCAGGTGAAGAGGGCGCCATTGGGGCAGTGGACCACGCGGTGATTGGCGGCGTCGTAGCCGTG<br/>         GTGGTGTGTTGCCATGCTATGTTTGTCTCATCTCTGGGCCGCTATTTTGCCAGACATAAAGGTAC<br/>         ATACTTCACTCATGAAGCCAAAGGAGCCGATGACGACGAGACGACGACACAGCTATAATCAATG<br/>         CAGAAGGAGGACAGAACTCCGAAGAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTGTT<br/>         CCAATGANGTGTCCAACNGGCTGCTTAGATGATAAAGAGACAGTGATNCTGGGAAAAA</p>                                     |
| RCT-141 | <p>ATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCG<br/>         GCACGAGGAAACAACTCCAACTCTGAAACAGCTGAAGTGAATCCAGCTCATGAAGATGCAGAT<br/>         GGAGGTGAAGGAGAAAAACCTCTGATTTCCAGGCCCTCTGTCTATCCCCACTGCTGTTCAGG<br/>         AACCGATCTCTTGGTTGAGAGACTCAATCCAGGCATTAACATCCATCCCATGTTTTCAGATGAGA<br/>         CCAATATATGCAATGGTAAGCCAGTGGATGGACTGACCACTCTGCGCAACGGGACGTTAGTTGCA<br/>         TTTTCAGGTCATTATTTCTGGATGCTGAACCCATTTCAGACCACCATCTCCACCACGAGAAATCAC<br/>         TGAAGTCTGGGGTATTTCCCTCTCCCTTGACACAGTTTTTACTAGATGTAACGTGAAGGAAAAA<br/>         CTTTCTTCTTTAAGGATCTCAGTACTGGCGCTTTACCAACGATGTAATGGATGCTGGGTATCCT<br/>         AAATAATTGTCAAAGGCTTTGGAGGACTAACAGGGAAGATAGTGCTGCTTTCAATAGCCAA<br/>         GTACAAGGACAGACCTCAATCTGTGTACTTCTTCAAGANANGTGGCAACATCCAGCAGTACACTT<br/>         ACNAACAGGAGCCCCGTGANGAATGCACAGGGAGGCAGCCTGNCATC</p>   |
| RCT-142 | <p>TCTCCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAG<br/>         AATTCGGCACGAGGCTCTGGGGTACTTCTATGAGAGATACGAGTGCTACAAGGTTCCAGAAT<br/>         GGTGCTTAGATTACTGGCATCTTCTGAGAAAGCAGTGTATCCTGATTACTTTTCCAAGAGAGAG<br/>         CAGTGAAGAACTGAGGATGTGGAGCTGGGATCGGGAGGTTAAACAGCTGGAGGAAGAACGTC<br/>         ACCTGATGGTATTATGACTGAAGCTTTGCCTCCTGCCAGAAAGGAAGGCGACTTGCCCCATTTGT<br/>         GGTGGCATATTGTGACCAGACCTCGGGAACGGCCACATAGAGACAGGCACCGCACTGTTTCATGC<br/>         TTGCAAGTGAGAGTTACAGAACACATTCACACTTGCCCTAATAAAAGTAACCTAGAGACCANNNA<br/>         NAAAGAANNAAAAAAGAAAAAANGTTGTGNGGCCGCAAGCTTATCCCTTTAGT<br/>         GAGGGTTAATTTTANCTTGGCNCCTGGCGCTGTTTTACAACGTCGTGACTGGGAAAACCTTGGCG<br/>         TTACCCAACCTAATCGCCTTGCAGCACATCCCCCTTTCCAGCTGGCGTAATAGCGAAAANGCCC<br/>         GCCCCGATCGCCCTTTCCAA</p>  |

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| RCT-143 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACCAGGTGATGTACCGCTGAGCTCGTCACTGCTGCCCGGGCCTTGGCCAGGCCATGCGC<br>ACAGGACATCTTAATGGCCAAAGCCTTCATAGCAGTGCAGTGGCCGCTACGTACAAGTATGTGAA<br>TATGAAGGCACAGGAACCTTGATGTGGACATGAAGCTGCGACTGACAGTGCAGTTCGGATTCTGA<br>TGTGGACAGAACTCTTCCGAGGCCTGGGCATGACCTAAGCTACCTCTTTCCGGAGCCCGCCACC<br>ATCAACTACCCCTTTGAGAAGGGCCCACTGAGTCCGCGCTTCCGTGGGGAGCATGCACTGCGCCG<br>CTACCCGTCTGGGGAGGAGCGTTGCATCGCCTGCAAGCTCTGTGAGGCCATCTGTCTGCACAGG<br>CCATCACCATTGAGGCTGAGCCAAGCAGATGGCAGCCGCGGACTACACGCTATGACATTTGAC<br>ATGACCAAGTGTATCTACTGTGGTTTCTGCCAGGAAGCCTGCCCTGTTGACGCTATCGTGGAGGG<br>CCCCAATTTTGAGTTCTCCACCAGACGCATGAGGAGTTGCTGTACAACAAGGAGAACTACTC<br>AACNATGGTGGACA   |
| RCT-144 | TTATNANATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>CGGCACGAGGATTCCCTTTCAGGAGGTAAATGAAAAACCTAAGAAGAAAAAGCTAAAACCCCA<br>GGAAACCTTACAGGAAAAATGGAATGGAAGACCCACCTGTCTCTTTGCCCTAAAACCAAGAAAAAGA<br>AAGCTTTTCCCAAGGAGGAGTTGGCCAGTGATCTTGAAGAGATGGCTACTAGCAGCATAGTGT<br>CCTTAAGAAAAAGAGTCTTACCTAAGAGGAAGTGGCCAGTGAACCTGAAGAGGCGCAAGCCC<br>CATCACCCTTAAGAAGAAAAGGAAATTTCTGAGGAGCCTGAGGCTGCTGCAAGCTGCACAAAGA<br>GCAGCACAAAAGAAAAAGAAAAAGTCCGAGAAGGCCCGGGAGGAGGATTAGAATGGACCTGCTTGG<br>TGGGAGGGGCATACTTTATGGTGGCAGTTCTCTTCCCATGATAAACCCCAATAAAAAACGAAA<br>ACCCGAAAAANNANANNNNNNAANN<br>CAAGCTTATTCCTTTAGTGAGGGTTAATTTAGCTTGGCACTGGNCGTCTGTTTACAACGTCGT<br>GACTGGGAAAACCTTGGCGTTCCCACTTTATTCGCTTGCAGCACTTCCCTTTCCGCCAGC |
| RCT-145 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACCAGGGCCGAACCTCGCGGGGCGGGAAGCCGCGAGATGGACACCCCTCCGCTCTCAGACTC<br>GGACTCCGGGTCGGATGAGTGCCTGGCCTCAGATCAAGAGTTGCAGGATGCGTTTCCCGCGGAC<br>TCCTAAAGCCAGGCCTCAATGTCTGTAGAGAAGCCGAAGAAGGCGGTGAATGACGAGAATGGC<br>CTGAAGCAGTGTCTGGCTGAATTCAAACGGGATCTGGAGTGGGTTGAAAGGCTCGATGTGACCCT<br>GGGTCTGTGCTGAAGCCAGTGAAACTCAGTCAACACCCAGAACCAAGGACCAGAAGAAAGGTG<br>TTAATCCAGAAGACGACTTCCAGAGGGAATGAGTTTCTACCGCCAGGCCAGGCTGCTGTGCTT<br>GCAGTATTACCCGACTCCACCAGCTCCAGTCCCTACGAAGAGGCCCACTGATTATTTGCGAGA<br>AATGGCCAAAGTCTGATCAACAGATGCAAAAGATTTCGACAGAAGCTGCAGACTAAACAGGCTGCCA<br>TGCAGAAATCTGAAAAGGCCAAGCAACTTCGAGCGCTTAGGAAATACGGAAGAAGGTGCAAACT<br>GAGGTCTTCCAGAAGAAGCAGCAGGAGAAAGCGCATATGA                     |
| RCT-146 | GGGGGGGCTCNANATGATTTCGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCA<br>AGAATTCGCGCAGGAGGACATCTGTAGCTGGGAGTCAAGTTAANGTGGTCTCTTCTGCGCAACT<br>ATGGTTTCGGACCAAGCAAACTACGTCCNGGAGCCTACAGNNAGTGGTGGCTTCTCAAGCCCC<br>TAGGAAGGTGCTTGGCTCCTCCACCTTTGTACCAATTTCTCCGGTTCGTCNAGAAAAGCTGAAA<br>ATAAGTATGCTGGAGGGAACCCAGTCTGTGTGCGCCCACTCCCNANTGGCAAAAAGGNATCGGN<br>GAATTCCTTCAAGCTGNCCCTCANGATTCTAANGGATAAAACCNAGATTCTNTGTANANGCCCGNGG<br>CTGNGGCNTTTNAAAATNCNATANTNGATNAC  |
| RCT-147 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACCAGGCTCAAATGTATTTAATTAAGTCTGAGCCTTCTCTTCCAGTTTCTAGACCAACACTG<br>CTCACCCCTGCCTACATCCCTGGCCCAAGAGGAACTGTATAAGGCCTCTGGGCTCCCGTGGGGG<br>AGGGCCCAGGAGCGGCAGGACCCCTGTGCCTAAGACACCACCAGAACCAGAAGGAACAGACCCG<br>ATAAACAGATCTCTGCACCCAAATCCCGTGGGAGGGAGAGCTGAACCTTCAGAGACGCGACAAAG<br>CCTGGGAAACCAAGAGACTGCTCTCTACACACACATCTCGGACATGGTGTGGCCACCACCCAC<br>GTCTCTCTCTGGCCCTGGAGCCCCAGTGGGCTGCATCACCCACCGCTGGTGCCTGTGATGGCT<br>GTGCCCGAGCAGGCTCAGGCAGCTCTCTCACCCACTGCACCTGCCATCACACCTTCTGTGGAGC<br>TACTTAATAAACACAGCACACTGTGAAGTGTTTTAAATCCAAAAAAGGCTGAGGCTGAGGCTG<br>AGTTGTGCGGCCGCAAGCTTATTCCTTTAGTGAGGGTAATTTTANCTTGGGCACTGGCCGTG<br>TTTTACAACGTCGTGACTGGGAAAACCTTGGCGTTTCCCAACTTGNGGGGNGNGNGG        |
| RCT-148 | TTTTTTTTTTTTTTTTTTTTTTTTTTTGGAGGAAGGTTTCAGCATTTTATTTCTTGGTGTCTCCAGGA<br>GCTCACTTAAGAATGGCACAACAACAAGCAAGGTAGTAGTGAGTACTGCTCTGCACTTCTCGA<br>TGGTCTCATCATGGCCTTGGAGAGTTGGGACCCAGAGCAGAGCGAAGCTAGGCTCTCAGAAGGA<br>GGACCCCGACTGTGGAGGAAGGCCTTTAGGGCTAGCCTTCAGATCCAGATGTCAGAACTGCAATC<br>ACCCCTGGGTAACGAAGCTCATGAGCCAGTGTGGCCCAAGAGGCTCTTTCCCAAAGTCCACCA<br>GAAAGTTGGGGTTCAACTTCAGCCCTCCATTTGCTGTATCTACATCAATTTGCAGCATCACAGAG<br>CCTTCCTAATGAGATTAGGGTAAACTGCTTGTCCAGGCGCTGTACAGTGTAGTGTAGTACGTA<br>AAGACGCTTCCCATCAAGCTGAGCTGGATCATCTGAGGACCTCCAGGAACCTCGTTTTCCTTGA<br>CCACTAGGGGCTCCGGCTG   |

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| RCT-149 | CTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCGGCACGAGGGGCGCGCTACTCGGACATGAGAAAGGCCAAGTGGAAAACTCAGACAAATAC<br>TTCCATGCTCGGGGGAACATATGATGCCGCCGGAAGGGGTCTGGGGGAGCCTGGGCTGCTAAAGT<br>CATCAGTGATGCCAGAGAGGGTATTAGAGATTAACAGGACACGGAGCAGAGGACTCAAGAGCTG<br>ACCAGTTTGGCAACAAGTGGGGCCGGAGTGGCAAAGACCCCAACCACTTTCGACCTGCTGGTCTG<br>CCCAGGAAATACTGAATTTTCTCTTCATGTTGTTCCCGGGCGCACAGCCCCCAAGGAAAGGGGC<br>AATTTACTGAGTTGAGTTATTTCTAAACCTGGATCCCTAAACATCCCAATGTGCTGAATAAATG<br>CTTGTAATGCANNANANNNAAAAAAAAANNAANAAAAAAAAANAAAAAAAAAAG<br>TGAGCGGCGCGAAGCTTATTCCTTTAGTGAGGGTTAATTTAGCTTGGCACTGGCCGCTGTTTT<br>ACAACGTCGTGACTGGGAAAACCTGGCGTTACCAACTTAATCGCCTGTCAGCANATCCCCCTT<br>TTGCCAGCTGGCGTAATACCGAANAGGCCCGCCCCGATCGCCCTTCCACAGTTG           |
| RCT-151 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGCAGGGGCTGTTGAAAGGGCTGGGCCCCGCGGCCCTTTGAAATGGTGTACTGGACAGGA<br>GACATCCCTGCCCATGATGTCTGGCAACAGTCTCGACAAGATCAGCTGAGGGCCCTGAACACCAT<br>CACAGACCTCGTGAGGAAGTTCTTGGGCCCCGTACCGGTGTACCCTGCTGTGGGCAACCATGAGA<br>GTACTCCTGTCAATGGCTTCCCTCCCCCTTCATAAAGGGAACCAAGTCTTCACAATGCTTTAT<br>GAAGCCATGGCCAAGGCATGGGAACCTGGTTACAGCTGACGCCCTTCACACCTGGTCTACCG<br>CATGAGGGCTGATGAGCAGCTCTCCAGACCTTCTGTTTCTCTACCAATAAGGGCCACCCACCTT<br>CAGAGCCCTGCGGCACACCTGCGCCCTGGCCACTCTGTGTGCCAGCTCTCAGCACGTGCAGAC<br>AGCCCTGCTCTGTGTGCGCACTGTATGCCAATGGGAGCCTCCAGATGCCCATAGCTGTGGTC<br>ACGGCCCTGCTGTGTGCTAGTGTGGGAAAAGTTCACATATTAGCAAAGGGATGGATTCTGTAGTAT<br>CGCTGATCTACCTGAGGCAANCTTTTCNGGGAAGGAGGGGGGGGGNGN         |
| RCT-152 | TCCNAAGTGATTNTGCCNANAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGATGGGTTTCGGAGACCTGAAAACCCCGCGGCCCTCAGGTGCTCAACGATTACCT<br>GGCGGACAAGAGCTACATTGAGGGGTACGTGCCATCACAAGCCGATGTGGCAGTATTGAAGCAA<br>TCTCTGGTCCACCACCCGCTGACCTGTGTCTGCTCTGCGTTGGTATAATCATATCAATCTTAC<br>GAAAAGAAAAGGCCAGCTTGCCGGGAGTGAAGAAATCTTTGGGCAAGTATGGCCCTGTCTAGT<br>GGCAGATACCACAGGAAGTGGAGCAGCAGATGCTAAAGACGATGATGACATTGATCTCTCGGAT<br>CTGATGATGAGGAGGAAAGTGAAGACGCAAGAGGCTACGAGAAGAAGCCTTGCTCAGTATGAG<br>TCAAAGAAAAGCTAAAAGCCTGCAAGTTGTTGCGAAGTCTTCATCTTGTAGATGTGAAGCCTTG<br>GGCAGATGAGACAGACATGACGAACTTGAGGAGTGTGTCCGAAGCATCAAGCGGACGGCTTGG<br>TGTGGGCTCCTCTAAATTGGTTCCAGTGGGATACGGAATTAAGAAAGCTTCAAATACAGTGTGTA<br>GTTTGAAGATGATAAGGTTGGAACAGATATGCTGGAAANANCANATTACTGCTTTTT |
| RCT-153 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGATGTAAAGAAGCCATAAGAAGGCTGCCTGAGAACCTTTATAATGACAGAATGTT<br>TCGAATTAAGAGAGCCCTAGACCTGTCTATGCGGCATCAGATCTTGCTAAGGATCAGTGGACAA<br>AATATGAGGAGGACAAATTCTACCTTGAACCTATCTGAAAGAGGTTATTGGGAAAGAAAGGAG<br>AGAGAAGAGTGGCGAAGAAGTGTCTGTAGTTAAGATCTGTGGGTGCGCCTGGTCTCACCTTA<br>TTTTATGACATTGTTTCAACCTGAATCACAACCTAAGAATCATTTGCTCTACACATGCCCTCACTT<br>TAAATAAATGTCTATTATAACCGTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG<br>CTTATTCCTTTAGTGAGGGTTAATTTAGCTTGGCACTGGCCGCTGTTTTACAACGTCGGGACT<br>GGNAAACCTTGGCGTTACCCAACCTTAATCGCCTTGCAACACATCCCCCTTCCAGNTGGCGTAA<br>TANCNAANAGCCCGCCGCTTCCCAACAGTTGCGCNAGCCTGAATGNCNAATGGGAAC<br>NCNCCCTNTANCGGCGCNTTAAGCCGCGNGGNGNGNTGGGCCCCCCCCNTGNCCCC        |
| RCT-155 | NCTCNAACATGATTACGCATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCGGCACGAGGATACGAGAGACCTGTTCTGCACCTGGTGTCTCAACACGCCGGTGGCTGGG<br>GACATCCGAGCAGATTTCCAGTGTTCACAGCAGGCCAGGGCTGCAGGACTACTGTCCACCTCCG<br>AGCGTTTCTGTCTACACACTTGCAGGATCTCTCCACAGTTGTGCGGAAGGCAGAGAGATTAGTC<br>TTCCAATTGTGAACCTCAAGGGCAAGTGCTTTTAAACAACGGGACTCAATATTTTCTGGTGAT<br>GGAGGTCAATTCAATACACATTCGATATACTCCTTTGATGGTGGGACGTGATGACTGATCC<br>TTCCTGGCCGAGAAAGGTTGTTTGGCACGGCTCCAACCCCAAGGTGTCCGCTCGTGGACAAGT<br>ACTGTGAAGCCTGGCGAACACGGACATGGCAGTAACAGGATTTGCCTCCCCACTGAGCACAGGG<br>AAGATTCTGGACCAGAAAGCATATAGCTGTGCTAATAGGCTAATCGTTCTGTGTCAGAAAACAG<br>TTTCATGACAGACGAAGGGAAGTATAACCTCCCCATGGTTCTTAAAGAATATTCTAATATTT<br>CTTATGTGAAAAGTTGACACTGNAATCTAAAAAANNNNANNNNATNNANNNNNNTN        |

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| RCT-158 | ANGACATGATTACGAATTTAATACGACTCACTATAGGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGGCAAGCGAACAGGGTCTAGCAAAGAGGAGCTACGGANACAGACAGACATTTTAAGT<br>TTTCCAAAGAATCATCACCTTCTGCCGAGGTGCGTTCTCATCCCTGGACACAGCTCCGCTAAC<br>CCANCCGGACTGTCTGACGAGTCAGGCATTTGGTCCACCAAATGCCGGTCTCANAGTTGCGCTG<br>AGACCAATTGAAGGCACCGCTGGCGGCTCCCGCTGACATCCAAGCTCTCCTGCGCCGGCACCT<br>TGCAGGCGCTCTTGGGGGGGCGCGGGGTCTGTAGTAGAACTCGGGCAAGCTGCCCTCTCCACC<br>TCCTGCCACTCGTATCTGCCCTCCAGGGGCTTATGATTCTGAAAGTCGAAATTCACCTTGCCTG<br>CTCGCTTCTTCCATATCTCGGCAGTGCTTCTCCAAGTCCCGGTTAATCTTCATGATTGACCG<br>GGCCGAANAAGTTTCTGCANGCGAAGGCTTGGGGTGCTCGGTTTGTCTGGCGTTCATCGCTCC<br>AGGCTCGGGCTCCGTANACACTCTCACGTTTGACATCTCTCTCCCGGGCGGGNGTGACACCG<br>CCTCTNCTCTCTCCGAAAAAAAAAAAAAAAAAAAAAACATTGCGGCCNCAA             |
| RCT-161 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGGAGGGCACTGGGTAACCTGGCCAGCAACCTTCTCTGAAGCTGAATCAAAAATAA<br>ATAGGAGAATATGGCAAGTGCAGACTGGGGATATGAAAGCAAAAATGGTCTGACCAATGGAGCA<br>AACTATATCCCATTGCCAATGGAACAACAGTCTCCTATTGATATTAACACAGCGAAGCCAAA<br>CATGATTCTCTCTGAAACAGTCAGCGTCTCTACAATCCTGCAACTGCAAGAAATTTGTAA<br>TGTGGGACATTTCTCCATGTAGTTTGTATGACAGTAGCAACAGTCAGTGCTGAAAGGTGGCC<br>CTCTTGCTGATAGCTATCGGCTCACCCAGTTCATTTTCACTGGGGCAACTCAAACGACCATGGC<br>TCTGAACACACCGTGGATGGAGCCAAATATTCTGGAGAGCTTCACTTAGTTCAGTGAATTCAGC<br>CAAGTACTCCAGTGCTGCTGAAGCCATCTCGAAGGCTGATGGGCTGGCAATCATTGGGGTTTTGA<br>TGAANGTGGGTCCAGCCAACCNAACTGCANAAAGTACTGGATGCCCTAANCTCAGTTAAAC<br>TAANGGAAACNANCCCCATTCCNCAATTTTGACCTTCCAGTCTCCTTCTCT                   |
| RCT-162 | ATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCG<br>GCACGAGGAATTTAAGCATATTAGTCAGCGGAGAAGCTTCGGCGAGCAGAAGTGGACTTGGAGCG<br>CGTGCGGGTGTGGTACAAGCTGGACGAGCTGTTGAGCAGGAACGTAATGTTTCGCACAGCCATGA<br>CCAACAGAGCAGGATTGCTTGCCCTGATGCTGCACCAACCATCCAACAGATCCACTTACTACC<br>GACCTTCCGCTCTAGTGCTGACCGCTGAAAGTCCAGAGCCAGAGCCTCTCAGCCCTGCATTCAGT<br>CAGGGAGGGGCTCTGCATTTACGCTCGCTCTTCTCCTCGTTTCTGTTTATTTCTACCACCTTAG<br>TTTTCTTCTTACCATCCATGTTTGGCTTCTGTTTGGCCCTTATCAGAAGGGTCTCTGCTTTCCT<br>TTGTCCTCTCCATAGTCAGTGCTGGGTGAAAGTCAAGTTTACTCAGCCTTGCCATACCCCTCC<br>CCCAAAATAAACAGGTTTGTGTTAAATAAAATTTTGAACAAGATAAAAAAAAAAAAAAAAAAAAA<br>ACAATTGCGGCCGCAAGCTTATCCCTTTAGNGANGGTTAATTTTACTTGGCACTGGCCGTCGTT<br>TTACAACGTCGTGGACTGGGAAAACCTGGCGGTTACCCAACCTAATCGCCTTGC |
| RCT-164 | NNCNAATCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCC<br>AAGAATTCGGCACGAGGATCTTACTGCCAGTTGTTCTGGCATTTCGAAAAAGGACTGTAGACTA<br>TGGTCTAATGTTCAAGGATGTGGATGGACAGGACTGTGGAATAAGTGAGAACTGGTTCTCCGC<br>TGGAGGAAGTAGGGTTAGGTTTAGGACCTTTGCAAGTGGGGGTCAGGCACACCACAGGAACAGC<br>TCCTTCGATAAAATAAACAGTTATCACATTTCCACAACAACCTAAACACAGACTACCTCTTCCT<br>TACCAGATCTGCTAAGCTGTGAGGTTCTAAGAGGTTCTGAGTGTTGTTTAAACTTTTGGAGATG<br>GTTTTTCATTATAACAATTCAAGCCAGACATTTGAAAGTGACTGTTCTTATAGTGTCCTCAAGTC<br>TACTAAGTGGGGCCACCTTCTAGTTTCTAGTTGCACCTTCTGAAATCCCATGTTTGTGTTGCTG<br>GGACCTGAGTTTGGTGCTTTTAAATACAGATGAGATCAATTTATCCGACTTTCATGAGTNATCC<br>TNCATTTCTCTCGAGAAAAANCTGATTTTCNATGTNAATTAATTGTACTATGACC  |
| RCT-165 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGATTAAAGACAGGGGGGCTACCTGAACAAAGCTGCAACCTCCTGCCCATTAGGAT<br>CCTGCTTACATCTTGTGCTGCTGCACTCTGCCGTGGAGTCGGCCATCGCTGCAGTCCACAGGC<br>TGGTGATGTGGCTCCCTGATATCCATGAAGATATCCAGTGGCTACAGTGGGCAACATCCAGGTG<br>TGTGCCGAATGACCATGTGCTGCTCCCTCTACCAGATCCAGAGCATCCAAGGATAACCATCA<br>AACACTCAAGCATGGATATCACCATCTCTCCACAACCCCAAGGCAGCTCTGCCGGTTGTAA<br>TTGCTGTGCTCCGTGCTTCCGATGAATTTGGGCATTCTCCCTGTGGATGGTTCCAGGAGAGGCCA<br>TAGCTGAAGGCACCTGCTTCCACCCCAAGTCCAGTTTGACCTTTATCTAGAGCAACAGTGTCT<br>AGATGATAGGTGGGTGGGGGTGCTGTCTCTGTTTCCCTCTGGGAAGGGTCTGTGTTAACTTTT<br>GGAGGCAGCTAGGAATTTCTCTTCAGGAGCTGAGCCTGTGACGCTGCCCCCTTGGTGCTGTGTG<br>GTAACCTCATTGC  |

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| RCT-166 | CTTCANATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGCGCGTTCAGCTGCTTCTGCCCTGTGTCCACCGAGGCAGTTCACCCGAGGCCGATC<br>TCCGAGGTCTGCCAGCGGCTACTTCCCACAGCCTCCGCCATGGGTCTGGAGCTCTACCTGGACCT<br>GATGTCCAGCCCTGCCGTGCCGTCTACATCTTCGCCAAGAAGAACGGCATCCCTTCCAGCTGC<br>GTACCATCGAGCTGCTTAAAGGTCAGCATTACACTGATGCCTTTGCCAGGTGAACCTTTGAGG<br>AAGGTGCCGGCTTTGAAGGATGGGACTTCGTCTTGGCAGAGAGTGTGGCCATCTTGTGTATTT<br>GAGTAGAAAGTACAAGGCACCTGACCACTGGTACCCTCAGGACCTACAGACCCGAGCTCGTGTGG<br>ATGAGTACCTGGCTTGGCAGCACACAGCCCTGCGGAGCTGTGACAGCAGGGCCATGTGGCAGAAG<br>ATGATGTTCCTGTGTTCTGGGACAGCCGTTCTCTGAGAGGTTGGCATCCACCTTTGGCCG<br>AACTGGATGGATGCCTGCAGATGCTGGAGGACAAGTTCTCGCAGAACAA   |
| RCT-171 | CTATGACATGATTACGAATTNATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGCTTTCCATCCATATTACCACCTGTTATTTCCCAAGCCAGCTCCACCCCTCTA<br>CTGTTACCAAAACCCACCTGATTCCCAAGCCACCTGGATTACCACCAATCTTCCACTNCTTTC<br>TAACTGTNTATTGCTATTATGCTTAGGTTCAGCATTTGGATATATGCACGCTGATTCTTAAATGA<br>TCAAGTCTCTCCACAAAGAGACTGGGCAACCTTATCATCTGCAAAGGTAACAAAGGCAAAAGCT<br>CTGAATGGTTTGGGAATGAAGACATCTACCACTTCTCCATACTGACAGAAGAACTGCTGAAGCTC<br>TTCAGCAGTCATGCTCTGTACACGTCCAAAAAAACCTTTGCGGCCGCAAGCTTATTCCTTT<br>TAGTGAGGGTTAATTTAGCTTGGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCT<br>GGCGTTACCCAACCTAATCGCCTTGCAGCACATCCCCCTTTCCGACGTGGCGTAATAGCGAANA<br>GGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGGAATGGGACGCGCCCTGT<br>ANCGGCGCATTAAGCGCGGCGGGTGTGGTGGGT  |
| RCT-177 | CCNNNNNNNCTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGA<br>GGCCAAGAAATTCGGCAGGAGGAAGCCTCGGGGAGGAGACAGCTCTGTTCCGTTTGTGTTCT<br>GGTGAAGAGTGTGGGATTTTCGTCCTGGCTTCAAATCCGTCCTAAGCAGCACAGCGGTCAAAT<br>CTCCTGCAAGTCTCAGATTACCACTGACTAACTGCACCTAGGCAGACCAGCCATGAGAGCCAC<br>TCAGCAGGACTTCGAAAATGCAATGAACAGGTGAAACTCTTGAAGAAGGACCCAGGAAATGAAG<br>TGAAGCTGAGACTGTATGCGCTGTATAAGCAGGCCACAGAAGGACCTGCATATGCCTAAACCA<br>GGTGTGTTTGACTTTGTCAATAAAGCCAAGTGGGATGCATGGAATGCTCTGGGCAGCCTACCAA<br>GGAAACTGCCAGGCAGAACTATGTGGACCTCGTATCCAGTTTGTAGTTCTCATCTGAAGCCTCGA<br>GCCAGGGAAGGGTGGAGCTGATGGGAAAGCCAGGAGTCCAAGGCACTNCTGGTAACGTGTA<br>NGTGGCATCACAAGATCACGTTCAATCGCCCTTCAAAGAAAGCAGCCATAACCTTCCAGATGTAT<br>CAGGATATTACTCGCGCTTAAGAATGCCAGCAGGATGACACAGTNCATCACCGTTTTCACAN<br>GAGCTGGTGACT                                  |
| RCT-179 | TCCTCATAANATGATTACNAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGA<br>ATTCCGCACGAGGGTTCGCGGAACAGTAGGCAGTTGTTTCCGTCGGCTTCTCTCACACTCAA<br>GTGCGCGCCTCCACCTCATGGAAGACTCGATGGACATGGACATGAGCCCTCTTAGGCCCTCAGAAC<br>TACCTTTTCCGTTGTGAACATAAGGCTGACAAAGATTACATTTAAAGTGGATAATGATGAAAA<br>TGAGCACCAGTTATCATTAAGAACGGTCAGTTTAGGAGCAGGGGCAAAAGATGAGTTGCACATCG<br>TAGAGGCAGAAGCAATGAACATGAAGGCAGCCCAATTAAGTAACACTGGCAACTTTGAAAATG<br>TCTGTACAACCAACAGTTTCCCTTGGGGGCTTCGAAATACACCACCTGTGGTCTTGAAGTTGAA<br>GNGTGGTTCTGGCCCTGTGCACATAAGTGGACAGCACCTAGTAGCTGTAGAGGAAGATGCANAGT<br>CANAAGATGAAGATGAGGAAGATGTNAACTCTTAGCATGTCTGGAAANAGATCTGCTCCCGGAG<br>GTGGTAACAAGTCCCACAGAAAAAAGTAAACTTGATGAANATGATGATGATGATTTTGATC<br>GATGAGGATGAATGAANATGATGATGATGATGATTTTGATC  |
| RCT-18  | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGAAGTTATACGCCCTGGGAATGGCTGCCCAAACTGAAATCATTTTCTGGACCAA<br>GGCCAAGAAAGCTATATGTGTGAATCCTACTGCCAGATGGTTACCAAAAGTATTAATTTGTCC<br>GAAGCAGAAGTATTACTTCAACTCCCCAAGCTCCAGTGAGTAAGAAAAGAGCTGCCTGAAGCCAC<br>TGTCACCCCAAAAGAACCTGCACCTTTCTTAACTCCCTGCTCGGAATCTTAGTGTTACGTTCTTA<br>GTTGAAGAATTTCCAAGAAAATAACTTCCCTCTACAAACACGGCTGTAGATTAAGAAAGAAAAAT<br>CCTGCAGTAGCTGAGAGGAGACACTCGAGCTCCTTCCCTACTCAACCCATATTCTTGTCTCTTA<br>AGGGAGGATATTTTCGAGCAGGCATTTAGTGACAAGCCACTTTGGTAATAGACCTGTTGTGTAGT<br>GTTAAACTATCTTAGACCTAGAGGAATAAAGCATACATGTGCAATCTGAACCATAGCTCCTACT<br>AACAAGAGGTTTATGAGATGGAATTCAGTTAGTTTGCACCTTGCAAAAATCAGGCTTCCAGAAT<br>AGTTTCCAGAAAGTCCCTAAGAAGCAGACGCATTACCAGCCTAAGGNGANGCAGAGCAGGTCTCC<br>NTTAGAGAGAATCTTCTGGAGGGAATAATGNTTN |

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| RCT-180 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGGTGGTGGCCAAAGTTCAACGCCTCGCAGCTCATTACCCAGCGGGCTCAGGTGTCTCTGTTGATCCGAAGAGAGCTGACAGAGCGTGCCAAAGGACTTCAGCCTCATCTGGACGATGTAGCTATCACAGAGCTAAGCTTCAGCCGAGAGTACACAGCTGCTGTAGAAGCCAAACAAGTGGCCAGCAGGAAGCCCAGAGGGGCCAGTTTTTGGTGGAGAAAGCAAAGCAGGAACAACGACAGAGAATTGTGCAGGCTGAGGGGAGGCGGAGGCTGCTAAGATGCTTGAGAGAAGCACTGAGCAAGAATCTTGCTATAGCAAGCTCCGAAAGATCCGGGCTGCCAGAACATCTCTAAAACGATCGCCACATCAACAGAACGGATCTATCTCACAGCTGACAACCTTGCTGCTGAATCTGCAGGATGAAAGCTTTACTCGGGGAAGTGACAGCCTCATTAAAGGGTAAGAAGTGAAGTGTGGACATCAAGAACCCCCACCACAGAGAAGTTGGCACACTTCTCCAGTTTGGAGGGGCCAGCTTAGGGGGTCAAGCATACCCANCCCTGACCCAAGCATCATGNGATGGATTCTTCTGTATCTGCTCTCTTGGGATTAAANGGAACTGAAGAC |
| RCT-181 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGTGAACATCTACGTGCCACCGTGCGTGGGATTACAGCCAGACATCTGTAAGGACTACAAGGAACTGGCTTCTGTGGTTTTTGGAGACAGCTGCAAATTCCTCCATGACCGTTTCAGATTACAAGCACGGATGGCAGATAGAACGGGAGCTCGATGAGGGCCGTTATGGTGTGTATGAAGATGAAAATATGAAGTAGAAAGCGATGATGAGGAAATACCATTCAAATGTTTCATCTGTCGCCAAACCTTCAGAAATCCGTTGTGTACTAAGTGTAAACATTATTCTGCGAGACCTGTGCATTGCAGCATTTCCGTAACCACTCCACGGTGCTATGTTTGTGAGCAACAGACCCATGGGGTTTTCAATCCTGCCAAAGAACGATTGTCTAAACTGGAGAAATACCGAAAAGCGGAAGGTGGTACTTCTAACACTTCCAGAAGACCCGATGGAATCTAATTGCCTTTACTTAGATTTTTTTGCAATTGTCAAATCTCAAAGTACTTTTTGTTTTTGGTCACTTCAAACCAAGCAACCGTAATTGAAGAAATATTAAGTTTTCTAAGAAGAAATATCCAAATTTGTATTATATGACAGTGCTACAGATGGGAA                       |
| RCT-182 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGGTGAATGTCTCCAGCCAGGCTCCAGCGTGCACTGACCAACCATAACCGTCTACTGTTCACCAAGGGTGCTTTAGACATGTTGACCAAGGTGATGGCCCTAGAGCTTGGGCCCCACAAGATCCGTGTGAATGCAGTAAACCCACAGTAGTGATGACACCCATGGGCGGGCCAACTGGAGTGACCCGCACAAAGCTAAGGTCACTGCTGGATCGTATCCCACTTGGCAAGTTTGTGAGGTGGAGAACGTGGTANACACCATCCTCTTCTGCTGAGCAACCGAAGTAGCATGACTACTGGTTCCGCTTTGCCAGTGGATGGGGGCTTCTTGGCTACCTAAGCCCTCCCTACCAATACCTGCTCAACTCATGTTTCAGAACATCGTGCCCTCCATCCCTCCAATAAAGCTCTCTGCCAGCCTGTGTGCTGATTCTCCACCCCNANAAAAAAATTCACANNAANANANAAAAAAGTTTGGCGGCCGCAAGCTTATTCCTTTAGTGAGGGTTAAATTTTAGCTTGGCACTGGCCGNCGTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCCACTTAATCGCCTTGCGAGCANATCCCCCTTTTCGCC                        |
| RCT-185 | NCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGGTAAAGCTTAAGCTCCAGCAGACAGCTGCCTGAAGAAGGACTGGAAAAAGCCGGAGTGTACAATCAAACCAATGGGAGGAAGCGGAAATGCCCTGGCCTGCATCAAACCTGGACCCCAAGGGTAAAGTTCTAGGCCGGATGGTCCACTGCCCAATACTGAAGCAAGGGCTCAGCAGGAGCCTCAGGAATCCAGTGCAGTAAGATAGCACAGGCCGGCGAGGACTCCCGCATCTACTTCTTCCCTGGGCAGTTTGCCTTCTCAGGGCTCTACAATCCAATAAGCCCTGGACAGGGTTTCATCTTACTTCTCTGTACAGCCGTGGCGGTACCCACCATATGGCCTCCCAAAGACTTTCAACTCCAGGCTAATAAACTGTTCTTTTCCAAAAAAGGTGTGGCGGCCGCAAGCTTATTCCTTTAGTGAGGGTTAATTTAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTA CCAACTTAATCGCCTTGCGAGCATCCCCCTTTTCGCCAGCTGGGCGGNAATAANCGAAANAGGNCCCCACCNN   |
| RCT-192 | CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGGTTTCCGCTTGCTGCTCCGCCATGGCTCGCGGTCCCAAGAAACACCTGAAGCGTGTGGCGGCCCCACGTCACCTGGATGCTGGACAACTGACCGCGGTGTTTCGCGCCCCGGCCATCTGCCGGCCCGCACCGCTGCGGGAGTGCCCTGCCGCTCGCCATCTTCTGAGGAATAGGCTCAAGTACGCTCTGACCGGCGATGAGGTGAAGAAGATCTGCATGCAGCGCCTCATTAAAGTTCAGCGCAAGGTCA GAACCGATGTGGCTTACCCAGCTGGCTTATGGATGTCATCAGCATAGACAAGAGCGGTGAGAATTCGCGCTGGTCTACGACACCAAGGGCCGCTTTCGCGGTGCACCGCATCAGCCCGAGGAGGCCAAGTACAAGCTGTGCAAGGTGAGGAAGTCTTCGTGGGTACCAAGGGCATCCCGCACCTCGTGACGACGACGCGCAACCATCCGCTACCTGACCGCTCATCAAGGTCAACGACACCGTGAGATCTCGCTAGACAGCGGCAAAATCACCGATGCCATCAAGTTTGATACCGGCAACCTGTGCATGGTAACCCGGAAGGGCCAACCTGGGCGCATCGGC                                     |

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| RCT-193 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGTTTTTTTTTAACTTTTAAAGAAATACCTTTATACATCATGAAAAAGGTATCCAA<br>CAACTAGATTACACTTGTCTGAATCTATAAAACAAACAAACAAACAAAACTGAAAGTTTAT<br>TCATTAGACTGTATGTGGGTCATGTTCCACATGGGAACAGAGAGGCACAGGGCTTCTAAGTAT<br>TGCACAGTCTTGAAAAAAGGAGTTGGGAGGAGAGATCACATGATACTGGGAACGTCT<br>CACATTATGAGAACTACCAAGAAACATTGAAAAGAAAACCTCTGTTTCTACAGTAGCTTTAG<br>TCTGCACTTCTTGGAAAGACTATTCCATTGAAGACATCTTAGTAACAGGAAGCTTCGTTGAGCA<br>ATCCCATGTGCAAAATATTAATAGGAAATATATAAAATAAAAAACCTTTGCGGCCGCAAGCTTAT<br>TCCCTTTAGTGAGGGTTAATTTTAGCTTGGCACTGGNCGTCGTTTTACAACGTCCTGACTGGGAA<br>AACCTGGCGTTACCAACTTAATCCGCTTGAGCAGATCCCCCTTTCGCCAGCTGGCGTAATA<br>GCGAAAGAGGCCCCACCGATCGCCCTTCAACAGTTGCGCAACCTGAATGGCGAATGGGACGCG<br>NCCTGTANCGGCGCAATTAACNCGNGGGGTGNGNG                   |
| RCT-194 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGTTACAGCGTAAGCCACGACAAGCTTCCTAAGGTTTCAGTGTATGACCAGTGTGAA<br>AACAGATGGACAGTTCCAGCCACCTGTCCCCAGCCCTGGCGTTACACAGCCGAGCTGTGCTGGG<br>GAACCAAGATTTTATCATGGGTGGGATACAGAATTCTCAGCTGCTCTGTTACAAGTTCAACA<br>GTGAACTTACCAGTGGACCAAGGTAGGAGACGTGACAGCCAAGCGCATGAGCTGCCATGCCGTG<br>GCCTCCGGGAACAAGCTTTACGTGTTGGAGGATACTTCGGCATTTCAGCGCTGCAAGACGTGGA<br>CTGTTACGATCCGACTTTAGATGTGTGGAACAGCATAACCACGGTTCCCTACTCTCTGATCCCTA<br>CCGCGTTTCGTAGCACTGGAAACACCTGCCCTTCCTAATGCAGAGCAACCAAGGAGCAGAG<br>TGAGCTCACTCTGACACACAGAGATGTGTTCTGCTCTGAAGAAGGCAAGTTAATGAAGAGA<br>AAGAAAAAAGTGAAGCGCCGCAAGCTTATCCCTTTAATGANGGTAAATTTACTTT<br>GGCACTACCCGTCGTTTACAACGTCGTNGACTGGGAAAACCTGGCGTTACCAACTTAATCGC<br>CTTTGCA   |
| RCT-196 | TTTTTTTTTTTAAAACTGAATAATCATGTATGGTTATTTAGTACAATGATTATAACCTATAAT<br>ACAATAAACGTCCTCCATAACTAAGGAGTGATATGCCATGTATTTCTCAAAATTTGTATGAG<br>TATTTTATTAATGTCTTTGCTGTTCAAGTAACCTACTGCTTTTCTGATAATGGGAAGAAAA<br>AACATAAAGACAGGAAAAAGCTACTACCCCAACAGGAAGTCAAGGGACAATTGGGCGTTGTTC<br>TTTTGTAGAGGCAGTCTCAACTCTTACTTCCCTTCCTGCTTCAGGGCCACGTGGTTATGGCCTGC<br>AGCGCTGGAGAAATCTCGGGTACAGCACACGCTTCGGATGTGATACCTGTTCAAGATCCAGCTT<br>AGAACTGTTTCAAGCCCAAGCCTACCTCCGTGAGGACATGTACCATATTTTCTCTG   |
| RCT-197 | TTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCGGCACGAGGGGAGGTGCCTTCTGTGTTCTAGCCTTGGTGATCTTAGCAACTTTAAGCTGTC<br>AACAATATCTGATTTTAAAGATGTAGCAGTGTGGGAAGATGGTCATGGACCTTTAGATGTCCTAG<br>GAAGTGAAGTTTACAGACATCTAAACCACACGCTCTACACCACCATGATCCTGATGAAGTCAA<br>CGGCTGCGATGAAGTCAACTGCTGCACCCATTGCTTCCAGCAAATAGGAGAGAAATTAATTGCA<br>GTTACTAATAACATGACTGTTCCAGAAAAGCCCCCTTTGGGAAAGTTTGTGTTAGCATGATT<br>CAGAATAGTAGTACTCTTAGAAAGATCATGGATAAGTTCCAACAAGTTGAGCAAATTTATCAAG<br>AGTTAACTAGAAGGAAAAGAGAACTAACATTGAGCAAGAAACGAAAGAAATATAGAATGGTTA<br>CAAAAGTTTCTTTTATTCTGAGGGCCCATAGAGTTTAACTTTATTAAAAATAAGGTAAATGT<br>TAAATGTATATCTGGGTACCCACAAGTCTGGTAGTATAACTGCAGNTTCTAAACTATTGTTTGC<br>GGCTGAGAA  |
| RCT-198 | TTNACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCG<br>GCACGAGGGGAAGGAGAAGGAGCTGGTGGTGGCCGAGACAGTGAAGAAGTGAAGAAAGCACCTG<br>TTTTGGTGTGTCCACCTTACGAAGCCGAGCATACACCACCCAGTGATCTCCAGAGTCGCTTG<br>GAATCTCATATTAAGAAGTTCTTGGGTTCTCTCTTCTAATAATGGCAAGATATCTCCCTGG<br>ATGATGGACATGTGAAGTTTCAAGTCTTAGCAAAATTTAGCTGATGACTTAGGCCATGCAGTACCT<br>AACTCCAGGCTTACCAAAATGTGCAGGGTCAGAGATGTTCTTGATTTCTATAATGTTCTGTTCA<br>AGACAGATCTAAATTTGATGAAGTCAATGCTAGTAATTTACCTCCCAATTTGAAAATCAGTTGGA<br>ATTACTGAGCAGTCCAGTCAGAACACAGTGAGATCATTCTATTCTTCTATTGGGTGACTGACA<br>GCGAAGCTTTGTGAGATGTTACCTATTAGAAGTTGGTTGAGAACTTCCTTTTTTTTTTTCTTTCT<br>CCTTGGAGAAGACACATTTTTTTTTTCTCTCTGGAGCATCCACAAAGAAACATTATCACATTTGC<br>TAAAGCTATTATCCCAATAAAATCAAGTCTTGGTAATTATGAAAACATTTCTATTCTGGTAT<br>ATAGTCAGGGTTGTTGAGAGGACANAAAGTGGTAACATGN |



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| RCT-205 | CAACNNCNCNNTTATGNCATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCC<br>TCGAGGCCAAGAATTCGGCAGGAGGTGTGTGTAACTGGATCAGCAGCATGTGTCCAGTCATG<br>GTTGACCTTAGCAGACATTAGCAGGATTAACACTGGAGGGAACAAGAAGCAAAATAAATATTT<br>CCTCTGAGGTGGTATCTGCTGCTTGAAGTGTGTGTCATTGAACTTTGGACTTCAGAGGTTG<br>CCTTATTGCATCTGAAATTTCTGGTCTAAAGTGAGATCCGAATTTCTTTTGGCCACCTTCACGAA<br>AAAGTATAGAACCATATAGTTGGAACTTGTGTGGGTATGTCTAAACCTAGGAATAAATGCTG<br>GGTTTCTTTTCTGTTGTAAATTTAGTCAAGTTACTGTGAGGGAAGCTGTTAGGTACATTTTAAA<br>TAAATTACAGCAAAGCGCTATCCTTCTGATCACAGCCAAGCTAACATCTATCTCCGAACATCAT<br>GTCTGCCGCTGCTGAAAGGCTGTAANGGTCTGGGTAGTTTTTCAATTAATATTGATCAAAGAAGC<br>GTTTATTTATAAGNGCAAAGTGTTTTTTGGACGTTAATAAAAAAAGTGTGNCACAACTAAAA<br>AAAAAAGGCTGAAAGCGGCGCAAGCTTATTNCTTTANTGANGGTAAATTT<br>TAAGTGGCACTGGCCGCGNTTACAACGTCNNGAATGGGGAACCTGGNGG |
| RCT-206 | NNNTCTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCA<br>AGAATTCGGCAGGAGGCAGATAAATGCGGCCAGAAAGGCTGCTGCCGCCGCCGCCGCCACCACC<br>ACCACCACCGCTCCTGGATTGCTGCCATGGGTGCGCATGCTGTGGCAGACGCTGGAATTCGAG<br>CAGAGGGAATAACCTGACTTACTTGACATGTGATCCCCCTTGCTCCGCCACTGTGACCTTGAAC<br>CCCATGCACTGTGACCTCTGCTTCCCCCTTCCCACTGTGATTGGCATGTTGACAAGGGCTGTC<br>CCAAGTCAATAGAAAGGGAAGGGTGGGGATTAGGGGAGGATTAGGGGAACCTACCAAGGACTCA<br>GAGTAGAGGGTCAGACAGTGCCTTGGCCGCTTGGGGTAAAGCCAGTGCCAGCAATAACAGTTT<br>ATCATGCTCATTAATTTGGGATTTCAAAACACAAATGAGAACTCCCCACCACCCCAAGTGCAT<br>GTGCGCATCACTTAAAGTAAGTTCATGAAATATCCTTACTTTTCTTCTTCTTCTTCTTCTTCT<br>TTGTTTAAATACAAATACCTGATTTGCAGAAAAAAGGCTTGGGCTGAGGCTGAGGCTGAGGCT<br>GCTTATTTCTTTAATGAGGGTAAATTTTANCTTGGNCACTGGCCGNCCTTTTACAACG  |
| RCT-207 | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTT<br>CGGCACGAGGTGATGTGCGATGCTCTCAAGGCCATTGGCAGCGAGCCTGACTCAGACGCTCTT<br>CTCGGAAATAATGCACTCCTTTGCTAACNGCATTGAANNANGGGAGATGGGNGTCTCAACAATG<br>AACACTTCNAGGAACGAGGAGGTATCTGAAAGGCGAAGCTCGAGGAACATTTCAAAAATCAANAG<br>TTGCGGCAAGTTAAAGACAAGATGAAGACTACGACGAACAGGTGGAANAGTCNCTACAAGATGA<br>ANATGATAATGATGTTTATATACTGACTAAAGTCTCANATATTTTACACTCAATATTCAGTANCT<br>ACAAANAAAGGTGTTGCCGNGGTTTGAACAGCTGCTCCCATTAATTTGTCAACCTGATTTGTCCA<br>CATAAACCTTGGCCANACANACAATGGGGATTGNGCATCTTCGATGATATCATANANCAGTGTAG<br>TCCAGCTTCATTTAAGTATGCAGAATATTTCTTAAAGGCCAATGCTCCAGTATGTATGTGACAACA<br>NCCCGGAAGTCAGGCAAGCTGCAGCATATGGCCTTGGCGTCATGGCNCAATACGGNGGANATAAC<br>TACCGCC  |
| RCT-211 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGAAGAAGCAGCGAGGACGACCCCCGGACGGACCAAAACCGTGCGCCGCTGTAAACCC<br>GTGCTCAGCGCCGACGTCCTTGGCCGCCCATGCCCCAAAGAAATGCTGAAGGGGATGCTAAAG<br>GAGACAAGGCAAGGTGAAGGACGAGCCACAGAGAAGATCTGCAAGGTGTCTGCTAAACCTGCT<br>CCTCAAAGCCAGAGCCCAAGCCTAAAAGGCCCTGCAAAGAAGGGAGAGAAGGTACCCAAGGG<br>GAAGAAGGGGAAGCGGATGCTGGTAAGGATGCGAATAATCCTGCAGAAAACGGAGATGCCAAAA<br>CAGACCAGGCACAGAAAGCGGACGGTGTGGAGATGCCAAGTGACGTGTGTGCGTTTGTGATAAC<br>TGTGTACTTCTGGTGACTGTACAGTTTGAATACTATTTTATCAAGTTTATANNNNAAAAA<br>AAAAANAAAAAACAATTGCGGCCGCAAGCTTATTCCTTTAGTGAGGGTTAATTTTAGCT<br>TGGCACTGGCCGTCGTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACCTAATCGC<br>CTTGACGACATCCCCCTTTCCAGCTGGNGTAATAACGAANAAGNCCGACCGATCGCCCTTCC<br>AACAGTTTGGCG                           |
| RCT-212 | ATGTCAATTGTACCTGCTCAAGGGGNTGGTAGTTAGGGACAGCGGTGTGTAATGTGGCCCTTCT<br>TTCTCAAAGGGGAATAGGCTGGTGTCCGCTTTATGGTTCGGCATAGAGCTCTGTAGACTCAAGT<br>TTCAGCTGTTCCAGGGCTTCTGCTGGGCTTCCAGCATGGCTCTGTATGGCGTCCCTCTCCATCTC<br>ATGCTCCTGCTGCTTATACAGTGCCACCTCTTACGAGAAGAGCTCTCCGCTCACTCTTCTCA<br>AAAGAATGCTCCTCTGAGGTGCTGTCTTGATTTATCCAAGAACCCTACAGGGGTAAATAAATC<br>TTCAATAGGAACAGTTCTTGGGAGGCTCTTTCCAGTTTTCGGATCCTCTTTTCAAGCGATCCT<br>TTGCTGCTTATCTTTCTAGGGTCTACCTTCTTCTTCTTCCGTAGAGGTTAGCTCTCATGGGG<br>ATGAGCTCCAGAAGGACAGCAAGGAAGCTCTCTGGTGGGTGTGTGACCTGTGCTGGCTGGCAGGT<br>TCCTGGGATCCAGCTCCGAGGTGCGAGAGCCGCGCAGCACAGCATCGCAGCGGTAGCCATAG<br>C  |



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| RCT-214 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGGTTTCTCTGAGCTGCATGCCCTTGCTGGTTAGATGACAGCATACTTGACTCCCT<br>CTATGATATTGGAGGTGACAACAACAGGAGACATTTCTCCAGAAATAGCATTGGACTTCTCAGGC<br>AGACTCACAGCTACTGTTTTGGTCTTTCTCTCTCCCTCCCTACTTCTGTCTCTGGGTTCATT<br>ATCAGAAAGATAATACTAAAGTGAAAGCTTTGTTTAAGGTCTTAAAAATTGAAGAAAATCAGAAA<br>TTGTAAAGACAGTAAGACTTCAGACATACATTTTATAAGATCACAGTACAATAGTTAGAACTACT<br>GATGAGTGTATTCCCAATCCCTGGTCCCTAAGGCTAAATCCACTGCTTGTTCCTTGCTCCCTCGT<br>ATACTCTCAAGGTCTCTTTCAAAGATGGTTGCAGTGTTTGTCTCCATTGTTTTCCATAAAGTAT<br>TTCCATTTAAAAAAGTGAAGCGGCCGCAAGCTTATTCCTTTAGTGAGGGTT<br>AATTTTAGCTTGGCACTGNCCTCGTTTACAACGTCTGACTGGGAAAAACCTGGCGGTACCCA<br>ACTTAATCGCCTTGCGACATNCCCTTTCCGCGAGCTGGNGGTAATAACGAANAGNCCCCACCG<br>ATCC |
| RCT-215 | ATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCG<br>GCACGAGGGTAATTTGGAGGTTTCCCCACAGCAAGTCACTCTCTTTTTCAGCCCCAACTACAG<br>GTGGAAGTGCTGGATCAGTAAATGCTAATTTTGCTCATTTTGATAACTTCCCCAAATCCTCCAGT<br>GCTGATTTTGGATCCTTCAGTACATCCAGAGTCAATCAGACAGCATCAACTGTTAGTAAAGTTTC<br>AACAAACAAAGCTGGTTTACAGACAGCAGACAAATATGCCGCACTTGCTAATTTAGACAATATCT<br>TCAGTGCTGGGCAAGGAGGTGATCAAGGGAGTGGTTTGGGACCACCGGTAAAGCTCCTGTTGGT<br>TCTGTGGTTTCACTTCCAGTCAATCAAGTGCATCTCTGACAAGTATGCAGCCCTGGCAGAGTT<br>AGACAGCGTGTTCAGTTCTGCAGCCACCTCCAATAATGCGTACACATCCACAGTAATGCTAGCA<br>GCAGTGCTTTTGAACAGTGCCTGTGGGTGCTCTCTCAGACACAGCCTGCTTCAAGTGGGCCT<br>GCTCCATTGGAGCTACGCTTCTACGAATCCATTGTTGCTGCTACTGGTCCCGTCTGCANCGT<br>CATCTACAAATTCATTTAGACCAATGCCAAAGGANCAACAGCGCAACCTT           |
| RCT-22  | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGGAGTGGGCTACATGTGGGAATTTGCCCTAACTACCGAGTCAGGAGTGATTGGCTC<br>TGAGTAAGGCCCCAGAAGCTCCCTTGGGTCCCAAAACCCAGGCACTGGCTGCTCTTGGTCTGCT<br>GACTCTTCTCTTAACCCAGCCACTTAATTTTCTCTGTTGTTCCCTCGAACACACGGAAGCTG<br>TTGATGAATCCTTTTCTTTGCTGTGCCAAGGCAAGTCAAGACAGATCAATGGATAAGGGCAAGG<br>TGTCCGAGGAGCCAGCTGTCTTCTCTCCCTTTAGACCTCCACAGGGACAGACCTGATTTATT<br>TATTTTGGTTTAAAAAAGTGAAGCGGCCGCAAGCTTATTCCTTTTAGT<br>GAGGGTTAATTTAGCTTGGCACTGGCCGTCGTTTACAACGTCGTGACTGGGAAACCTGGCGT<br>TACCCAACTTAATCGCCTTGACACATCCCTTTTCCGAGCTGGCGTAATAACCGAAAAAGCCC<br>GCACCGATCGCCCTTCCCAACAGTTGCGCAACCTGAATGGCGAAATGGGACGCGCCCTGTACGGC<br>CATTAANCCCGCGGNTGTGGTGGTTTNNCCCCACCNGTGAC  |
| RCT-220 | CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>CGGCACGAGGGTGTAGTACCTGTAGGGAGTACGGCTCTCAGAACACTCAGGTTCTTTATAAACT<br>TTGCTTTGGTTTAAAGAGAAAAGGAATGTCAGTGAATGCTCTGGAGGCAGAGGCAGGCGGGTCA<br>CTGGGGGTTCAAGGACAGCTTGGTCTTCATAGCAAGTTCCAAGCTGTACAGGGCTACGCTGTAAG<br>ACCTGACCCAAAAACAGCAAAACAGAAGGAAGGAAGAGAAAATAGTATCTAGAGATGGAACCAAC<br>TGATGCAGCAGCAGTGGCGTGGGGTTTCCAGACTCAGAAATTTCTCTTTTCTAATTTCTTAAGGA<br>CATTTGGTTTCCATGCTAACCTTTCCCTTGACACAGACTTAAAAAGATCTGCAACAAGGGGAGGCG<br>CTTTCTCTTTAGAATGTAGAGAGGAGAGGAATTTGTTTTTATTTTAACTATTAAATCATGATAAA<br>CTGACTGCTGAGACTTCCCTAGCATTCCTTTAAAGTATTTTGTACAGAAGAGAAGAACCTCTCTG<br>GAGCGCCCCAGGTAGGTAAGTCTGTGCTGTACACAGCACCTCTCTGCCTTTCCACTGCTGTGTC<br>ACCT  |
| RCT-221 | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>CGGCACGAGGCTAACCTGTCCACGCTCCTGCCTGCAACCTCTCTCCTGCTTGGCACAGTTCGAGG<br>AGGAAGATGCTCTTTGCCTATCCAGCTGCACCTGGCTTCTGCTCAAGGGAAGTGAGCACCCC<br>ACTTCCTGTGCTAGTTAGTGCTGATTCTCTGGGTGAGTCCCCGGGCGGACTCCCTCAGCCCCCT<br>TCTCTGGTACAGTGGTGTCCGCCGACTGCCTCCTGTAACCCCATCTTCTAAGCCATCAATTTTA<br>TGTTACTATATTGCCCTTTGTGGGGTGGGAGAGGGATCTCTGGCTCTGCGACTTGGCCCTTTGC<br>CGAATAGTTACTGTTCTTGACTTGAAGAGAAGCAACGTGTGGGACCTCCCCACTGCCCCAGCCC<br>AGACTTCTTCGGAAGGGTTGGAAGTTGCTAGACAAATCAGAATGTAGAAGGTGGAGGATTTCTGAG<br>GAGGAGCAGAGAATTTCTGACTGGGAGGTATANGTTGGGTCTCTGCCTCCACGGCTGCAANG<br>TGTGCTGACCTCTGGAGCTCAGCCCCCTCCCCCTTTCTCTCAGTGCTGACAAGATGTCNATAA<br>ACTTATTTTTCATACAATTAATAAAAAA                                 |

49/73

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| RCT-242 | CATTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCCGACACGAGGGACCGAGAGCTGTGGGTGAAGCAAAGCTGTGAATCGCTCCAGATGGTCCCTG<br>TGTTCTGTCCACACACAGGTCCCGGCTTTTGAAGCAGCCTCCTGGTCTCATGCTTAAATCTG<br>TTCCCTCACTGCCCGTGTTCACCTTANAAATGGCAGAACACAGAGCTGGACTGTTGAGCAGGCCCT<br>GTCTCTCTCATTAAATAAAATAAGTAAGTTTGTAAAGCTATTCCGACAGAAAGACAAAGGTTAC<br>TGATTGTACAATAGCGCTTTATATGGAAGACTGTACAGCTTTATGGACAAATGTAAACTTTTT<br>TGTTTTTAATAAAATGTAGCAGACCCCAANCNTAAAAANAAAAATAAAATGGAAGCGGCCGCAA<br>GCTTATTCCCTTTAGTGAGGGTTAATTTAGCTTGGCACTGGCCGTGCTTTTACAACGTCGTGAC<br>TGGGAAAACCTGGCGTTACCAACTTAATCGCCTTGACACATCCCCCTTNCNCCAGCTGGCG<br>TAATAACNAAGAGGCCCGCACCCGATNCCTTCCAACAAGTTGCNACCTGAATGNCGAATGGG<br>ACCCCCCTGTACCGGCCCNNTAAACCGCGGGGTGG         |
| RCT-244 | CTTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGA<br>ATTCCGACACGAGGAGCGGATTTACCGGAGTTGCTTGGCGGTCTTGAATGATTGGCCTGATGTGT<br>TTGATGTCCGGTGCCTGGGTGTCTTATGGAGCTGTGGCAATCTACTAAGTCGGGACATGACAGTG<br>ACTTATGAGGATGTGCATGTGAACCTTACGCGGGAAGAGTGGGCTTGTCTGGATCCCTTCCAGAA<br>GAAGCTCTACAAAGATGTCTGCTGGAGACCTACAGGAACCTCAATGCTATAGGCTTTAATTGGG<br>AAGACCAAAATATTGAGGAACACTGTCAAGATCTAGAAGACAGAGAAGGTACTTCTTAAATGCA<br>AGCTCATACAAATATGCCTCTGAAGAAATTTAATGTGTTTTGAAGTTTGAAGTAAAGCAACA<br>GTGTAATAAAGAACTGCTTTAAGTATATTGGTGATCAATACATTCTAACAAACCATGGTATTCC<br>ATGTGCTTTTATCTTATTGTMTTCAATGCAATTTTTTAAATAAGTGGACTTTTAAACAGTGCC<br>TTAGTGATATATCAGCATTTGAACACAGCCCTATTACAACACTCTGTACAACCTGGCAGTAAAT<br>TCTGTAAATTTTTTAAAGCTCCACATGGTGAATAGTTG |
| RCT-245 | CTTTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGA<br>ATTCCGACACGAGGTTTTTTTTTTGTTTATTCTTGTGTTTTAGGTAAGGCTCAGGTTTTCTTCCA<br>GGTCCGTCTGATGGGGCAGTTTCTCAACTGAGGTTTTCTTCTTCCCAATGACTCTAGCCTGTGT<br>AAAGTTGACATGAAACTAGCCTGAACAATCACTCAGTTCAACCACTAACACACTGAATCCATGA<br>TCCCTATCCACACACTAAAGAACTAGAGAGAAGGCCAGATTTGGGATAGAGTTGCCTGCCTAGC<br>ATGACAAGGCCAGAGTTCTATGCCCACTGTCAAGGTGCTGGGCACAGGAGCACACTGTAAT<br>CCCAGCATTCATGAGACTGAGGCAGAAGAACCTTGAGCTACACATTGAGTTCCAGACAATTTGA<br>ACCCTTGCTGAGATATTATCTCCAAGAGACTTGGGCAGTTGAGACTGGAGAAGTACAGTTCA<br>AGTTTATCCTCAACTGGANGCCAACCTGAGCCTTACCTAAAAACAAAGAAATAAACAAAAA<br>AAAAAAACCTTTGCGGCCCGCAAGCTTATTCCTTTAGTGAGGGTTTAATTTTANCTTGGCAC<br>TGGCCGTGCTTTTACAACGTCGTGGACTGGGGAAA              |
| RCT-246 | TTTATNACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCACGAGGCATTACTCCTGAATGTGTAATAAGCTGGGTAGCTCTCTGCAAATAGACCGAG<br>TAAATATTGGCTCTAAACCGGCATTATCTGCCTTAACAGAAAGAAATATAGTTAGCCAGTGAACA<br>TGTAAGTTAAACCGTCCCTGGTCTTGAATGGTGTATGTGGTGTATCTGCGAACAGGAAGGGAAGCC<br>AATCGTCTTTTCAATTGCAATGTCCATTGCTAATGCTAGTAGCACAGAAAGGGGAAAGGAAAT<br>GTCCGGCGGAGAGGGGAGATGCATCCTCTTTTCTTGGAGCCTGGGAAAGCGGGTCACTCACT<br>GGCTCATGCATCATAATCACTTGAAATGATATGGGTATGATTTTATCTCAAGTGGCCTCTGCT<br>TAAAGACAAAGACACACAGCTAGAGAAATACCCAGAAGGTCTGCAACAAGAACCCAAAAAGACAAA<br>TTCTGGGTTTACTTCTGTTCCACATTATAGATTCTTTTATAGATATCCCTCTCTTGGAGAGGTC<br>CTTCCAACGGGGGTGTCTCAATTAATAAAAAAAAAAAAAAACCTTTGCGGNCGAAGCTTATTC<br>CCTTTAATGAGGGGTAAATTTAGCTTGGCACTG       |
| RCT-251 | CNNNNNNNNNNNTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCT<br>CGAGGCCAAGAATTCGGCACGAGGAAAGAAATGCCCTTCAAAGACTTGACTATTGGCTAATCTCAT<br>GGTGGCATTCTTCAATTGTTGCTCCCTTTCCAGAAAACCTCCTTGGGTCAAGGTGACAAAA<br>ACTAACCAGCGTGCCTGATGTCATTGCTATGGTGTAGAACAGTATCTGGCACAGAAATCATGATA<br>GACGGCGTTATCAGCTGTATCTGCTTTAGAATCACTGGAATCTCCATGAAGGTATATTTGATT<br>AGGGCAGCCTCCGAAGATGTTTCTGGGCATTATTTGATTACCTTAACCTGAGGTGGGAAGACAT<br>GCTTACTGCTGAGGGTGACAGTGGGGAAGTGTGCTTCTTATACCTGCTCCCCCAATGCTGACCA<br>TCTGATGGAGAGCACACAGTAGTTACATGCTTCATGTAACGTTTTTGTCTCTATTATGGATAA<br>AGCATCAAAGGCCTTTTATATTTGGTATTTTGGAGACAGGGTCCATACCATGTGGCCTAGTCTG<br>GTCTTAATCTCAAGTTCAGACTTAACAGACATGTACTTTAAAGATCAGATAAGGAGTCGGAAA<br>GTTCAATGGACTGGTAACC                        |

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| RCT-252 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGCAGGGGCAATACCTCTACTGGCAAGACCCTTCATCAGGTACCTGCTGGAACAGGATTT<br>TCCAGGCATGAGGATTGGGCTGAGCCAACCACTGATTCTTCATAGCAGTGATGCAGGGAGATG<br>TGGAGGGGATCATCCCTGGGAACGCCCTGGTGGTGGATCCGAAGAAACCCTTCAGAAAGCTCAAC<br>GCCTTCGGCAATGCCTTCTGAACAGGTTTGTGTGTGCGCAGCTGCCAACGCTGTTCTAGAAAG<br>TATCAGTGTATCGACACACCGGGGATCTCTCTGGTGAGAAACAGAGGATCAGCCGAGGGTATG<br>ATTTTGTCTGTCTCTCGAATGGTTTGTCTGAGCGGGTGGACCGAATCATCTGTCTTTGACGCC<br>CACAAGCTTGACATCTCTGATGAGTTCTCAGAAGTCATCAAGGCCCTCAAGAACCACGAGGATGC<br>AGGATCAGCTGCAGGCCAGGACTTCAGCAAATTCACCACTGAAGAGCAAGCTGCTAGAAGTG<br>GTTGATGACATGCTGGCCCATGACATTGCCAGCTCATGGTGTGTTACGCCAGGAAAAGACCCA<br>CGGCCTGTTTCAGATGGTGAANGGCGGAGCATTTTGANGGAACCCTCAAGGGCCCTTTGGGCATG<br>GGCTTT   |
| RCT-256 | TCTCNTAANATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCGGCAGCAGGAATTGAGTGACATATCACTCCTGAGTATGCCACTAGATGCGGTGGAGATGCA<br>GAGGCATCCGGACCCACGCCCCACCCCTCCCTCACACACTTACTCTCTGCTAGTAATGCCA<br>CAGAGCTTCCATCCCCATCAAAGGTATCAGGCATGGCTATCAGTTGGCTCTCAGGGTGGATTT<br>GACATTTCTCAGATGATTAGAAGTTGGCAAGAAGCAACCTTGGTGAATAACTCTGGTGTCTAACT<br>CTGTACTTGAGTTACAGTCTCAGTAGAGGAGACGCCAAAGCTGTGCGAGTGACGCCAGGATTAT<br>TGAACAGTCATGATGCTTGGCTTTCAAAGGCGATTATCGCTTTAAGGTCTTAGAATTAGTAAGTG<br>CATCTTTATAACCAGGCATAGCTAGATCATAAATACTGATGGCCAGGACCATAGAACGTGCTT<br>CTTACCTTCTCTCTAGTTAGCATTACGACAAACATAATCACCACGCTCAGGGAACACTTGCT<br>GATTCAAGTAAATGCAATGAACCTTGAAGACCTTTCTAGAAGTCAGAGATCAAGTTTCATCTTGN<br>TCTAGCACTTTCACATTTCATGTTTGGGTTGTATGCTGCGCCCTAN  |
| RCT-258 | TNATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>CGGCACGAGGACCAGTCAGGGAAGAATGTGATGGTGGAGCCCCATCGGCATGAAGGAGTCTTTAT<br>CTGTCCGCGAAAGGAGGATGCCCTTGTGCACAAAGAACTCTGGTTCTGGAGAATCTGTGTATGAG<br>AGAAGAGAGTCTCTATCTCCGAAGGAGATGACAAAATTGAGTACCGAGCCTGGAACCCCTTCCGC<br>TCCAAGCTGGCCGAGCAATCTGGGTGGCGTAGACCAGATCCACATCAAGCCGGGGGCCAAGGT<br>GCTCTACCTTGGGGCAGCCTCAGGCACACCGCTCTCCACGTGTCTGACATTGTTGGCCCGGATG<br>GTCTGGTCTACGCAGTTGAGTTCTCCACCGCTCTGGCCGTGACCTCATCAACTTGGCCAAGAAG<br>AGGACCAACATTATTCTGTAAATTGAAGATGCTCGGCACCCACACAAATACCGCATGCTTATTGC<br>AATGGTGGATGTCATCTTTGCCGATGTGGCCAGCCAGACCAAAACCCGAATTGTGGCCCTGAATG<br>CCACACCTTCTCGCGAATGGANGACACTTTGTGATTTCATTAAANGGCCAACTGCATTGATTC<br>CACAGCCTCAACANAANCTGTGTTTGCATCTGAAGTGAAGA   |
| RCT-260 | GGGGGTGAACATACAAGAAGGTTGNTGTCTTTTGCACANAAAAATTTTGTGTTGAACTGTGANTG<br>GNGAGTACACGAGTTTCTCTAACCAGTCACCACACTTCTGAAATAACGCGTGTAAACATTCAAC<br>TGATAAAAGGGACCGTCCCTTGGGTAAAGTGTCAAGCAGGGTTAAATATGTATAATAGACAAGCA<br>CCATGAGGAATCTGCTCCTGCTCGATGGGTCTGTGTCTCAATGTCCNTGTGTACCCCTCTTTTGT<br>GCAAGTTGATTACATGTTTGTGGCTGACTCCAAAAGCACATGGTCACAAGACAAACATTTTPTT<br>TTAAAAAACATTCTCATGAATGATTATCTACAGTACGGTTTCTAATACACAACGATCCTTCTTT<br>ATTGCTGAAACTGGTGGTACTTAAGTGTCTCCTTTCTCTTTTCTTGACAACTAAGCTTCCAACC<br>CAGTCCACCAACTCTTTCAAACCTAAAGTCTCCTGTACAGATGACAGGATGCAGAAGAGACCTG<br>CTGGGATCGGCTTTTGCACCTGTGCTGCAGCCTTCGCCCTCCTTGGGTGTGAAGTTGAT   |
| RCT-264 | CTANNCCNTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCC<br>AAGAATTCGGCAGCAGGCATCTCGAGCAGAGAGCTGTTTCCAGCACCCGTTCTCTACCACCAA<br>GTCACACTCGTGGCTGGCACAGAGAAGGTGCTCACTGTTTGTCTGTTTCAGACCGCGTCACCAAAA<br>CATGGAAAACCTATTGAGTTTAATATTCTGGGCTTAACAGACTGATTATTTTCAGGAGCAACTG<br>AAGGATATTCTGAAGTATGCTGAAGTGACAGGTGGAGAACAATTCCCATTAATTATTATGTCTAA<br>TTATTCCACTTAATAATGATGAGATGCAATAAGACCAACCAATAAAAAATGAGGAAAATACACA<br>AGTATAATGTATAGAAAAGCACAAAGTATTACCATTCTTCAGCTTCGAACAAGACCATGATCA<br>ACATCAAAGGACAACCTATAGCCCCAAGACATGTGCTGTCTGCACTCCAGGCTTGCTTACCTTGC<br>TACGGATGATGAGAGGGAGTGGCAATAAAACCAAAACAGTGGAAAACCAAGGAGAAAGCGACG<br>ATACACCAAAAGCGTAATTGAGGAGCTTCATGCTGAGCAGGTGCTTCAACANTTCCCCCTCACT<br>CTCAGGCAGAAGTTAATAACAGCTGGGATTAATATTTCTCTACCTCATCATCTTTACCTACTGG<br>CTCAGANAGAACCAACCGTGGTTAAAAATAAATCTCATTTTTATGGTTTN |

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| RCT-268 | ATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTTCG<br>GCACGAGGGGCTGTTCTCCAGGAAAGATAAGGTTGACTTTGTCCAAAGAATGCTCTTCAACCAAC<br>AGGAGCTCTTTGGAAGGAATGGATTGGAATATAGGATGTTCCAGATGTTTGAATCTCACATAAG<br>GACCTGCTTTTCAGTGATGACACAGAATGCTTGTCTAACCTTCAGAACAAAGCAACCTATAAAAC<br>ATACCTAGGGCCACAGTATCTTACCCTGATGGACAACCTTATAGACAGTGCTTGTCTCAGAACCTGC<br>TGGATGCTGTACATTTACAAAACATTAAACCATTACGCTGGGGGGGTAACCCAAGGACTGGGGA<br>CCCAACTGCTTGCTCCATCGGACCTGTGCCGACATCTCTATAACTCAGTGCTCATAGTGGAAAC<br>AAACAAAAAATGAATAAAAGTATCTTCCAGAAAAAAGAAAAAACAACATGCGGCCGCAAA<br>GCTTATTCCCTTTAGTGAGGGTAAATTTAGCTTGGCACTGGCCGCTGTTTACAACTGCTGAC<br>TGGGAAAACCTGGCGTTACCAACTTAATCGCCTTGCAGCACATCCCCCTTCCAGCTGGCGT<br>AATANCAGAAAAGCCCGCACCAGATCGCCCTTCCAACAGTTGCCCCACCTGAATGGCGAATGGGACN<br>CC                                |
| RCT-271 | CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGCACATTTCTTCAGTCATCATGGAGAAGGTGGGCACTACCACTACGATACCAACCC<br>AGACACAGTGGAGTATCTCGGCTACTTCTCGCTGCACAGTTCTCTACCGAATTGACAGCCCA<br>AGGAGACCCATGCCCTTTGGGAGGGATTAAAGCAGCTGCTGCTTGATTAGGGGAAAAATGGTTAGC<br>TAAGGTTATATTGCTAACCCAGCAATTGACAGTAATTAATAAATATAGTAGGACCAAGAGAGAG<br>AGAGAGAGACCCGAGCCAACAACAGTCATTTCACTACATTAGCACTGTTTTATGGCATCCATGT<br>GGATAAGGGACACTCGTGTTATTTAGCATCTTTATGTGAAGGAGTCTTGGGAACAAAGATAACTA<br>ATTGAGATGCTCACTTTACTCAACCAATTTTCTGTCTTTATAGCCAGAGTCCACCTTCCTTCT<br>CTTCACACCTCAGGTATGGGCATGGACAGGGACCTTTTCATTATCCCTGCTATCGAGTAACATTTG<br>GGTCACATTGCTGAATTTTCAAGTTTCATCTCACAAGGCTAAGGGGTC   |
| RCT-274 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGCAGGGCGGCAGCAGAGCCAAGTCTAGATGCTATGCAGGACAGCTTCACTCGGGCGTCTGG<br>CATCATAGATACGCTTTTCCAGGACCGGTTCTTCACCCATGAGCCCCAGGACATCCACCAATTTCT<br>CCCCATGGGCTTCCACACAAGCGGCTCATTTCTTGTACCCCAAGTCCCGCTTGGTCCGCAAGC<br>CTCATGCTCTCTCCCACTACGGGCTCTGAGCTTCCACAACATGTTCCAGCCTTTCTTTGATAT<br>GATACACCAGGCTCAACAGGCCATGGACGTCAGCTCCATAGCCAGCTTTACAGTTCCCGGATG<br>TGGATTTCTTAAAGAAAGGTGAAGATGACCGCACAGTGTGCAAGGAGATCCGCCATAACTCCACA<br>GGATGCTGAAGATGAAGGGCCAGTGTGAGAAGTGCCCAAGAGATCTTGTCTGTGGACTGTCGAC<br>CAACAATCTGCCAGGCTAACCTGCGCCAGGAGCTAAACGACTCGCTNCAGGTGGCTGAGAGCT<br>GACCCAGCAATACAACGAGCTGCTTCATTCTCCAGTCCCAGATGCTCAACACCTCATCTGCTG<br>GAACAGCTGAACGACCACTTACGCTGGGTGTCAGCTGGCTAACCTCACACAGGGCGATGACCAG<br>TACCTTCGGTCTCCACAGTGACAACCACTTCTTN |
| RCT-276 | ANNNNNNNNNCCNCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTC<br>GAGGCCAAGAATTCGGCAGGAGGCTGACCCGTGTGCAGAGGCAATTTTCGTCCCCCTTTGCTTTA<br>TTTCTACCTACAGTACTATTTACCTTCCGTGTCTAGCCCTGCCACCTGTGTATTTTGGGGTG<br>CTATGGAACAATGAAGAGAAACGGGGTTTCAGAAGAAATGTAACCAAAATTCATATGCTTTG<br>TATAAGTTTTTGATATCATGATCACAGGTGATTACACGCATACACATCCACACCCACACGTGCA<br>GCCTGAAGTGATGTCCATGGAACCCATCGTCTTTGTACAGCGTATGTACATGGCAATCATTTCAT<br>ACTTTTGACTGGTCAGAAAAAATAAATTTGTGATTTCTAGTCTTGCAAAGCTGTATGTAGTT<br>AGATGATGTGACCTCTAATATTTATCTAATAAATATGTATTTCAGATGAAACCTGTAAAAACAAA<br>AGTTGCNTAACANAAAAAAGGGNGCGCGCAAGCTTATCCCTTTAGTGAGGGTTAA<br>TTTTANCTTGGCACTGGCCGTCTTTTACAACGTCGTGACTGGGAAACCTGGCGT  |
| RCT-277 | TTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCGGCAGGAGGCTGAGAATCTGTATTGTGGTGATAAAGTGTCTTCTAAGAGCAGTAAAGGA<br>CAAATTAAGCAGACTTTCTTTTCAAGCTTATGACTTAGATTCTTTAGAAATATAGTTCTTAAATC<br>TTTAAAGATGAGATTCTAAGCCTAGAATTTTAAACCACATTTCAATTATGGTGGCTTACTGATCTC<br>AAATTTTCTACAATTTGGTTTTTTAGACTAAAAACAGCTAAACAAAACCTTCCTTTATCTTTC<br>TCATCACATCCAGTGGCAGAGGGGACTGTCTGAGAGTAAAGTCCCATGATTGAGAAGGACATAGC<br>AGGTGAGGATGTACCAATAAAAGTTATGAATGTGATGTTTATTAGAAAGAACTGAACAACAGG<br>TACAGAAATGAATATCAGCAAGAAATTTGTTTTAAGGATTTTCCAGATTTTACTTTGTATCTTGAA<br>GTGTGTGCCATATGCCAAGAACTAACAGAACTTCTGTTCATCTCTGTACCTTCTCTTTTTTA<br>AAAGTGAACCTATGGGTGCTTCAATNCTGGGGGCTTATGGGATGGGTGGCTTGGACTGGTTG<br>CCACTGGATGCTGCAGTTNCTTTAAT  |

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| RCT-279 | <p>ATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCG<br/>GCACGAGGGTGTGACTGATGGTGGAAGCAGGCCTTTCTTTATTATCCAAACCTTCTGCCACTGA<br/>ACCATATCTCCTTTAGTACCAACTTCAACACCTTTCTGCTTTTATTTTCAGTTCTCTAGATTTT<br/>GTTTTTTTCTGAGTCTTACTTTCTCACTGAACTTTTGTTCCTCATGATAAGGTACCCTGTGTG<br/>CACCTCCCTTCCCTCCTCCCTCCAGAGCACAGCTCACTGGCCGCTTCAAGCCTTGTGCTGG<br/>CTTACTTTGTGTGAGGGCTATTATAAAGCTAATCTTCAAAATTAATAATTTAAATTAGGAA<br/>GTGTTGTATTCCAGCCCAACAAATGTCATGTCTATAACCCAGCCTCTAGGAGGCAAGGCTAACT<br/>GGGGCCCAAGGATTGCCAGGAATTGACAGCCAGCCGAGCTACATAACAAGATGGAAAGAAAACA<br/>CTGGTGATATTTAATCTGATACATTGGTTGGAGGAGTATTTATATGAACATGTATCTGTGGATT<br/>AAGAAGTTATTTTATTGGCTATGATACAGAATATCTAAGCCCNCTGGTTACTTNAATGAGCCGCC<br/>TCTTACTTTCTTATCTCGGCAGANAACCTGGTGGTAAGTGGATTTTTTGGCAGNAAAGCTCAAA<br/>ATCTCTGGCTGAATAATTGGGAAANATCTTCTAAGCGNGGGGAA</p>                      |
| RCT-28  | <p>CNNTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br/>TTCGGCACGAGGGAATTCAGCCTCGCGGACGGCTGTCAATTTCAATTTGAAGTTCCCTTTGTGGA<br/>AGTTGACCTGAAATCTTTATCACAGTAATAAATCTTTAATCGGTTTTTAATATTATAACTGAT<br/>TCCCTTTGTTTACAGTTACTCTATATGGCATTGTGCAATGTTTCATGACTCCTTGTTTATTGTT<br/>CCTGTTTTCTATTCTTTGGAATCCTTTCTTGGTGACAGAATTTGTAAATTTGTATACTACCTC<br/>GGAGCCCCCATTTGTCAGAAGTTCTATTTTCCAGAGTCAGGGCACTGTGTTAGTCAACCGAGCCG<br/>GCATTTTANCAGTTTGCAGAAGAAGTGATTTGAATGGACAGCTGCAAGTGAGACAGCCTAGACCT<br/>GAAGAGATGAAACACTCACTTCACTTGGAGGAAAGAGGAAGCAAGCCTAGGGCTTAACAGACCT<br/>ATCTGCAGTACGTCCAGCCCTCCAGAGCCTGGCCCANCCATTGGACGCCCTCGGCTTTTATTG<br/>CCTTGGACAGCGGATGTACCAGGNCCTGGCCAGCGGGATCCTGCNAAGGCTGAACATGAAGAGCT<br/>ATGAAGAGTACCAGTTGGNGATANATGGGGGAACCCNNGGCCNAGNTTGGGTTTCGATGTACAC<br/>AGAAATGGTNCAGANAATGGAGGANCATTCCGATTCTGGCTTACTGG</p>            |
| RCT-280 | <p>CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br/>TTCGGCACGAGGCTCCTCTCCACGCCATCTGCGCATCCTTCTTGCCTTGTCCACTCCCTTTCTCT<br/>CCTGCCTCTTCTGCCCCGAAATTTGCACTATGTCTCTGGAGGGGAACACTGGGCAGAGGGCGT<br/>GTGATGTGGGGTTACAGCCCCCACCCTATTTAGACACAAGGATGCTGGGTCTCTATGCGGATGG<br/>GGACAATGTTTACAGGCACCCAGTCACACATTACGTTGTGCACACAGGCACACGAGAGGGC<br/>CCCAGCACATAGCTTGTAGTTTGTGCAATTTGCTTCTCCAGGTAATAGGATGGACAAAGGGCC<br/>CACACCCCCAGTTTAAAGAAAGAGTCCATCCCAACCCCTCCTGCTCCTCCCTGGAGCAGGG<br/>CACCATCCCTCCTGCACACCTTGGCTGGTGGTGAGCAGGGTTTACTGTGAGGTGAATTTGGGA<br/>TTACTTTCTTTCTATTTGGTTTGTGGTGAGCTTGTCTGTCTGAGTCTTGTGTCTACCCCTAGACC<br/>AGTAATGGCTAATGAATCTTAGAAATTTCTGATTGATCTTGGGGTCCCTCTGTGATATTTCTTTG<br/>TGCCCAAAAGATATTAAAAAAGACCAAAATATGTGAAT</p>   |
| RCT-281 | <p>CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTT<br/>CGGCACGAGGGTTGGATGAAGAGAACATATGAGCTTGTGAGAGAAGACCGTGACAGCAGCGATT<br/>TTTGTGACGTGGAGCACTGCTGACTCATAAAGGGAAGACAGAGAATCTTTTAGAGATCGCATGTT<br/>TTTCAGAAAGGCTTGGCCCCATACAGCCTGTTGTTGTTGGACATTCATAGTAGAACTCCTGTGTG<br/>GCTTGTGTGATTTGAAGAAAGAAAAAAGCATATTGCTAAAAAATCTGGCTGAAAAATACCTTAA<br/>TGAATGGCAGGATGTGGGAAAAATGGATGGTTGGTCATTTCAGATGTCTAGTGATACAAAGACAGA<br/>TGAGTGTGGCCCCAAGCGCTGGCACTTGTCTGTGTTTGGGGGAATCGTATTGGTGGCACATTGGA<br/>TATTTCTAATATGATATAAGCTGTGTATCTTGAATCACCTTTATCCTTTGCTATGTCTGCGTAT<br/>CTCTCTTAAATGCCAAGACCTCTCTTTTGTCTGTCATCGATCCTTTGGAACAATTTTGCTTCT<br/>TTAGTTACAGGTTGTCATTGACCTTTAGGAATTAATCTGAGGGGT</p>  |
| RCT-284 | <p>TNCTAACATGATTACGANTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTT<br/>CGGCACGAGGGGTTACTCCATTCAAATAACATACTTTGAAAGCAAGTATAGGAAAGCCTTTTCC<br/>TATTATTTTCTTCTTAGCTTCCCATTTGTCTGAATTTGGGAAACAGGAAAGCATTGCTTTGTAG<br/>CACCTGCAAAATGGTTTAAATGCCCCCTGCATAGTTCCATATCTTTCAACAATAGATTTAGCATGGG<br/>AATCTAACTAGACACCCTGAGAACATCTGTCTTCTCCCAAGCTCTAAACCCAGGCTTTTGATTA<br/>TGTGTGGCTTGTGAATCCTATCAACCAAAACAGGGGGACAGACATACCTCACCACCTGTATACCC<br/>TGATGACTCCTTACTCAAGGGCTTTTGTAGTACCTGTTCTTGATAGTACCTGTCTATTTTCAGATG<br/>GGGACCCCTGGAGCTTTCATCCTTCCCATCTTACTTGCAGGGCGCAAGTGGCTCCTCTTTTGCAAT<br/>TTACCGAGCCCCCTCAAGCTTAAGTTTCATTTGCGGATCAGGATTAAGCCTGGAATTTGTCTTG<br/>TCCCTGGTGTGAGGGGTTATTGTAAATGGTAGTAATCTACCCCAAGCCCTCAGTAAGAACATA<br/>AATATTTAAAAAATATGNGCATTTGNAATCTGGTCTGGATCCTGGAACCTGTGGGCTGNTCANGC<br/>AGGAGTGGACTTTAATCTTCTAGTGAATAATTGCCCACTTTGNGGGAAGGN</p> |

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| RCT-287 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGCAGGCCAAAACCTGACGGACAGATCAGTTTGGACCTCTTATCCTCTGTGGCTCTGAGTGG<br>TACTAATCATGAACATGACCAGCCAGCACATTTAACCTTGAAGGATGACAGCATACCTGTTAATA<br>GAAATCTGTCAATATATGATGGCCCTGAGCAGCGATTCTGCCCTGCAGGAGTTTATGAATTTGTT<br>CCTCTGGAACAAGGTGATGGATTTTCGGTTACAGATAAATGCTCAGAACTGTGTGCATTGTAAAAAC<br>ATGTGATATCAAAGACCCAAAGTCAAAATATTAAGTGGGTGGTCCAGAAAGGTGGAGGAGACCTG<br>CTTACAATGGCATGTAAAGCCCAAGTGGCTCCACTTACTGGCAGACTTGACAGCCAGTTTCTAGA<br>ATACTGTAAATGTATGCCAACTAACCTCCCATATGTTTGGATAACTTCTGAACAAGTGTCTCTC<br>AAACACTGAAGTAAAAAACTTTGTATCTAACGTCCCATAAAAATCATGAAATATTTGTCAITTAATA<br>AAACTTTATAAATAAATAAAAAAATAAAAAAATCTCGCGCCGCAAGCTTATTCCTTTAGTG<br>AGGGTTAATTTAGCTTGGCCTGGCCGTCGTTTTCAACGTCC                     |
| RCT-288 | TCCTNATNAGATGATNACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCCGGCAGCAGGAATTAACACTATATAAATAAGAAATAAGTAAAGAAATAAACAG<br>TAGTAAACACCTCTGGTTTATCAACGTTTAAATCATAGAAGGAACCCCTGATGTCACTTTCTTT<br>ACGTATGACTCTGTGAAGGAATGTAAATGGTACATTACAATAGGAGCTAATGTTTAAATGTGTAC<br>AGTAGTGAAATAATTAACAATAAACTGGAGTTCAAATGCCAGTCAATGTAAGTACATTCTATGA<br>TGGGGCTTTGAAAGTGTATTATCCATGAAGCAATTTACAAAGAACATTGATGAGCAATATGGGT<br>AAACTGTTTGGAAAGTGTCTGGGCAATAACTGGAATGTCTAAGTGGCTTCACCGCACTGTACCA<br>GAAACATATTTCTGAAAGTCAAGATCCATCAGTGTCACTGTGTGCGCAACTTCACAGTAATTTAC<br>TTTACTGTGTGAAAAATAAACATCGCTCTTGTAACTGTGGTGTAAACATTTTCTTAAATGT<br>AAAGGAGGCATTCTTTTACAAAGAGAAATGCTTTATCTTTCAGAAAAAATGAAGCAAAAC<br>ATCTTATCCATTATCTGAATGTTGATTCTTTGCTTATAAGTTTATAGGTGCAGGTGGCTTCTCCT<br>ATTGCTTCTCTT |
| RCT-291 | GTCATCTTCAGCTATGCAGTGAATATGAGGCCAGTCTGGACTACAGGAACCNCTGATTGGACAG<br>AGCTAGAAGATCATACAATCAGGAATGTGGGTGTAAACAGCACTTACTTTTAAAGGATAATGGATAA<br>AACTCGAAAGAACATGAATTCGGAATGGTCTAGTTTATAGTGGTGTCTGTTGGACATTTTGTAGA<br>CGGGCTCTAAGATGACATTTAAACGAAAATACCTGCTGACTTTAAAGGGAGGGAAAATATGGAA<br>AGTTACATGTAAATAAACCAATTAAGAGGTAGTGTGGGGCTGCCCTTACACAGTGCCACGTTCTG<br>GCCAAGAATGTTCTCTACTCATTAAAGGTCAAGTCCAGTACAGTCAAGTCAAGTCAAGTCAAGT<br>CCTCCTCTGCCCACTTCACTACATATACTAAAGCATGACAAACACTATGGTCTTCTGAAAAGTGTG<br>AAATCTACTGTCTGTTTCTATGTGCTTATAAAAAATCAACTCCCTGTGTATCCACACGCTCCAG<br>ATTGAGTTGTCCAAATCAGTCCAGAAATTTAGAGGAACACACCTCGTGCCGAATTTCTGGCCCTCG<br>AGGGCCAAATTCCTTATAGGAGTCGTATTAATTCGNATCANGTNAATCANNNG   |
| RCT-292 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGCAGGCACGTACTAAGCAGACCGCTCGAAAGTCCACGGGCGGCAAGCCCCGCGCAAGC<br>AGCTCGCCACCAAGGCCGCGCCGCAAGAGCGCTCCGGCCACCGGCGGCGTGAAGAAGCCCCACCGC<br>TACCGTCCCGGCACCGTGGCTCTGCGCGAGATCCGGCGCTACCAGAAGTCCACCGAGCTGTGTAT<br>CCGCAAGCTGCCGTTCCAGCGCCTGGTGCAGGAAATCGCGCAGGACTTCAAGACCGACCTTCCGT<br>TCCAGAGCTCGGCGGTCTATGGCCCTTCAGGAGGCCAGCGAGGCCCTACCTTGTGGGTCTGTTTGTAG<br>GACACCAACCTGTGCGCCATCCACGCCAAGCGTGTGACCATCATGCCAAGGACATCCAGCTGGC<br>CCGCCGATTCGTGGAGAGAGAGCTTAAACGGTCTACGAGCAGTTAACCAGAGGCTCTTTTCA<br>GAGCCACACNANTNNATNANTAGNANNNNAANAAAAAATTTGCGCCGCAAGCTTATTCCTTTT<br>AGTGAGGGTTAATTTTACTTGGCACTGGCCGTCGTTTACAACGTCGTGACTGGGAAAACCTGGC<br>GTTACCCAAATTTATCCCTTGACGACATCCCCCTTTCCGCCAGCTGGNGTAATAAC         |
| RCT-293 | GNNNTGTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCC<br>AAGAATTCGGCAGCAGGCTCGCTCCTCAACTTGGCAAAAATGCCTACAGAGACTGAGAGATGCA<br>TCGAGTCCCTGATTGCTGTTTCCAGAAGTACAGTGGGAAGGATGGAATAGCTGTCTCTCTCC<br>AAAACAGTGTCTCTTCTTCTCATGAACACGGAGCTGGCCGCTTACGAAGAACCAGAAGGACCC<br>CGGTGTCTCGACCGCATGATGAAGAAGCTGGACCTCAACAGTGTGGGCAAGTAGATTTCCTCAAG<br>AGTTTCTCAACCTTATTGGTGGCTTAGCTATAGCATGCCATGAGTCTCTCTCCAGACTTCCAG<br>AAGCGTATCTAACCCTCTCCATTCCCTTCCAGCCACCAAGTCATCGCTCCTCCACTCCTTCCCC<br>CATCCACACCTGCAGTGAAGCCACACCTACACACATGCAGCCACGCTGACAGGGAAT<br>AAAAAATGTCAATTTTAAATGTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA<br>GCTTATTCCTTTAGTGAGGGTTAATTTAGCTTGGCACTGGCCGNCGTTT   |



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| RCT-296 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGCAGGATAACATTAATCTTTTTAACAAAAATATGGTCACTTTATCTAAACCCATCCTATCC<br>CCAAGTTTAAACCAGGATAAGCTATTTTCATTGGCCAACTATCTATTCTCCACACCTTTCTGTCT<br>GATTTTCTGATATTCTCCCTGTAAATCTGAATAAATTCAGCAAGTAATAACAATGCCACAATTT<br>AAATAATGTTTCTTGAAGGAATCATCCAGGGAATACCTTTCCCTCTAACTTCTTTACTTCAC<br>CCTGAACAGGCAGGTGAACCTATACATCCGAAATTTCCATATCTGATACCTATGACCTTAAAG<br>ACATGCTGGAAGACCTGAACATTAAGGACTTGCTACCAACCAATCAGATTTCTCAGGCAACACC<br>AAAGATGTTCCCTTGACATTAACGATGGTCCACAAGGCCATGCTACAACCTGGATGAAGGGAATGT<br>GTTGCCTAATTTCTACCAACGGGGCTCCCTTACACCTGCGCTCTGAACCACTTGACATCAAGTTCA<br>ACAAGCCCTTCATCCTCTGCTCTTTGACAAGTTACATGGAGCAGCC   |
| RCT-31  | TCTATNACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGCAGGGAACGTTGCTTTCACATGTTTTTACAGGATGAAATCATAGATAAAAGCTATACT<br>CCATCTAAATAAGACATGCTGAGTTTGGCAAGAAGAGGCAAAACCCCAAGACCATGAATGATTC<br>GTCCGTACCAATGAAGACGTTGTAACCTAATCTAGCATGCTGCAGACACTGCTGTAAACAAACGCGC<br>ACGCCCTGGATGTACTAACACTACGCTCCCTTTCATTCTGTCTGTTTGGCAAGACGTTCAATTTG<br>CTTTAGTGGAACTCCCTCACTTCTCCAGCCTTTCTAAGTAGCCCTTCCCACCGTGTCCCTCCGT<br>GTGCACTGTAGCCTCAGCCCTGTAGACCTGCAGTGTCTGACTAAAGCTGCCGACTTGCTCGAAT<br>TTGCACTTCTGTCTGCTGCTTCTTGAATCTGATTGACTAGGATATTTCTCCCAACCTGATG<br>TGTGATGTCACCACTTGCTCCTAATTTATGTGCAGGAGCAGACACCAATTTGTCTCCAGTGCCAC<br>ACATACGAGGTGACTTTGTGTGCAGAAATGTGCTTCTTCTGGCTGTAATCCCTTCACATGA<br>GAGATTAATGAGGGAATCTTTATATCTGTATAAA  |
| RCT-34  | ACTAAANNAANNCTNTATGACNTGNTNACGAATTTAATACGACTCACTATAGGGAATTTGNGCC<br>CTCGAGGCCAAGAATTCGGCAGCAGGCAAAAGAACTACAAATCCTAGATTGCTCTGAATATACA<br>GACTCAGAGAATATTTAGTTTCATCTGAAAAGGAAAACCTTTTCCNTCTATGTACACCAAGAGCT<br>CTGTCAAATGCTGCTCTCCATTACCACCTGTCTGACCTCTGCTGAGAACAGTCAGTGCAGC<br>CACCAGGTTTCCGCCCTCTCAAGTTTGGCTGTAGCAGATTGGCAGACTGTCTTCTAACAGCCAT<br>TCATTTTCAATCCAGATTTTCCAGGGGAATAGTCTGCATCCTGCTTGTCTGTATAAACTTA<br>CAAATCAATCATGAAATGCNCTAATTTTGTGAATCAGGACCTAAGTGTTTAATGNAATAA<br>TTTTGTTTCATAGATTGCTTTAGGTTTGTGTTATCTTTTAAATGTTAACTGNAATTTAATCTAC<br>NTCTAAAGTAACCTGGAACCTGCAGATTAAAGCCCAAGGCTTTACAGATAAAAAAATAATTTACTGG<br>NAATGNCATAAATTTGGAAGAATGGCAATTAAGCCCACTTTTCAAGGCTTAAAGCCTTTTAAANAC<br>CACCNNNTANTCATCTACACCTCNCNCNTCAGNNGTGGGCGGCCCCCANANCTTTATTTCCCC<br>TTTNANNGGAGGGGTTAAATTTT                         |
| RCT-36  | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTT<br>CGGCACGAGGGCGCGCAGGGGAGCGTGCCACGGGACTGTTGGGCCGAGTCTACCTGGTTTTAG<br>AACGATCCAAAGAAATGGCAGGAATGCATTCACTGTATTCTCTTTCTAGCCCTGTCTCCAGATCT<br>CTCACAATGAACCTACCCGCAACAATTTATAGTACTCAATGGCAGACATCTGTCTCCTCCCA<br>AACGAACGGTTGGCTGGAGGACTCTAACATGCCCCAAGTGTGCACACCTCCTCTTTAGATTAAA<br>CCTCAAGGGCTCCCTTCAGCTGAGTGCAATGTGTCTGATTACCAAGAGATCTCCAGGGTTTGCA<br>GGGAGTTTAAAGGTCAATGTGATTTTCAATATGGAGCTAAGGAGAGAAATGACACAAATTTAGTCA<br>TGCTTCTATATACACACCTATGAGCAATAAAAATGACACTTTTCCCGAAAAAATAAATAA<br>AAAAAATAAATAAAGGTTGTGCGGCCGCAAGCTTATTCCTTTTAGNGAGGGTTAATTTTACTTG<br>GCACTGGCCGTCTGTTTACAACCTCGTGGACTGGGAAAACCTGGCGTTACCCAACCTAATCCCT<br>TGCAGCN  |
| RCT-38  | TNATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTT<br>CGGCACGAGGGTCCCTTCCCTATCAAAGCCAGATGCTTGAGAAGCCATGAAAGAGACCTCTGAAGT<br>GACAGAAAGGAGGAACAGCCTCAAGCCCCATCTGGAATCTTCTGGCTGCTGTCTCAGCCCGT<br>TCTTCTGGCTGTTGAGCATCGATGAGCTGTCTCCCTTCCAATTGAGTGACATATCACTCTGAG<br>TATGCCCCTAGATGCGGTGGAGATGAGAGGCATCCGGACCCCAAGGCTTCTGAGGAGGAGGAGG<br>CACACTTACTCTCTGCCTAGTAATGCCACAGAGCTTCCATCCCCATCCAAAGGTATCAGGCATG<br>GCTATCAGTTGGCTCTCAGGGTGGATTTGACATTTCTCAGATGATTAGAAGTTGGCAAGAAGCAAC<br>CTTGGTGAATAACTCTGGTGTCTAACTCTGTACTTGAGTTTACAGTCTCAGTAGAGGAGAGGCC<br>AAAGCTGTTGCGAGTGACGGCAGGATTATTTGAACAGTCATGATGCTTGGCTTTCAAAGGCGATTA<br>TCGCTTTAAGGCTTANAATTAGTAAGGCATCTTTATAACCAGGCATAGCTAGATCATAAATACT<br>GGAGGGCCAAAGGACCTAGAACGNGCTTCTTACCTTNCCTCTAGNTACATTACGACAAACATAA<br>TCNCCANNCTCAGGGGAAAACCTTGCTGATTCAAGTA |



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| RCT-39 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>TCGGCAGGAGGGTAAACCTGGCCAGGCTCATGTACAAGAAAAGACATGGTCCTCTATGGTTGTCT<br>GAAACTCCTGGGGAGCCCTGGAAACCTTGTAGAGGGCACTGGGGACCTCATTATATACAGAAGT<br>CACTGATGTGGACAAAGCTGGATACAGCTATGACCAGGCTGGAGGGACAAGAAGCAAAGGGGTAG<br>GTAAAAGAGCTCATGGTGTCAACTGCAGACAAGCCAAGTTGTGAATCCTGGTCAGCACACCCAGA<br>GACTTAGTCTAGAAATCCCTCCAGGATGCCCTGGATACCTGTGCTCCCACTGACCTCAGATGAGGG<br>CCTGCTGTGGGACTGTGGTCCTTGGAAATCACTACCCTCTTGACGACCCAGGCACAACGGCATT<br>CGTCATTCTGTTCTCATTATATTGTTTGTCTCATGGTCAAGTTTGGCCATGGCTTTGGTAGGTGT<br>CTTGAGCATTGGCTTGTGTTGGGGAATGGGGGAGCGTTGGGAGCAGAGTCCATGAACAATTTTGT<br>CCCTCAGACTGTCTTCATTTTGGATGAGAGTGAATAACTCTTTCCACATGGCCCTTTTGTGAGG<br>CACACGCTCTCCCCGAA   |
| RCT-40 | NTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGAAAGATCCAGTCACTGGGTTAGACTACTGGATTGTCAAGAACAGCTGGGGCTCTC<br>AATGGGGTGAGAGTGGCTACTTCCGGATCCGACAGGAACTGATGAATGTGCAATTGAGAGTATA<br>GCCATGGCAGCCATACCGATTCCCTAAATTTAGGACCTAGCTCCCACTGTCCCATACAGCTTTTT<br>ATTATTACAGGGTGATTTAGTCACAGGCTGGAGACTTTTACAAAGCAATATCAGAAGCTTACCA<br>CTAGGTACCTTTAAAGAATTTTGCCCTTAAGTTTAAACAACTCCTTGATTTTTTCTTTTAAAT<br>CCTCCCTATCAATCACCGAAGTACTTTCTTTTAAAGTACTTGGTTAAGTAATACTTTTCTGAG<br>GATTGGTTAGATATTGTCAAATATTGCTGGTCACTTAAATGCAGCCAGATGTTTCTATGTT<br>AAAAATCTATATAAAGTGCAAGCTCCTTTTTTAAATTACATAAATCCCATGAATACATGGCCAA<br>AATAGTTATTTTTTAAAGACTTTAAATAAATGATTTAATCGATGCTATAGAATTCCTATGTGTG<br>TTAC   |
| RCT-42 | TNN<br>CCCTCGAGGCCAAGAATTCGGCAGGAGGGTGGGTGGGACCACCCCTGGTAGTTCTGGGAACATATA<br>AGAGAGCAAGCAGAGCAAGCAATGGGAGGGAGCAAGCCAGTAAGCAGCATCCCTCCATGGCCTC<br>TGCATCAGCTCCTGCCACCAGGTTCCCTTGTGCTGGGTTCTTATCTCGACTTCCCTCCGATGAC<br>AAACGGTGATATGGAATGTAAGCCATATAAACCTTCTCCTCAATTCGCTTACGTTACAGTGTGTT<br>CATCAATAATAACCTGAGACAAGCAGGAAGCACTCTTAACCACAGAACCACTCTCCAGCCCCA<br>CGGTGACACTCTTGTCTCAAAGAAGGTAACAGCCACAACCACAAGCCAATCAGAACCATGTGCA<br>CGGAACACACAATTCACGATGCTGGGTTAAAGATCAGAACACGTTCTTACAGAAAAAAGGGA<br>AAAACCTTTGCGGCCGCAAGCTTATCCCTTTAGTGAGGGTTAATTTTAGCTTGGCACTGGCCGT<br>CGTTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTTAATCGCCTTGCAGCACAT<br>CCCCCTTTCCGACGCTGGGCGTNATAGCGAAANAGNCCGACCGATCGCCCTTTCCAACAGTTN<br>CGCAN |
| RCT-43 | GGCAGGAGGCAACAGAACCCAAAGAGGATGCTTTCCGGAAGCTTTTCCGCTTCTACAGGCAGAGC<br>CGGCGGGGTACGGCGGACCTAGGAGCGGTCATCGACTTCTCAGAGGCTCACGTGACTCAGAGCCC<br>GAAGCCCGGCGTGCCCAAGGTGGTCAGATTCCCTCTGAACGTGTCTCAGTGACTGAGCATGATA<br>CCTCTAGGGCAGGACTTCAACCTGCCCTGGAGACACCTCTCCAGCTGTCTCTCCCTAGCGGATCAT<br>TGCTTGAGCCCTGTTCTGTGGAAGACTGGCAGGTGTGTGCCACCTACTTGAAAACCTGCCCGAGTT<br>AATATGACTGTTCCGGCAGGTACTGGCCACAGGCCAGGACTTCTCTTAGAACCCATGGAGGAGCC<br>AAAAAGAGACATTACTGCAGATGGTTTGTGCCATCTGCATGACCAGAAAAGCCCTGTAAACCGGA<br>AGAGGTTAAATACCAACGACTAAAGCTTAGGGGACTCTCTGGTTGCCCTCACACAGGGGCAGGGAA<br>GAACTCACCTGTCTGCTTCTGCTTGGGCTCATCTTANAGCATAACTGAGTTTGTCCAGANAA<br>ATGTCCTACTCGGCCAGTTCTAGCTCTTATTANGNNGNNGNNGNNGTTTGTCTATACCC  |
| RCT-45 | TNNTNACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGCCAGGCTACCCCTGTCTCTCCAGGCACACAGGTGCACACACAACCTCATGCACATG<br>CATATAAATGACCACAAATATATACTGACACCCACACATATGTAGACACCTGTATATGCACAGG<br>TCCCACTACCACACAACTCAGCTGGGAAGGTTTCTTTAGATGAAGCGTTCCCTACCTGGTATC<br>TCTTCTTCCAGCCTGGTGCCTGGTGGTGTGCTCTCTGAACAGTGTGGGTAGAGGTGAGAG<br>GAAGCCCTACTTTCTACCTCTCCCCAGCCTCCTCTAGGCTGTGGCTACAATCTGATTCTCTCTGA<br>AGAGACTGCTTGGTCAGCTTCTTACCATAACACCTACCCAGGGCTTATCTTACTGGGAGCTGAG<br>ACAGGTCCCAATGAGGTCCCACTGTGCACTGTGCTTATCTCACTCCAGGGCAGAAGAGCCAC<br>AACATCACCAATTCTGCCACTTACAAGGTGGAGAAAGACAGGTCTGGTGGCTTANGCATGACCTGG<br>ANGTCCTCACAGCCCATTTAGCCTGTCTCAATGTCTCAGTTTGGCGGTGCTAATGGGGGTANCT<br>CANANACCCNCTNAANTTCANGGGGAG   |

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| RCT-49 | TTATCCATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGGTGAGGTGTTCTCGTGGTTACGATAGGTCTCTTCCCTGTGATATTCAATTGCAGAT<br>GGCTGGACTGATCAAGCAGTACAGAATGGAGGTCGGAGGGAGAGAAGGTCCTCCAGGGAGATGAG<br>AAATCGCCGAGCACCTTAAGTCTCAAGGTTTGCTGACGGCCAAGACCAGGCTTTGAATGAATGGT<br>GAACTCAGAGGGGAGCGCGTTGGCCTGAGGAACCCACGGATGCCAGTGTGGTCTATTCTTGCTT<br>TCAGGTACCCCTTGAACACAGAATAGCAGTCTAGTCTGCTGCCACCCCAAGGCTGGGCAT<br>GGTTCAAAGGCATGCAGGATGCAAAGAAGAGTCAGCTTTGGCTGGGGAGGAGTGGTTTGGTGTAC<br>ACTGCTACTGAAATAGAACTTTTGGCCTTCTGTCTGTAGAAATAAAATCTGACTTGGTGATGT<br>TTTTAAAAAAAAAAAAAAAAAAAAACATTGCGGCCGCAAGCTTATTCCCTTTAGTGAGGGTTAA<br>TTTTACTTGGCACTGGCCGTCGTTTTTACAACGTCGTGACTGGGNAACCTGGCGTTNCCCACT<br>TAATCCCTTGACACATTCCCTTTTCGCCAGT  |
| RCT-50 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGGCAATCATGGCTCGGGTTGGCCGCGGCCCTCTGCCGAGCTCCTCGTGTGGGATT<br>CGGGTTGGTGTGATACGCGCCACGGCCGGGAGCAAGCACCAGGCAACGCCCATGCTCAAGCG<br>GCAGCTCCTGGAGCGCGGACCTCGACAAGTCATGGACTGCGCTTCTGTCCAGCGGACACAC<br>AGCGACTTCTGCTGGGATGCGCAGCAGCCTCTGCCCACTTCAGGATGCTATGGCCATTCT<br>GGGAGGCGCTCTTAGTCTGGCCCTGGTTTGGCGCTGGTTTCTGGTTTCTGGTTTCTGGTGGAT<br>GCCGCCGAGAGAAAAGTTTACTACCCCATAGAGGAGACTGGTGGAGAAGCTGCCAGGTGTGG<br>CACTGATCCAGTGAGGAGCACC CGCGCTGGTGGCCATTTCATCGTCCATTTCATTCTTGGAGCC<br>AGCTTGGCTTTCAGAGACAAGCCGCGCCAGACTCTTCCAACCAAGGGGGTGGGGCGAGGTGG<br>TGATTACCTCCAAGGACTGGGCTTANGGTTCAAGGGANCTTCCAGGGTGTCTAATTGCCCTGT<br>CTCTGGNTCTGGGGCAGACAGANANCCTCAAGCTAGGTCACAA   |
| RCT-53 | ATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCG<br>GCACGAGGATTTATTACTTTATGTATGTAGTACACTGTGTCTATCTTCAGACACACCAGAAGA<br>AGAGGGCATCAGATCCCATTACAGATGGTTGTGAGCCACCAAGTGGTTGCTGGGATTTGAATCA<br>GGACCTCTGGAAGGGCAGTCAGTGTTCCTAACCGCTGAGCCATCCCTCCAGCCCAAGCTGTTTT<br>TATGGAAGTGATTCTCAACTCATGGGTCTATGACCCCTTTGGGGGTAAATGACCCCTTCACATAT<br>CAAATATCAAATCAAATACCCTGCGAGAGCAGATATTCAATTGCAATCCGCAACAGCAGCAAAAT<br>TACAGTTACGAAGTAGCAAAGAAAATAATCTTACGGTTGAAGGTCAACACAACACGAGGACCTGT<br>ACTACAGAGGTCTCGGTGTCAAGAAAGTCTAGAACCCTGTGTCTATGGGGGGGTGTCAGATCAGCC<br>GGGGCTACACAATGAGACTCATCTCAAGAAAGAAAAAAATGACAGGAAATATAAGCCTGACT<br>GTGCGCTCCACAGCTCTACCCCAAGCCCTCACCTACAACCACGCAAGGATCTGCTTCTGCTCCG<br>AGAGAGTGACTTCCACATTGCTTTATGCTCNAAGTCATCCCTACNATGNGGGCC   |
| RCT-59 | CCNNNTTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCC<br>AAGAATTCGGCAGGAGGCAAGATGGTGCTCGGGGGCTGAGGGAGCTCAGGAACTGAGCAGTG<br>ACTGGTCTCTTTCCAGTATTGAATACTGAGCCCTGTGGGTGTGCAAGCACTTAGTGGGTCTGGC<br>CCCAACCCCAACACCCCTGTTCTGTAAACCCCTGAGCTGGACTGTTTATCTTTAGCCGGGAGA<br>ACATGTATTTTGGTCCCTTCCCTGTCTCCGCTCAGATTGTAAACCTCCACGTGTGGGATCACA<br>CCCTGCACTGTCCCGAATCTTTACACCCATCCCAAGCTGGTGCTCAATAAATATTCTAGATG<br>ATTAAAAAAAAAAAAAAAAAAAAAAAAAATTTGGAAGCGGCCGCAAGCTTATTCCCTTTAGTGAG<br>GGTTAATTTTACCTTGGCACTGGCCGCGCTTTTACAACGTCGTGACTGGGAAAACCTGGCGGTA<br>CCCAACTTANTCGCCTTGCAGCACATCCCTTTTCGCCAGCTGGGCGTAATACCGAAAAGGCCCG<br>CACCGATCGCCCTTTCCCAANAATTGCNCAACCTGANTGNCAATGGGACCCCCCTGTAAACGG<br>CNNATTTAANC GCGGGC   |
| RCT-6  | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCAGGAGGTGCTAGCCCTAGAGAGCAGTGCTCACTTCAGACCAACCAGCCTCCGGTGCTTCTC<br>GCCCGAGCAAGAAAGTTTTCAGCGAGGAAAGTAAGTTTCCATCTGTCCAGCCATGGGAGAGGACG<br>CTGCACAGGCAGAAAAGTTCCAGCACCCAAATACAGACATGCTCCAGGAGAAGCCATCCAACCC<br>AGTCCAATGCCTTCTCCACACCGAGCCCAAGCCTGAATCTGGGGTCCACAGAGGAGGCCATCCG<br>AGACAACCTCACAGGTGAATGCTGTCAACGTCACACTCTCTTGATAAATTTGGTCAACATGCTGG<br>ACCCGCTGAGGGAGAACCAGCACAAATGGAGCAGCGGCAGATCAACCTGGAGGGCTCGGTGAAG<br>GGCATCCAGAATGACCTACCAAGCTCTCCAAGTACCAGGCCTCCACCAGCAACACAGTGAGCAA<br>GCTTGCTGNAGAAGTNTCGCAAGGTGAGCGCTCACACGCTGTGTTCGGGAGCGCTAGANAA<br>GCAGTGTGTACAGGTGAAGAAGCTGGAGAACCAANGCTCAACTCTCCGANGCAACCACTTCA<br>AAGTGCTCATCTTCCAGGAAGAAAGTGAGATCCCTGCGAGTGTGGTTGTGAAGGAGCCNGTCCC<br>AGCACNTGCNNAAGCNAGGACTTGCTTGATGAAAACNAGNCCTTGGGAGGAACTNT |

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| RCT-60 | <p>TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br/> TCGGCAGGAGGGCCAGGTGGAACCTCTGGACCTCTCGAGGCTCTGCCCTGGTGAACGGGTAT<br/> TTGTACAGGGCTATGAGAAGGGCCAACCTGACGAGGAGCTCAAGCCCAAGAAGAAAGTCTTTGAG<br/> AAGCTGCAGGCGGACTTTAAGATTTCTGATGACTGCGTCGCACAGTGGAAAGCAAACCAACTTCAT<br/> GACCAAGCTGGGCTTTGTCTCTGTAAATCACTAAAAGGGGGCAACATCAGCTAGCCGCTCGGCT<br/> GCTCCCACCATCTGTCTGCCGGTCTGTCACCTCTCACCCGCTCCCATCTCAGGACACTGAAGC<br/> ACCGGTCTGGACTGCTGACTAGACGAGGACTTGAAAGGGACAGCTACCTTCTTACCATGTGG<br/> GCTCATCCCGCTGGCTGAAAGGAGACGGAGTGCCTGGGCTAAGGATCTTGCTTGCAGCAACA<br/> GCTCTACCTTCTTCCCTTGGCAGCTGACTTGAGAAATCTGGTTCAATAGAACCCACAGAAAAAG<br/> TTTATTCTCGGTCTTGTAAATGGAAAAACACTGGTTCCTCAAGATTCCATGGGGTTTTNCCTGC<br/> AGCTGTACCTCTAGCTGAGATCTGNTGCTGGTCTGGGCTAATTACAGCTTC</p> |
| RCT-61 | <p>CNNNNNNNAATNNNNNNNTNCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTT<br/> TGGCCCTCGAGGCCAAGAATTCGGCAGGAGTGTATTATTGTACAAAGCAGCGTCTCTGTGTTTT<br/> GATCCCCCATNGTTTGAATTTCTCGNCTTTAGCTGGTAGAGTCTCANATATCCCTGACACGGGGCA<br/> TTCTGTGTGCGGTGAGGGGTTCCCGAGAGGNTCCGGAGCCCTGCGTGAAAGCAAGCTCTCAGNCT<br/> ACGGNGATTTGTGCAAGNTCAGCACGGCANAGCATCTCTGGTCCAGGTCTCACTTCTGCTCTT<br/> TATTGAAGACAAACATTCNCCANTAAGAAAAAAGAGAAAGATGTTTTGAGANAACTAAT<br/> TTTCTTTGACAAGAGTATTACTTAATTTTGGCCTATTAAGGTTCCCTAGTTAGNACTCNATT<br/> CCCTGTGCTAATCGTTCACTGTATATTGTAAACACACTGCTGATTCTGTACCAAACTGGTCT<br/> CAAAANAAAAAGAAAAAACAACNTCTAGCGGCCGCAAGCTTATTCNTTAAGGGAGGGTTA<br/> ATTTTANCTTGGCCCTGNCNGCTTTTACAACGTCGNGACTGGGAAAACCTGNCGTNACCCCA<br/> CTTAATCGCCTTGACGACATCCCCC</p>                                     |
| RCT-62 | <p>ATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCG<br/> GCACGAGGATTCCTCAAACTGAGTGGCCCTTATTACAGCAGATTCTGTGACTTGGGATTCATTC<br/> CTCATGTTTACCTTAAATTCACCAAGAACTGTAGACATCAGGACCAAGGTCTCTTACAAGCT<br/> AGATTACAGTGTGTAGTCTGAAGACCTTTTGTGTTGTTGAGACAGGTCTTTATGTTGTCTT<br/> GGAGCTTGCTGTATAGACAGGCTGGCTCAATAGAGACTTGCCTGCTTCTGCTTTCTAGTGC<br/> TGGGATTAAGGTGTGTGCTCTCACACCTGCCCCCTGTTGAGCATACTGACGGCAGAACTCTGAT<br/> ACAGCATCCATTTAAGGACGACAGTGGCAGAACGTGAATAGAACTAGCTAATAGATGTTGAGTC<br/> CTGAAAAATGCTCATCTGGACATGTCACTTTATGCTTTCTGTTGAAGCAATGATGGTAACATCTA<br/> GGACCTGAAGCACCACATTAAATTTTGAACATTTTGAATTTAGACAGTACAATTTTGAATAA<br/> ATTATGAATTTATTCTAAATATACNAATGTAAGGAGGAACTGGAAGTTCTTCTGNATTGC<br/> ATAAGTAAGTTTANAATTTCTTGGGGGAAACCATNAAG</p>                        |
| RCT-64 | <p>CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br/> CGGCACGAGGCTACTAGGTGGGCACAGCTCTCTCACCTGGGGACTTCAGGGTTTGTCCAGTG<br/> AATAACTGGCTGCTCTCTGAGGCAAACTGAATGGGGCATCTATGTTCCGTGTTTGTGTTT<br/> GTTTGTGTTGTTGTTGTTTGGCTTGGGATGGGGATCGTGCTCGGGCGCTCCCTGTCTGATCAGA<br/> AGACACATGTGGTTTCGCACTCAGTCCCTGGTTAAGCCAAAGAAAATGCCAGATGAGACCCGAGAA<br/> AACGTCTTTTGTGTAATGAGGCTTATTAGACTTCTAGGCATCCAAGCAGGGGCAAAATGATTCCC<br/> TCTTTTCTTTTCTCAAGAGAATAAAATGACATTTGTTCTTCAAGTGGCCCCAGTAGGGCAGGA<br/> CAGCCATCTTATGGACAGGCTATCTCCAGAGGTACAGGGGGAATGGATAGGAGGCTTGGATACGC<br/> CATGGCTGGCAGAGACCACTGCCCTCGGACTCCGGGCTCTGTAAGCCCTTCTTCCCAAGTGGA<br/> GCCAACACTGGGCTTCACTCCATGCTCTGACAGTGGCCACCCTCATGGTACCATGAGTGGC<br/> CTACT</p>   |
| RCT-66 | <p>TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br/> TCGGCAGGAGGACACTTTGCTTTAATCCACAAGAGGCAGAGGCAAAACACACAACCTGAGATCCAA<br/> GCCAGCTGGGCTACATAGTGAGACCTTATACATCTAAAAACCAAGAAATCCATAATCCAGG<br/> CTATTTGGGGGAACCTTGAAGAATACTTAGAAATGGCCGTGGATTGTCTACACGGGTGACCTAAA<br/> AAGACAGTGGGGACCTTGTCTGGGTCTCTGGGGTGCCCACTGTCCAGCCACTAGGACACTGTAA<br/> GGAGCTCTGTGCTATGGCACCGGGCCGGTCTTCACTGTATATTCAAGGATAGCACACATATATA<br/> TTAACTCTATTTATTTTGTCTGACCTGACTGCTGCACTTGTCTGGTGACGTTTCTCAGGTTAGGC<br/> TGGGGTGATACTCTGGGATGCTCTGCGTACAAAGATTATTTGAATGAAGTATCTCAGGCCGTGTC<br/> CTGTGTGTGTTGCTTTGGGGGTGGGAAGTCTTTGAAACCTTGTTCGGATGTTTTATAGGCTG<br/> AGAATGCTTGTGTGATGATTAAATTCCTTTTGAAGAACTTAAANNNNNNACNNNNNNNN<br/> NNNAAAN</p>   |

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| RCT-68 | TATTACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGCAGGTTGATAGAATCAGTAAGTTTCTAAGGGAAAGGAAATTGATATTTTCAGACCAATTT<br>TGTTCTAACCAGCATCCCAACTCTAGCTCTGTGAGCCACGTTACCGCATCCACCCTTTACTGCAT<br>GCTCAGGTCGCTGCAGTCTGGTTCTCCTGGGAGATTTTCATCATGTAGCTATTGGATACAATTTAT<br>GAAAACCAACTGTTTGAACATATTTGGAGTAGCTGTTCTTTCTTAGAGAACCAGCTGTTTCAG<br>CTGGTAGAACAGGTTGAAGCCCGCTGCATTAGCTGTGCTTTCCGTATGTTTAGAGGGATGCAC<br>AGGCACGACATCATTCAGGAAGGAAATTTGTGGTTAAGAATTTCCAGTAAGATCATACTTAATA<br>GCTGAGATTTTAAAGGCATTTTATGTTTTCATGACATAACAAAAGTCAACTCATGCTTATAGC<br>AAGGTGAACAAACCCTAGGTTCTCTTCAGACGTTAATTGATAGTATTTAATGTACGTTGAAAGTT<br>AACCTCCATTAATGACATCTTTCTTTGTGGTANGGCCCTACCTTCTGCTTTCTCGGAAAAGATGA<br>AATATACATCATTTGAACCTATTTTGTAGTTTCTGTTGGGGGGGGGGGGGGTT     |
| RCT-69 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGCAGGGTGAAGGAGGAGGATCTGTTCATAGCTACACAACCATCATGGCTCTCGTTACCT<br>GGGGGCCCTCCAAGTGAGCTGCCCTGTTGAGTGGATTTACATTATGTAACCTTTGGGCTTTCTCT<br>TTTTTAGAAAAATGGAATCTCGGATACAAATATTTTAAACAAAACCTAGCTATTGTGTGTTTGT<br>GCTTTGATTGATGCTCTGAGGTCACCTCGGGATGATTTTAAATACGCAGATGAAGGACACGCTT<br>AACATTGTGAGCACACAAGTCAAGAAATGAGGCTGTTGTAGTGCAAGCAGCCGCTGTGGCTGAA<br>CAGATTCTGCGGCCACTGCGTAAGTGCCCTGGGAGGTTGAGAGGCCACCCGGAAGGTGGAGGTTT<br>AAGTAGTGGTTGGTGACTTTTACGAGAATCATGAGAAAAATTAAGAAATGGTTTGAAGTCTTTT<br>CTCTGCTTTTCTGTTTTTTTACAGAAGCTGTAAACAAATATTACTGACTGTTCACTTTTTTGTAGAG<br>TTAGTGTTTTCTCTTCTTAGTAAAGAGACTGCAAGGGAACAGTCTTTATCACATAATCTATAAA<br>ATCATATCACCATATTTTTGTTTTACACCAATAAAATATACTTGAACCCCAAAAAA |
| RCT-72 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGCAGGCTCAGACACTGAGGATTGGAATAAGGGCCCTGGAGTAATACCCAGTCTTCAGTAAC<br>CATAGGCCCAGCCAGAGACCTGTGGTGGTTTCAGCCACAGCAGGGGCTGGCAGAAAACCCCTCTG<br>AGCTGCCAAAGCTTGTAAGTGCCAAAGTAAGCCCTTTCTCCAGCATGCTCTGGCTGAAGGGT<br>TGGCCCTGCCCTGACACCTTCTCAGTGCCCTCTCCCTATGCTTCCCAATGATGGTGGCCAGCCTG<br>GGGCTGGGCCCCACATATGCCAGTATGAAGGCCGCTGGATGAAGAGGGCAGGCTCCCACTCCCTT<br>CATTTCCCTAATGGGTGCTGGCTCCCAAGTTTCAAGACTGACATTTCAAGGCAGCTCTCA<br>GGACTGCCATTTTCTCTACACCTGTGGGTTTAGCTTTTGTATTTTAAAGTCAACCTTTGATA<br>CAAAAGTGTTCCTATCTTACTGGTTGAATTTAGCTTACTAATTCACACACCTTGAAGCAGCAACT<br>TGTAGCATGTAACCAAGCCAGTTGGTTACTCTGGAATGGGACAGTATGATGCCATCCCATGTTG<br>AACACTGCGCTCCNATNAAACAAGCTGGAATTC                               |
| RCT-74 | CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>CGGCAGGGAACCTTTTTTCCGAGATATCCGCGAGACCCCTGAGTTTGAACAATTCACATATCA<br>ATACTTTTGTCCCTCAGGCGATGTTTGCCTGCAAAATCCGCTCAGTGGTGAGCCTGCTCATTTG<br>ACACCTGAGAAGGCATGACTCCTCCCAATAACTAGCCAGGTGGACCAAGGAACCCGGCTCCCAT<br>TCCCAGCAATGGGACCCATCGCGGAACCATCGGCACCCACACCAAGTCTCTCATGACTCAAAGT<br>CCACTGCGAGCCTAGGAGGGTTGTTTCCAGAGAAGGAGGATATAGGCTAATGCTCTGTAACTGG<br>GAACATTCAATTTCTTCAGAGGCTCTTCAAAAAATGGCTCAGCAACGCAATGTTTCTCATCTCT<br>TCAATATGCAGGATAATTTTGGGGTTTGAACGTTAATTTTTCATAGATGTGTATTATTTTGAAG<br>TATCCAAATAAAGTCATTTATTTTACTATTNNNNNNAANAAANNAANAAAAAGTTGTGCGGC<br>CGCAAGCTTATTCCCTTTAGNGAGGGGTAAATTTAGCTTGGCACTGGCCGCTGTTTTACAACGT<br>CGNGACT  |
| RCT-76 | ANCNGAGANNNNNTNNTCACATGATTACGNATTTAATACGACTCACTATAGGGAATTTGGCCCT<br>CGAGGCCAAGAATTCGGCAGGAGCGCTTGCTTAGCAAGTGCAAGCCCTGGGTTCGGTCCCGAG<br>CTCTGAAAAAACAACAAAAAACAACCTTCTGTAANTAGTTGGATTAGGCCCACTCCT<br>CAGCACTGTGAGATGAATTCACGTCATTTATGTTTACAGNGTTTGGAAAGCATAGCTTGTA<br>CATCAGTTATACTACTTCTTGATGACTTCATGTAACCTTCGAAGTTAACGNGAAGCGATGCTTCA<br>TCTTTGCTCCGNAACCTCAGTCACTGTTTTCNATTAACCTGTAAANAGCNANACGGNGAAAN<br>NAGAAGAAAAAAGAAAAAGGTGGGCGGCGCAAGCTTATCCCTTTANTGAGGGGTANTTT<br>TAGCTTGGNACTGGCCGNCGTTTTACAACGNCGTGANTGGGAAACCCCTGGCGTTACCCAACCTTA<br>ATCNCCTTGNACAACATCCCCCTTTNCNCAGCTGGCGNTAATAACCNAAAAGCCCCACCGATCG<br>CCCTTCCCAACAGTTGCCNCAGCCTGAATGGNCAATGGGACNCCCTGTANCGNCCCCATTA<br>AACCCCNCGGNTGNGGNGGTTACCCCGCAAGCNTGACCGTTACNCTTGCCAGNCCC                        |

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| RCT-8  | CTAANNCTAANNMTTNNACATGATTACGAATTTAATACGACTCACTATAGGGGAATTTGGCCCTC<br>GAGGCCAAGAATTCGGGCACGAGGGAGATATGGATTCCAAAACGCCGTTCTGGTTTCGATACACCC<br>AGAAAGCACCTCATGTGTCGACCCCACTCTCGTGGAGGCAGCAAGAAACCTGGGAAGAGTGGGC<br>ACCAAGTGTGTACCCCTTCCGAAAGCTCAGAGACTGCCCTGTGTGNGAAGACTATCTGTCTGCCA<br>TCCTGAACCGTCTGTGTGTGTCATGAGAAGACCCAGTGAGCGANAAGGTCACCAAGTGCTGT<br>ATTGGGTCCTTGGTGGAAAGACNGCCATGTTTCTCTGCTCTGACAGTTGACGAGACATATGTCCC<br>CAAAGAGTTTAAAGCTGAGACCTTCACCTTCCACTCTGATATCTGCACACTCCAGACAAGGAGA<br>AGCAGATAAAGAANCAACNGCTCTCGCTGAGCTGGTGAACACAAGCCCNAGGGCCCAGAAGAT<br>CANCTGAANACGGTGGATGGGTGACTTCGCAAAATTCGTGGACAAGTGGTTCCAAGGCTGTGNAC<br>AAAGGATAACTGCTTCGCCCTGAGGGGCCAAACCTTTGTTGCTAGAACNCAAAAANCTTAACC<br>TTAAACACATCACAAACCATCTCAGGNTACCTNGAGAAAAAANACCTTGANTAN  |
| RCT-80 | CTTATGACATGATTACGAATTTAATACGACTCACTATAGGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGGAGGTTGTGCCTGATGGCTGACAGAAAACAAGCAGGAGAAATATACACAAGGGCTGC<br>TTCTAGACTGTTTCAGAGGAAGTTAGGTGGCTGACTACCTGACCGTAACCAACCTGCCTCTA<br>AGTATGGCCACGAACAGATCAACACCTGCTCCTTCCCTGCCATACCTCAAAGTGTAAATACAAGG<br>GAATTCAAAGCAGTTCATGTCTATCAGCTCTATCCAGAATCTTTCAATTTAAAAATCTTCTT<br>GGTTTTTTTCAGAAGTGACATTTTGGCTTTATTTCTTCTTAACTCTTCTATCTTATCAGTATGA<br>TGATACCTTTTACAGAATAAAAGTGAACATGAGACACTCTTACCTTAGAAGTTACCAAAAA<br>AAAAAATAAAGAAACATTCGCGCCGCAAGCTTATTCCCTTTAGTGAGGTTAATTTAGCTTG<br>GCACCTGGCCGCTCGTTTACAACGCTGCTGACTGGGAAAACCTTGGCCTTACCAACTTAATCGCCT<br>TGCAGCATATCCCCCTTTCGCCAGCTGGCGTAATANCGAANANGNCCCCACCCGATCGCCCTTCC<br>AACAGTTGCGCAACCTGAATGGCGAATGGGGACC  |
| RCT-83 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGGAATTTGGCCCTCGAGGCCAAGAAT<br>CGGCACGAGGTGATTATTTGTGATGGAAATTCCTTTGTACCACCTTAAATTAGTTTGTAAATCCA<br>AAGTGGAGGAAGACAGCAATAAAATGAATCCAAGTTTAAAAATGGGAAGACATAGGGTAAGAGCT<br>CTCTATTATAAACTGATTGCAATTTGTTTCTTCTTACACATCAGTATATTGCATAGCTCTCAAT<br>GAAACATTTGACGAACCTGCTAAGCTTACTTTTACAAACTCAAAAAATCCTTTAAAGGGCATAGG<br>AAAAAATAATCATTCAACAATAATACCTTTTGTCTTCTTAGAGCTATACTAAAGTATAGAAATTC<br>AAAACAGGACACCTTAGATTTTCCACCTATTCTGTAACATGGACGCTGGAACCTCACAGGAGAGCT<br>GTCGTGTTGCCACAAACATCATATTTTGGTGAGTGACTGTGGTTGTGATTACAGAGCAAGAA<br>GTAAGGCTCTCCAGGCAGTGATGGCTACTTCAGGTATGACTACCATGAAAGACTATGTGGAATTT<br>CTTTTACCTTTGGAATGTTTGAAGCTAGTAAAAAGAATTAGGGAATTTAAATTTTCANGGGA<br>AAAAATATG  |
| RCT-84 | TNATGACATGATTACGAATTTAATACGACTCACTATAGGGGAATTTGGCCCTCGAGGCCAAGAAT<br>CGGCACGAGGACAAAAGTCACCATGGCGTACCTATGAAGAGACCAACAGGTACCGTCTTGTATGC<br>ACATATATTACCCACACACGCATCAGCATATCCGCACCGTTTGTTCCTATATACAGGCATAAA<br>ATAGAGTAAGCCCAGGTAGTTTAAAGTACCTTCCGTGTGACTACCGTTGTGCTTCCGAAAGC<br>TGAGAATAAAAAGTTGTTTATTATGCTGGAAGGAGTTCGAGTTTGTCTGTGAGCATGTCGGG<br>CTAAGAAGAACATCAGGGCTCCCACTAAGGTTATCTTCCCGCTGACAAACCGTAAGGGAGCCATC<br>GGAGCTCACAAACCAATGTTCTCTGTGGAATGAAGCTAGTGCCAGCCTGTGGCTTTCGGGCTCA<br>GCAGGAGCTAGGGTAAGGNAAGTGTCTTGGTACATTTCAATGCTGTGCTTACTAAAGGTTTTAA<br>CCCCACACGCACTTGGCTGCGCGCGCGCACACACACACACACATATGCTTCTTTCCCTCT<br>GCAGTCTGGTTTGGCCTTGTGCTTTTGTGTTTGCCTTCTGNCAGCCACTAAGGTCACATGTTGTC<br>TTTGGTGTAGTGAGATTACATGCGTANAGNCCNCATATGGACTCCTCCGTTTCCATTTCCGGAN<br>CATACANAANGNCAGAGGGTTTTTGGTTTNGGTTGGNTTTTCTTTAAAAA |
| RCT-87 | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGGAATTTGGCCCTCGAGGCCAAGAAT<br>CGGCACGAGGCCAAACTGCACAGAGGGGAAATCAAGCTGAATTCGAGCTGGACTTAGATGACTC<br>CATTTTAGAGAAGTTTGCCTTCTCCAACGCTCTTTGCCTCTCAGTGAAACTGGCTATTGGGAAG<br>CAACACTGGACAAATTTATGTAGTCTATTCACTCCATCCAGAGGCTTTAAAGCTGGGAAGAAA<br>GTCAAAGTGTCTATAAAGAAGTTATGCAGAAAATGGGTGAGCTCTTGGCCCTCAGGCATCGAAT<br>AAACCTGAGCTCAGACTTCTTGATCACCCCTGACTTCTACTGGGACAGAGCGAACCCTGGAGGAGC<br>TTTACGACAAGACCTGCCAGTTCTCTCAGCATCACTCGAAGAGTTAAGGTCATGAATGAAAACTG<br>CAACACTGTCATGGAACCTAAGACCTAATGCGCAATCACCTCAATGAGAAGCGAGCGCTCCGCCCT<br>GGAGTGATGATCGTCATCTCATCACCATTGAGGTAAATGTTTCGAGCTGGGAGAGTCTTCTTCT<br>GATCTTGTGATCATGAAAGCACCCTGGAAGAGAGTAGTCAAGTTCTGCAACCAAAAAACAGCG<br>TTCTT   |

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| RCT-88 | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGCTCCTGGGTTCACAGTCTGAGCTTTCCAGGTATTGATGCTTCACAGGCACTGCTA<br>CATACTGCTGAGGGAACATGCTCGGTGACTTTACTGGGAAAATTCCTAGCAAAAATTTGTG<br>CCTGATTTCTCTGACGTGTGCTGAATAGACTTCCACAAGAGTTGTGCACACACATTCCTGAAA<br>TCCTTCTCTGCTTCCTGCCCCGGAATCTAAGTGCCTCAGCCTAGAGGAATTTCTAATCATTCCTC<br>GCTCACC CAAGGACCGCTGGCCCTGTTTATCTGTGCTATTACCTAGAAAATTCCTTCTTATCAGAAG<br>GCGCATGCTTTTCATTGTGTCCTTTTCCCTCGTCCCTTCACTACTTATAGAGGAATATTTAAAAGA<br>AACACAGAGGGGATGAATTCACTCGAAAATTTGTTGATGAAATTTCTCAAGGAGTTAAACCATGT<br>TTCAAAGAACAATGTGGACAGCATGCTGCCATTTGCTTAAAGGAAGTGAGATAGAGAAATGCA<br>CCGAAGGATTTCTGGAGGCGTCCAGGCTGCTTCTTGTCTACTTCAGCAGACTGGTGCCCACTGGTG<br>GGCCCTCTCGGGGTTCCTTCTGGACAGAA |
| RCT-89 | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGTGTGTTCTCTGAAATTTCTGGACTGATTTGGACAACCTGAATCTGGAGCGTGTGGG<br>ATACACAGGGGAGTTGATTTTTTATAAGCACATGAAACAGACAGTAGATTTCACACTTTTCAGGA<br>CCATAGTGTGTTGTCATGCTTTAGTTATATGTAGTGAAGTGGCAGAGGAGGTCATGAGGCACTTG<br>GATTCGACTGTACTGGAACCTGACCTTAAATGAGTAGAGAACATTCCTTGGCCAGAACGTTGGCACT<br>GTGTAGAGGCAGCCCCAACACTACCTCTTAATTTGGTTTATTACATGTAACCTTCCATATTTCCC<br>TCCCTTTTAAAGTCAGCAGTATTTTCGTTTAAATGTCATCTTAGAGCCGCTCTACAAAATGTTT<br>CAACAGACACCCTAAACTAGACCATTCCGAATTCATGTTCTTTTCGAGTTTATCCATTATCCT<br>TAAAAGTAAGTGTGTTACACCCACATTCCTGATGTATGATCTTCTAGCTCTGTACCAATACAG<br>GGTTTCTGTAGTCCAGACTGGCCCTCATATTCATGTCATAGCTGAAGATGACCTTGAACCTCTGA<br>TCTT                         |
| RCT-91 | TCTATGACATGATTACGAATTTAATACGAATCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAT<br>TCGGCAGAGGCTTTGCTCCAGCATGGCTGCCTTAGGGACCTGGCTATCCATAGGTGTCCGGAGG<br>TTGCACAGTAGTGAGTGGCGCGGGCCGGCAGCCAGTGGCGACTCCAGCAAGGGCTGGCTGCCAA<br>TCCTTCCGGCTATGGGCCCTCACGGAGCTTCCGTACTGGTCTTTTCGCGGATGGCCGCCCTGCTC<br>CCCCAATGAAAGGCCAATTCGAAGAGAAGCTCAAAGGGAGAAGCTTGCAAGACGAGTTGTGCTG<br>CTGACACAGGAAATGGATGCAGGATTCAGGCATGGAAGCTCAGGCAGCAGAACTGCAGGAAGA<br>AAGGAAGCAGAAACATGACCTTAAACCTAAAGGGACGTCAGTGAGGAACCACTTCCAAATCAAT<br>AAAAAGCTCCTGTGTCCTTCTCAAAAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT<br>TATTCCTTTAGTGAGGGTTAATTTTACGCTTGGCACTGGCCGCTGTTTACAAAGCTCGTGGACTG<br>GGAAACCTGGCGTTACCCAACCTAATCGCCTTGACAGCACATCCCCCTTTCCAGCTGGCGTAA<br>TAGCGAAAA                         |
| RCT-92 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGAGGTGCTACCCGGTCTCATTTGTTTCATGACTGCATATCATTAGCGCGCTTCAAAGGTGT<br>TCATATTTTCGAAGATCTGGGGGGTTTTTTCTATATCGCAGGATATTTTGTACATGCTTAGAG<br>ACCTCATTCAGTTGATAATCCCAACATGTTTGTGTCATCCTTAAATCATGAGAGTAAACCCAAGTA<br>TGACAAATTAAGAAAGAACTCTAGTCTTTCTAAATTTGCTTTGCTTAAAGAAATATGTTCCCATAG<br>ACTGCCAGCATTGCTCTCACCTAAGGACGAACCACTCCTCCTCATTCCTTGTCTTCAACTCATGC<br>ATTTGTAATGATGCTGGCAACCTACATGAACAGACAACATTTGCTCCTTGGCTCTGGACAGCCT<br>TACCAGCTGGTCTCATCTTCTGTCATGGCCACACCCCTAGTGATGGAACCTCAGGTANCATAGCAC<br>AACGTGAAGTTGTAGTCTGTTGAGCCTCCCATACCAATGAGAAAAGAGCTTTGGAATTCAGTT<br>TTCTGAGATTCTGGTAGTACCTTCATATTTTCATGTTGTAGACATTTGAAACTGNGGTAAACTTTA<br>TTTTT                       |
| RCT-94 | TTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCGGCAGGAGGAAACAGTTTATTTTAAATATTATAAATACTGTTATTTTGGAGCTCTTTGGCAT<br>GTAGGAGTTCCGGGTCTCAATGTATATTCGTTGGTGTATGATTAGGAAAGAAAAATTAATCA<br>AGAAACACATGGTTCTGTGACAGAGAGAGCTGTTTCTGGGAGGTGTTATCCACCTTTTCATTG<br>TGGATCATGTTCTTATTTATATTTCTGCTTCCATCTAGTTTCTTACATTCAGCAGCCCTCTT<br>GTCCCCCACTAATAAACTGACTGAAATCAAGAGAGCACCCCAAGTTATTTGTAAATAGTTACG<br>TGGGAAAAAAGACATATTAACCTGGAAGATAAAATGTGNCAAAACAAANAAAAAAGAAAAA<br>AACCCATGCGCGCGAAGCTTATTCCTTTAGTGAGGGTTAATTTTACGCTTGGCACTGGCCGCTG<br>TTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACCTAATCGCCTTGACACATCCC<br>CCTTTCCCAAGCTGGCGTAATACGAANAGGCCCGCACCGATCGCCCTTTCCCAACAGTTGCGCA<br>NCCTGAATGGCGAATGGGACCCCGCCCTGTAACCGGC         |

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| RCT-99                                       |           | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACGAGGGATCTCAGTATTTAACTGTTCTCAATTTTGTGAGGCTGTGTTGGAAATAACCCG<br>CCTCTGATGCTGTTGGTATGCAAGGCAGCGGTGCTTACACAATATTTCTGTGCTCTCCAGAGAC<br>GATGGACTGATTTCTGACACTACTCTCCCTTCACTTCCGTGGTTACCTTGAGTCTTGACTTACA<br>AGTGCCACGATGGGTGTAGCCCTTATTAAACAGATCGTGATTTCTGATCTCTCGCTGCAGCCAC<br>AGTGCAGCTCCCTATAAACCTGCAGCCCAACCATTGTATCAGGCATCACCTACTAACACAGAC<br>GTGCGCGGCTTTTCTGCATCAATTGCTGTGACGGTTCAGAATGTTGGTATACAAGAAGGAATAGA<br>AAACTGATAAGGTTTAAATAATCTGTAATTTCAATCTTTTCTGAAATACATTATATTGTA<br>TGTTTGAAATAATCTAGTACAAAGTATAATAAACTAGATGTATAATAAACCCCTTTAAATCATT<br>GCTAAGTGTATAAGTGGGAAGTGAAGCATTTATGGACAAAGTAATGTTACTCTAATGGTTACTT<br>GCTCGCTCTCGCTGGGCACACTGCTTATNATTT        |
| Phosphatidylethanolamine-<br>binding protein | NM_017236 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACGAGGCTGAAGTGGGAGCGGCCCCAGCACGCCCTGAGGGTCGACTACGGCGGAGTAACGGT<br>GGACGAGCTGGGCAAGTGTCTGACGCCACCCAGGTCATGAATAGACCAAGCAGCATTTATGGG<br>ATGGCCCTTGATCTCGGAAGCTCTACACCCTGGTCTCACAGACCCCGATGCTCCAGCAGGAAG<br>GACCCCAAAATTCAGGGAGTGGCACCCTTCTGTTGGTCAACATGAAGGGCAACGACATTAGCAG<br>TGGCACTGTCTCTCCGAATACGTGGGCTCCGGACCTCCCAAGACACAGGCTGACCCGCTACG<br>TCTGGCTGGTGTATGAGCAGGAGCAGCCTCTGAAGTGTGACGAGCCATCTCTCAGCAACAAGTCT<br>GGAGACAACCGCGGAAGTTCAAGGTGGAGTCTTCCGCAAGAAGTACCACCTGGGAGCCCCGGT<br>GGCCGGCAGCTGCTTCCAGGCAGAGTGGGATGACTCTGTGCCCAAGCTGCATGATCAGCTGGCTG<br>GGAAGTGGGGCGCTGCAGACCCGACGCCGGGACCCACAGTACAGTCAAGTCGATTATAAG<br>CATGTGCTTGTGGGGTGTCCCCCAGNCCATCCT         |
| Phosphoglycerate<br>kinase                   | M31788    | TTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTT<br>ATCGCGGGATCCTGTTGGGGTATTTGAATGGGAAGCCTTTGCCAGGGGAACCAAGTCCCTCATGG<br>ATGAGGTGGTGAAAGCCACGTCTAGGGGCTGCATCACTATCATAGGAGGCGGAGACACCGCCACT<br>TGCTGTGCCAAATGGAACACAGAGGATAAAGTCAGCCATGTGAGCACTGGGGGCGGCGCCAGTCT<br>AGAGCTCCTGGAAGGTAAAGTCTTCTGGGGTGGATGCTCTCAGCAATGTTTAGTATTTTCTG<br>CCTTTGGTTCTGTGCACAGCCCCCTAAGTCTGACCTAGTGTTTTCCGCATCTCCATTGGTGTAG<br>TGCAGCTAGTGGCCAAGACGACGACCAAGCAACCTAAGCAGCTGCACAGCATCTCAGCTCGTCT<br>TTACTGCATCGGGATTCTACTACGTTCAAGATCCCATTTAAATTCCTTAGCGACTAAAACCA<br>TTGTGCATGTAGAGGGCATCTATTTATACTCTGCTGTGAAAGGAAGTGAAGCTGAAGCTTGCC<br>AAAAGGGCAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGA<br>TGG                                   |
| Poly(ADP-ribose)<br>polymerase               | U94340    | GTTATTTAGGTGNCACATATAGAATACTCAAGTTATGCATCAAGTTGGTACCGAGCTCGGATCCAC<br>TAGTACCGGCCCGCCAGTGTGCTGGAATTCGCCCTTCGCGGGATCCGCACAATGCCTATGACCTGG<br>AAGTGATAGACATCTTTAAGATAGAGCGAGAGGAGAGCCAAAGCTACAAGCCCTTCAGGCAG<br>CTTCAACAACCGGAGACTGCTGTGGCAGGGTCCAGGACCACCAACTTCGAGGCATCTGTGCACA<br>GGGTCTGCGGATAGCCCCACCTGAAGCACCTGTGACAGGCTACATGTTTGGGAAAGGAATCTACT<br>TTGCTGATATGGTGTCCAAAAGTGCGAACCTACTGCCACACGTCTCAGGGAGACCCGATTGGCTTA<br>ATACTGTTGGGAGAAGTTGCCCTTGGAACATGTACGAGCTCAAGCATGCTTCTCACATCAGCAA<br>GTTACCCAAGGGCAAGCACAGTGTCAAGGTTTGGGCAAAACCGCCCTGACCTTTCGGCCAGCA<br>TCACCCTGGATGGTGTAGAGTTCCGCTGGGAACAGGATTCCGCTCGGTGTTAATGACACCTGC<br>CTGCTGTATAACGAGAAGCTTGGCCAAGGGCAATTCGACATATCCATCACACTGGCGGCCGC<br>TCGAGCATGCATCTAGAGGGCCAATT          |
| Preproalbumin                                | V01222    | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACGAGGCCCCACTAGCTCTGGCACAATGAAGTGGGTAACCTTTCTCCTCCTCTCTTCATC<br>TCCGGTTCTGCCTTTTCCAGGGGTGTGTTTCGCCGAGAAGCACACAAGAGTGAGATCGCCCATCG<br>GTTTAAAGGACTTAGGAGAACAGCATTTCAAAGGCCTAGTCTGATTGCCTTTTCCAGTATCTCC<br>AGAAATGCCCATATGAAGAGCATATCAAATTTGGTGCAGGAAGTAACAGACTTTGCAAAAACATGT<br>GTCGCTGATGAGAATGCCGAAAAGTGTGACAAGTCCATTCACACTCTCTTCGGAGACAAGTTATG<br>CGCCATTCCAAAGCTTCGTGACAACTACGGTGAAGTGGCTGACTGCTGTGCAAAAACAGAGCCCG<br>AAAGAAACGAGTGTTCCTGCAGCACAAGGATGACAACCCCAACCTGCCACCTTCCAGAGGCCG<br>GAGGCTGAGGCCATGTGCACCTCCTTCCAGGAGAACCCTACCAGCTTCTGGGACACTATTTGCA<br>TGAAGTTGCCAGGAGACATCTTATTTCTATGCCCCGAAGTCTTACTATGCTGAGAAATACA<br>ATGAGGTTCTGACCCAGTGTGTCAGAGTCTGACAA |



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| Preproalbumin,<br>sequence 2 (alternate<br>clone 1) | V01222    | TTCTGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGTCTGTCTGCCATCCTGAACCGTCTGTGTGTGCTGCATGAGAAGACCCCACTGAGC<br>GAGAAGGTCAACCAAGTGTGTAGTGGGTCCCTGGTGAAAGACGGCCATGTTTCTCTGCTCTGAC<br>AGTTGACGAGACATATGTCCCAAAGAGTTTAAAGCTGAGACCTTCACCTTCCACTCTGATATCT<br>GCACACTCCCAGACAAGGAGAAGCAGATAAAGAAGCAAACGGCTCTCGCTGAGCTGGTGAACAC<br>AAGCCCAAGGCCACAGAAGATCAGCTGAAGACGGTGATGGGTGACTTCGCACAATTCGTGGACAA<br>GTGTTGCAAGGCTGCCGACAAGGATAACTGCTTCGCCACTGAGGGGCCAAACCTTGTGTAGAA<br>GCAAAGAAGCCTTAGCCATAACACATCACAACCATCTCAGGCTACCCTGAGAAAAAAGACATGA<br>AGACTCAGGACTCATCTCTTCTGTGGTGTAAACCAACACCTAAGGAACACAAATTTCTTTGA<br>ACATTTGACTTCTTTTCTCTGTGCCGAATTAATTAATAATAGAAAGAATNTTAAANNNNNNNCN<br>NNNNNNNNNNNAAAGTGTGGCGNCGCAGCTTATTCCTTTAGNGAGGGTTAATTTTACTT<br>GGCACT |
| Proliferating cell<br>nuclear antigen gene          | Y00047    | CNCAAGCTATGCATCAAGCTTGGTACCAGCTCGGATCCACTTAGAAAACGGCCCGCCAGTGTGCT<br>GGAATTCGCCCTTCGCGGGATCCGGGGCTGAAGATAATGCGTGATACCTTAGCANTAGTATTGA<br>AGCACCAATCAAGAGAAAGTTTCAGACTAGAGATGAAGTTAATGGACTTAGACGTTGAGCAAC<br>TTGGAATCCAGAACAGGAGTACAGCTGCGTAGTAAAGATGCCATCTGGTGAATTTGCACGTATA<br>TGCCGGGACCTTAGCCATATTGGAGATGCTGTGGTGACCTCCTGTGCAAAGGACGGGGTGAAGTT<br>TTCTGCGAGTGGGGAGCTTGGCAATGGGAACATTAAGTTGTCCAGACAAGCAATGTTGATAAAG<br>AAGAGGAAGCTGTGTCCATAGAGATGAATGAGCCAGTTCAGCTAACTTTTGTCTGAGGTACCTG<br>AACTTTTTCACAAAAGCCACTCCACTGTCTCCTGCAGTAACACTCAGTATGTCTGCAGATGTACC<br>CCTTGTGTAGAGTATAAAATTGCTGCATGGGACACTTAAAGTATTATTGGCTCCCAAGATCG<br>AAGATAAGCTTGGCCAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGGCCGCTCGAGCATGC<br>ATCTAGAGGGCCGATTC   |
| Prostaglandin H<br>synthase                         | U18060    | TGCGAATTTGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTC<br>GCCCTTCGCGGGATCCGTGGACTACGGTGTGAGGCACTGGTGGATGCCTTCTCAGCCAGAGGG<br>CTGGCCGATTGGTGGGGTAGGAACCTTGACTACCATTCTGCATGTGGCCGAGGATGTCAATC<br>AAGGAGTCCCGAGAAATGCGCCTGCAGTCTTCAATGAATACCGAAAGAGGTTTGGCCTGAAGCC<br>TTACACTTCTTTCCAGGAGTTTACAGGAGAGAAGGAGATGGCCCTGAGTTGGAGGAGCTATATG<br>GTGACATCGATGCTTTAGAGTTCTACCCGGGGCTGATGCTGGAGAAGTGCCAGCCCACTCCCTC<br>TTTGGGGAGAGCATGATAGAGATGGGGGCTCCTTCTCCCTCAAGGGCCTCCTAGGGAATCCCAT<br>CTGTTCCCCAGAGTACTGGAAACCCAGCACATTCGGTGGTGATGTGGGTTTCAACATCGTTAACA<br>CAGCCTCACTGAAGAACTGGTCTGCCTCAACACCAAGACCTGCCCTATGTCTNCTTCCGTGTG<br>CCAGATAAGCTTGGCCAAGGGCGAATTCAGCACACTGGCGGCCGNTACTAGTGATCCGAGCTC<br>GGTACCAACTTGATGCATAGCTTGA   |
| Proteasome<br>activator 28 alpha                    | D45249    | GAATCGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTCGCCC<br>TTGGGACGAAGACGACAAAGGTCTCTCCCTGTGGTCCAGTGAACGCAATGAGAAGATTGTGGTCC<br>TCCTGCAACGCCTAAAGCCCAGATCAAGGATGTCAATTGAGCAACTCAACCTGGTTACTACCTGG<br>TTGCAGCTACAGATACCTCGGATAGAGGATGGGAATAATTTGGCGTGGCTGTCCAGGAAAAGGT<br>GTTTGAGCTGATGACCAGCCTTCATACCAAGCTGGAAGGCTTCCAAACGCAGATCTCTAAGTACT<br>TCTCCGAGAGGGGTGATGCCGTGGCCAAAGCAGCCAAAGCAGCCTCATGTGGGTGATTATCGGCAG<br>CTGGTGCATGAGCTGGACGAGGCGGAATACCAGGAGATCCGGCTGATGGTCATGGAGATCCGTAA<br>CGCTTATGCTGTGTTATATGACATCATCTGAAGAACTTTGAGAAGCTCAAGAAGCCCCGTGGAG<br>AGACAAAGGGGATGATCAAGGGCGAATTCAGCACACTGGCGGCCGGTACTAGTGGATCCCNAGC<br>TCGGTACCAAGCCTTGATGNATAGCTTNGAGTATTCTATTAGTGTCAACCTAAATAGNTTTGGCN   |
| Protein O-<br>mannosyltransferase<br>1 (Pomtl)      | NK_053406 | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCACGAGGTTTGGCGTCAGAACGCAGGTGTTGTGAAAGCCACCGCTAATTCAAAGCAAAAATG<br>GGAAAGGAAAAGACTCACATCAACATTGCCTATTGGCTGCACCCAGGACAGTGCCAGATCCA<br>CTTGCTTGGAAACATCGTGATCTGGACTTCAGCCAGCCTCGCCACAGTGGCATAACCCCTACTCT<br>TCTTCTGGTACCTGCTCCGCCGTGCAAGGAACATCTGTGACCTCCTGAGGATGCCTGGTCCCAC<br>TGGGTGCTGGCTGGAGCTCCAGGAATGAATTCAAATTTCTATCTCAAGAGCCCTGTTTGAAGTGAT<br>TTCTCTCTCACAGTGAAGAATGTGCCAGCCACAGCATCACCATGAGGCCAACTCTGACCAG<br>TGTTTGAAGTGGCAGTGTAGGACTCACCTACACTACACCTAAGGCAGGAGGAGCAGCCAGTGAAG<br>GAGTGAAGTCCAGGCCCGCCAGCTGTGCGCCCAACATGGGGTCTTAGCTCTCTCCCGANGCC<br>CACAGTACTGCCACTCATTTGTGTGACAGTACAGTGGCCCTCTGTAAAGCCTGCTTTGAAANCTG<br>CCTTCACTCACACTGACTCCTCACCAATGCGACTCTANAAATC                            |



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| Protein tyrosine<br>phosphatase alpha | L01702   | GCTATGCATCAAGTTGGTCCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGC<br>CCTTATCGCGGGATCCTGCAGAGGCCACACATGGTCCAGACACTGGAACAGTATGAATTC TGCTA<br>CAAGGTGGTACAGGAGTACATCGATGCCCTTCTCAGATTATGCCAACTTCAAGTGACAGGGGACAA<br>GGCCACAGACAGGAGAATTGCCTTTAATATTTTGTAAATATCTGTTTGTTAATATACCCAAAA<br>TTGTATATATCTTATAACTGTTTTAGAAATGGCACATAGGCTTCTATTACCTATTAGGTGGAGAT<br>TTTGTATGTAAATGTGTAGCACTATAGTCTTTTCCAGTGTTTATTGGGGAATTAATAGTGT<br>GATATTGGAGTTGATTAAATGAAGTCTTAGCCTGGAAATGGGCCAGATTATTCTTTGCTTCAA<br>ATGTCTTTTCCAAAGAAGACAAACATAAGAGTCAATCCAGGTAACCTCGGTGCCAACTAAAACAA<br>AGCACAAGTTCTCGGAGCTCTTGAGGAAATGGTTGTCTCACCCTCCCGAGCCGCTCTTCCC<br>TTCCCTGAAGCTTGGCCAAAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGC<br>ATGCATCTAGAGGGCCCCAATT  |
| PTEN/MMAC1                            | AF017185 | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCG<br>CCCTTATCGCGGGATCCCTATTCCAATGTTCACTGGCGGAAC TTGCAATCCCAGTTTGTGGTCT<br>GCCAGCTAAAGGTGAGGATCTACTCTCCAAC TCAGGACCCACGCGCGGGAGGACAAGCTCATG<br>TACTTTGAGTTCCCTCAGCCATTGCCGTGTGTGGTGACATCAAAGTAGAGTTCTTCCACAAACA<br>GAACAAGATGCTCAAAAAGGACAAAATGTTTCACTTTTGGGTAAATACGTTCTTATACCAGGAC<br>CAGAGGAAACCTCAGAAAAGTGGAAATGGAAGTCTTTGTGATCAGGAAATCGATAGCATTTGT<br>AGTATAGAGCGTGCGGATAATGACAAGGAGTATCTCGTGCTCACCCGTGACAAAAAATGATCTTGA<br>CAAAAGCAACAAAGACAAGGCCAACCGATACTTCTCTCAAATTTTAAGGTGAAATATACCTTTA<br>CAAAAACAGTAGAGGAACCATCAAATCCAGAGGCTACAAAGCTTGGCAAGGGCGAATTCCAGCAC<br>ACTGGCGCGGCTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTA<br>TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGGTTCTCTG   |
| Pyruvate kinase,<br>muscle            | M24361   | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTC<br>GGCAGGAGGCGCATGCAGCAGCTGATTGCCGAGAGGCAGAGGCTGCCATCTACCACTTGCAATT<br>ATTTCGAGGAATCCGCGCGCTGGCGGCCATTACCAGCGACCCACAGAAGCTGCCGCGTGGGTG<br>CCGTGGAGGCCCTCCTTCAAGTGCTGCAAGTGGGCCATTATCGTGCTCACCAGTCTGGCAGGAGT<br>GCTCACCAAGTGGCCCGGTACCGCCCAAGGGCTCCTATCATTTGCTGTGACACGCAATCCCCAGAC<br>AGCCCGCCAGGCCCATCTGTACCGTGGCATCTTCCCTGTGCTGTGTAAGGATGCCGTACTGGATG<br>CCTGGGCTGAGGACGTTGATCTTCGTGTGAAC TTGGCCATGAATGTTGGCAAGGGCCGAAGCTTC<br>TTCAAGAAAGGAGATGTGGTCAATTTGTGCTGACTGGATGGCGCCCTGGCTCTGGCTTCAACAAC<br>CATGCGTGTANTGCCGTGATCATGATGATCTCTGAGCTTCTCTTCTAACCCCTGTCCCTTCCC<br>CTCCCTATNCTATTCTAATTAAGGCACAACGCTTGTAGTGCTCACTCTGGGCNATAATGTGGCGCT<br>GGTGGGCTGGGACACCACGAAAAAATAATGNCCTCTGAA   |
| RAD                                   | U12187   | GNAAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCG<br>CCCTTCGCGGGATCCCAGGGCACACATATGACCGTTCTATCACTGTGGATGGAGAAGAAGCATCA<br>CTAATGGTCTATGACATTTGGGAACAGGATGCAGGCTGTGGCTGCCTGGCCACTGCATGGCCAT<br>GGGGGATGCATATGTCATTGTGTACTCAATAACGGACAAGGGCAGCTTTGAGAAAGCCTCAGAAC<br>TCCGGGTCCAGCTGCGGCGGGCACGGCAGACAGACAATGTGCCCATCATCTAGTGGGCAACAAG<br>AGCGATCTGGTGCGCTCTCGTGAGGTCTCTGTGGGTGAGGGCCGGGCTGCGCAGTGGTCTTCGA<br>CTGCAAGTTTCATCGAGACCTCCGAGCACTGCATCACAACGTCCAGGCACTGTTTCAGGGGTGTCG<br>TGCGTCAGATACGCTGCGCAGGGACAGCAAGAGGATAATGCTCGTCGACAAGCTGGCACTCGA<br>CGACGGGAGAGCCTTGGCAAGAAGGCCAAACGCTTTCTGGGCCGCATAGTAGCTCGCAACAAGCT<br>TGGCCAAGGGCGAATTCCAACACACTGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTT<br>GATGCATAGCTTGAGTATTCTATAG   |
| Ref-1                                 | D44495   | GNATNTGCTCCACNANAATANAANGATGNANCNTAANNANAATTTAGCAANNATATANNNNNGNC<br>NTNGANNNNNNANANNNTTCCAGTGNNGATGGAATATTNTGCAANAATNTCGCCCNNTAATCG<br>CNGGGATCCCGAAANAACCCAAGTCCGAANCCAGAAGACCAAAANNANTAAGGGGNCANCAAAAN<br>AAAATTTAGAAGGAGNCCNCAAGGAAAAGGGCCCTTGTCTNTGTATGAGGACCCNTCCAAGTTCAA<br>GAAAACGTCAGCCAGTGGCAAAATCTTGCCCACTCAAAAATATGCTCCTGGAATNGGGATGGG<br>CTTCGAGCCTGGATTAAAAAGAAAGGCTTGGATTGGGTAAAGGAAGAAGCACCAGACATNTTGTG<br>CCTCCAAGAGACCAATGCTCAGAGAACAGACTTCCCGGCTGAAGTGAAGAGCGTGCCTGGACT<br>CACCATCAGTACTGGTCAGCCCCATCAGACAAAGAAGGATATAGTGGTGTGGCCCTACTTTCCC<br>GCCAATGCCGCTCAAAGTCTCTTATGGCATTGGTGAGGAAGAACATGATCAAGAAGGCCGGGTGA<br>TTGTGGCTGAATTTGAGTCTTTATCTTGGTAACAGCCTATGTTCCGAACGCAGGAAGGGTCTG<br>GTAAGACTGGAGTACCGACAGCGATGGGATGAAGCCTTCAGAAAGTTTCTAAAGGACTTGCTTC<br>CCGGAANCATCTTGTGCTGTTNTGNAANGNANTTAANAANCAATN |

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| Renal organic anion transporter | AF008221 | TGCGAATTGGGCCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTCGCGGATCCATCCAGGTGATTTTCGGTGCCGTGGACCTGCCAGTTTGTATGCTTCCTAGTCATCAACTCCATGGGGCGCCGGCCTGCACAGATGCCCTCCCTGTGTCTGGCAGGCATCTGCATCCTGGTGAATGGCATAATACCGAAGAGCCATACGATCATTTCGCACCTCCCTAGCTGTGCTAGGGAGGGCTGCCTGGCTTCCTCTTTCAACTGCATCTTCTGTACACCGGAGAGCTGTACCCACAGTGATTCGGCAGACAGGCCTGGGCATGGGCAGCACCATGGCCCGGTGGGCAGCATTTGTAGGCCCGCTGGTGAAGTACTGCAGAGTTCTACCCCTCCATGCCCTCTCTTCATCTTCGGCGCTGTCCCTGTGGTCGCCAGTGTCTACTGCCCTGCTGCCAGAGACCTTGGGCCAGCCGTGCCAGATACAGTGCAGGACCTGAAGAGCAGGAGCAGAGGAAAGCAGAATCAACAGCAGCAGGAACAGCAGAAGCAAGCTTGGCCAAGGGCGAATTCAGCACACTGGCGGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTG |
| Retinoid X receptor alpha       | L06482   | GCGAATTGGGCCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTCGCGGAATTCCTTGTGGAGTGGGCCAAGAGGATCCACACTTTTCTGAGCTGCCCTTGGAAGACAGGTATCTCTCCGGGAGGCTGGAAACGAGCTGCTGATTGCCCTCTCTCCACCGCTCCATAGCTGTGAAAGACGGCATCTCTGGCCACCGGCCCTGCACGTACACAGGAACAGCGCTCACAGTGTGGGTGGGCGCCATCTTTGACAGGGTGTAAACGGAGCTGGTGTGGAAGATGCGTGACATGCAGATGGACAAGACGGAGCTGGGCTGCTTGGCGCCCATTTGCTCTTCAACCTGACTCTAAGGGCTCTCCAACCTGCTGAGGTGGAGGCGCTGAGGAGAAGGTGTATGCATCACTAGAAGCGTACTGCAAAACAAAGTACCCTGAGCAGCCGGGAGGTTCGCAAGCTGCTGCTCCGGCTGCCCTGCACTGCGATCCATTGGGCTCAAGTGCCTGGACACCTGTTCTTCTTCAAGCTCATCGGGAAAGCTTGGCCAAGGGCGAATTCAGCACACTGGCGGGCGTTACTAGTGGATCCGAGCTCGGTACCAAACCTTGATGCATACCTGAGTA          |
| Retinol dehydrogenase type III  | U33501   | GNNNNNNNNTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTTCGGCACGAGGGCCTTCTCAGACTCCCTCAGGAGGGAGCTCACCTACTTTGGGGTGAAGGTGGCTATTATAGAGCCTGGTGGGTTCAGACCAATGTCACTAATATGGAGAGGCTATCAGACAACTGAAGAAGCTGTGGGACAGGCCACTGAGGAGGTCAAGGAGATCTACGGCGAGAAGTTTCGGGACTCTATATGAAAGCAATGGAGTCACTGGTGAACATGTGCTCAGGGGACCTGTCTCTGGTAAACGACTGCATGGAGCACGCCCTGACTTCTGTACCCCTCGCACCCGTACTIONAGCTGGTTGGGATGCAAGTTCTTCTACCTCCCATGAGCTACCTTCCCACCTTTCTTTCGGATGCCGTAATCTACTGGGCTCTGTAAAGCCTGCCCGAGCCCTGTGAATCTGCACATGTGTGCAGACTTGGGAAGTAAGGCGGTGGAGGGAGATAACAATGTGGGGTCCATTGTTTACCATACTCATTAAATAATCTGCTTCCGTACTAAAAAAGTGTGGCGGCCGCAAGCTTATT   |
| Retinol-binding protein (RBP)   | A858962  | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGCGTTTCTCTGGGCTCTGGTATGCCATCGCCAAAAGGATCCCGAGGTCTCTTTTGGCAAGACACATCATCGCTGAGTTTCTGTGGACGAGAAGGGTCAATAGAGCGCTACAGCCAAGGACGAGTCCGTCTTCTGAGCACTGGGAAGTGTGTGCAGACATGTTGGGCATTTTCACAGACACAGAAGATCTGCCAAGTTCAAGATGAAGTACTGGGGTGTAGCCTCTTCTCCAGCGAGGAACGATGACCCTGGATCATCGATACGGACTACGACACCTTCGCTCTGCAGTACTCTGCCCTGCAGATATCTGGATGGCACCCTGTGCAGACAGCTACTCTTTGTGTTTCTCGTGACCCCAATGGCCTGACCCTGGAGACACGGAGGCTGGTGGAGGACGAGGAGGAGCTGTGCCCTAGAGAGGAGTACAGATGATCGAGCACAAATGGTTACTGTCAAAGCAGACCCTCAAGAAACAGTTGTAGCAATGTCAAGGATGTATAAAGTTGGAACCTTCTGATTAGCTCTCATCCAGTCTTCA   |
| Ribosomal protein L13A          | X68282   | GGGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTCGCGGAATTCATTGTGGCCAAGCAGGTACTGCTGGGCCGAAAGGTGGTGGTTGTACGCTGTGAGGGCATCAACATTTCTGGAAATTTCTACAGAAACAAGTTAAAGTATCTGGCCTTCTCCGAAAGCGGATGAACACCAACCCGTCTCGAGGCCCTACCCTTCCGAGCCCAAGCCGATTTTGTGGCGCACTGTGGCAGGCATGCTGCCGCACAAGACCAAAAGAGGCCAGGCTGCCCTGGAACGCCTCAAAGTGTGGATGGGATCCCTCCACCCTATGACAAGAAAAGCGGATGGTGGTCCCTGTTGCCCTCAAGGTTGTGGCGCTGAAGCCTACCAGAAAGTTTGCTTACCTGGGGCGTCTGGCTCATGAGGTCCGGTGAAGTACCAGGCAGTGACAGCTACTCTGGAGGAGAAACGGAAGGAAAGGCAAGATCCATTAACGGAAGAAGACAGCTCTTGAAGCTAAGGAAACAGGCAGAAAAGAAATGTGGAGAAAAGCTGGCCAAGGGCGAATTCAGCACACTGGCGGCCGNTACTAGTGGATCCGAGCTCGGTACCAACTTGATGCATAGCTTGAGTATT     |
| Ribosomal protein L27           | NM_02514 | CNTNTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGGCCTGTGCTCGCTGTGCAATGGGCAAGTTTATGAAACCGGGAAGTGGTGCTGGTCTCGGTGGACGCTACTCCGGACGCAAGCCGTCATCGTAAAGAACATTGATGATGGCACTCCGACCGCCCTTACAGCCATGCCCTGGTGGCTGGAATTGACCGCTATCCAGAAAAGTGACAAGTCCGACATGGGCAAGAAGAAGATCGCCCAAGCGATCCAAGATCAAGTCTTTGTGAAAGTTTATAAATAAACCACCTCATGCCACAAAGGTACTCTGTGGATATCCCTTGGACAAAAGCTGTTGTCAACAAGGATGTGTTTCAGAGACCCAGCACTGAAACCAAGGCCAGCGGGAGGCCAAGGTCAAGTTTGAGGAGCGATACAAGACAGGGAAGAACAATGGTTTTCAGAAAGCTTCGCTTTTAGATGTATTTTGTCTTCGTCATTACAAAATAAAAAATANTAAAAAACAACAAAAAATCTCGCGGCCGCAAGCTTATTCCTTTAGTGAGGGTTAATTTTAGCTTGGCACTGGCCGTC  |

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| Ribosomal protein S8                  | NM_031706 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGAGGGGAAGCTTTGCGCTTCCTCTTTCCAGCCAGCGCCGAGCGATGGGCATCTCTCGGGACAACCTGGCACAAGCGCCGCAAGACCGGGGGTAAGAGAAAACCCCTACCACAAGAAGCGGAAGTATGAGCTGGGACGGCCGGCCGCAACACTAAGATTGGCCCTCGCCGCATACATACAGTCCGAGTTTCGAGGAGCAATAAGAAGTATCGTGTCTGTAGATTGGATGTGGGGAACCTTTCTGGGGCTCAGAGTGTGTACTCGCAAAACAAGGATCATTGATGTTGTCTACAATGCATCCAATAACGAGCTTGTCCGCACCAAGACCCCTGGTGAAGAACTGCATTGTGCTTATTGACAGCACACCCGTACCGCAGTGGTAGCA GTCCCACTATGCACTGCCCCCTGGCCGCAAGAAGGGGGCAAGCTGACTCCTGAGGAGGAAGAGA TTTTAAACAAAAACGATCAAAGAAAATTGAGAGAAATATGATGAAAGGAAAAAGAAATGCCAAA ATCAGCAGTCTTCTGGAGGAGCAGTTCCAGCANGGCAAGCTTTCTCGCCTGTATTGCCCTCAAGAA CAGGCCAGTGTGGCAGANCAGATGGCTATGTGCTCNAANGCAANGAGCTGGAGT |
| Ribosomal protein S9                  | X66370    | AGCTATTTAGGTGNCACCTATAGAATACTCAAGCTATGCATCAAGTTTGGTACCGAGCTCGGATCC ACTAGTAACGGCCGCCAGTGTGTTGGAATTCGCCCTTCGCGGAATTCTATGTGACCCACGGAGA CCCCTCGAGAAATCGCGTCTCGACCAGGAGCTAAAGTTGATTGGAGAGTATGGGCTCCGGAACAA ACCTGAGGTGTGGAGGTCAAAATTACCTGGCGAAGATTCTGAAGGCTGCCGGGAGCTGTTGA CGCTGGACGAGAAGGATCCTCGGCGTCTGTTTGAAGCAACGCTCTGCTGAGACGACTTGTTCGA ATTGGGGTGTGATGAGGGCAAGATGGAGCTGGATTACATTCTGGGCCCTGAAGATTGAGGATTT CTGGAGAGAAGGCTGCAGACCCAGGTCTTTAAGCTGGGCCCTGGCCAAATCTATTACCATGGCCC GTGTGCTCATCCGCCAACGTACATCAGGTCCGCAAGCAGGTGGTGAACATTCATCTTTTCATT GTTCGCCCTGGACTCTCAGAAGCACATTGACTTCTCCCTCCGTTCTCCTTATGGTGGCGGCCGCCC AGGACGAGTGAAGAGGAAAGCTTGGCCAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGCC GCTCGAGCATGCATCTAGAGGGCCCAATTACAA                     |
| Sarcoplasmic reticulum calcium ATPase | X15635    | GGAAATAGGCCCNNGATGATGCTCGAGCGGCCNCCAGTGTGATGGATATCTGCAGAATTCGCCC TTTGCAGAAATGTAAGGGTGTTCGGGTGCGTGCATGTGCGTTGTTAGCAACACATCTTCCAGCCC TCTGCATGACTGAGCTTGGGGAAAGAGAAATAGAACAGCCCCAGCTCACTGTGTGATGTGGAGG AAATGTGTATTACAAGTGGGGTTTTAGCTGTTGAGTCAAAATAATAACAAGTGTACAATTTAGCA TAAGGAATCGGAGAGCCTCTCCAGAGAAGTCGGTTTCTTTGCTGCAAGAAGATGAGGTTCTGAA CCCTTATCCAAGAACAGAAGCCATCAGCCAAGTCTCCACATTTCTCTGCAAAATGTTGTAGCCTC TATAACTGNATGATAGTGAATGCATGCCCTTCAGTTGTAAGTGGCCAGATCGCGCTTCAAN  |
| Selenoprotein P                       | NM_019192 | TTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT CGGCACGAGGGGCAAGTGAAGGCTTGCAACTTTCACTTGCCAGAGGAAGCTCTGACGAAGGGGA TGCATAAACAGCTCCTGTGTAAGTTATCTGAGGAGTCTGGGGCAGCTACCAGTAGCTGCTGCTG CCACTGCCGACACCTCATATTTGAGAAGTCAGGATCTGCAATCACTTGACAGTGTGCCGAAACC TCCCATCCTTGTGTAGCTGACAGGGGCTTTTCGCGGAGGAGAAAGTCATTGAATCCTGTCAATGT AGATCACCTCCAGCTGCCGTGACACAGTCAGCATGTAAGCCCCACAGAAGCCAGCCCCAAGTGAAG CTGAAATAATAAGACCAAGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG TCCCCAACCTCATCTAAAGACACAATTTTCATTTCTAGAATGTTTCCAATCCATTTAATTAATTAG TGAAGTAAAGTAGTTGAAATTTGATTTGTGCAAAACATGGAGAAATCTACCACATTTGGCTTCTAA AATTTAAATTTTATAGCCACAAACCATTTCATCCAAATCAGATTTGTACCGTGGGGCAACTGAA AAGTGATTGCGGNCATTGGGTAATATGGCTTTCTTTTCTTTCC    |
| Senescence marker protein-30          | X69021    | GAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCAGTGTGATGGATATCTGCAGAATTCGCC CTTATCGCGGGATCCCCAAGGGTCTTGTACTCCCTTCTCCTGATCACAGTGTGAAGAAATACT TTAGCCAAAGTGGATATCTCCAATGGTTTGGATTGGTCCCTGGACCATAAAATCTTCTACTACATT GACAGCCTGTCTACACTGTGGATGCCCTTGACTATGACCTGCCAACAGGACAGATTTCCAACCG CAGAAGCTGTTTACAAGATGGAAAAAGATGAACAAATCCAGATAGAAATGTGCATTGATGTTGAGG GGAAGCTTGGGGTGGCCTGTTACAATGGAGGAAGAGTAATTCCGCTAGATCCTGAGACAGGGAAA AAGCTGCAAACTGTGAAGTTGCCTGTTGATAAAACAACCTTCATGCTGCTTTGGAGGGAAGGATTA CTCTGAAATGTACGTGACATGTGCCAGGGATGGGATGAGCGCCGAAGGTCTTTTGGAGGCAGCCTG ATGCTGGTAACATTTTCAAGATAACAGGTCTTGGGGTCAAAGGAATTGCTCCATACTCGGGCAAA GGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGACCAAACCTTGATGCAT ACTTGAGTATTCTATAGTGNACCTAAATAGCTTGGCGTAATCN   |
| Serotonin transporter (SERT)          | M79450    | GNCCTATAGAATACTCAAGCTATGCATCAAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGC CGCCAGTGTGCTGGAATTCGCCCTTGGACATCCGCATGAATGCTGTGTAACACACCTGGGAGAG GACACCTCTTCCAGCCACCTCTCAGCTCTGAAAAGCCCCACTGGACTCTTCCCTCTAAGCC AAGCCTGATGAAGACACGGTCTTAACCCTATGGTGCCAGACTCTTGTGGATTCCGACCACTTC TTTCCGTGGACTCTCAGACATGCTACCACATTCGATGGTGACACCACTGAGCTGGCCTCTTGGAC ACCTCAGGGAGTGAAGGAGGGATGAACGCCACCCAGTCATCAGCTAGCTTCAGTTTGAATTA GGTCTGTGAGAGTCTGTATCATGTTTGTGTAAGATCACTACCCCGCATCTGTTAGCTTCTAA AGCCTTCAATGTTTCATGAATACATAAACCACTAAGAGAAAACAGAGATGTCTTGTAGCCATAT ATATTTTCTCGGTAGCATAGAATTCTATAGCTGGAATCTCTAGAACCTGTAAACCCAGTGTCTG CTGTGAGGTTAAGGAGGGAAGGTAAGGGCAATTCTGCAGATATCCATCACACTGGCGGCCGCTC GAGCATGCATCTAGAGGGCCCAATTCCG                                     |

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| Superoxide dismutase<br>Mn   | Y00497   | TTTNTGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAAT<br>TCGCCCTTATCGCGGGATCCACAAGCACAGCCTCCCTGACCTGCCCTTACGACTATGGCGCGTGG<br>AGCCGCACATTAAACGCGCAGATCATGCAGCTGCACCACAGCAAGCACCACGCGACCTACGTGAAC<br>AATCTGAACGTCACCGAGGAGAAGTACCACGAGGCGCTGGCCAAGGGAGATGTTACAACTCAGGT<br>TGCTCTTCAGCCTGCCTGAAGTTCAATGGCGGGGGCCATATCAATCACAGCATTTTCTGGACAA<br>ACCTGAGCCCTAAGGGTGGTGGAGAACCACAAAGGAGAGTTGCTGGAGGCTATCAAGCGTGAATTT<br>GGGTCTTTTGGAGAAGTTTAAAGGAGAACTGACAGCTGTGTCTGTGGGAGTCCAAGGTTCAAGGCTG<br>GGGTCTGGCTTGGCTTCAATAAGGAGCAAGGTCGCTTACAGATTGCCGCTGCTCTAATCAGGACC<br>CACTGCAAGGAACACAGGCCTTATTCCACTGCTGGGGATTGATGTGTGGGAGCACGCTTACTAT<br>CTTCAGTATAAAAACGTCAGACCTGACTATCTGAAAAGCCATTGGAAATGTAATCAACTGGGAGA<br>ATGTTAGCCAAAGAAN |
| Suppressor of<br>cytokine signaling<br>3                                     | AF075383 | ATTATAGAATACTCAAGTTATGCATCAAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGC<br>CAGTGTGCTGGAATTCGCCCTTATCGCGGGATCCGTGCCCGCTTTGACTGTGTACTCAAGTTGG<br>TGCACCACTACATGCCGCCCGCCAGGGGCCCCCTTCTCTTACCACCGACGGAACCTCCTCT<br>GAGGTTTCAGGAGCAGCCACCTGCCAGGCACTCCCGGGGGTACCCCCAAGAGAGCTTACTACAT<br>CTATTCTGGGGGCGAGAAGATCCGCTGGTACTGAGCCGACCTCTCTCTCCAACGTGGCTACCC<br>TCCAGCATCTTTGTGCGAAGACTGTCAACGGTCACCTGGACTCCTATGAGAAAGTGACCCAGCTG<br>CCTGGACCCATTTCGGGAGTTTCTGGACCAGTATGATGCTCCACTTAAAGAGCAAAGAAAGGGTC<br>AGAGGGGGCCTGGATCGGTGCGCTCTCTCCGAGGCACATGGCACAAGCAAAAATCCAGCCCCAA<br>TGGTCGGTAGCTCCAGTTAGCCACAGCAGAAGATAGGCTTCTCTCAGGCCCTCCACTCCAAGC<br>TTAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCC                                  |
| T-cell cyclophilin   | M19533   | GANANNNCNAANNANGNNNANGNNNGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>ATTTCGGCCCTTATCGCGGGATCCCTGTTCGAGCTGTTTGCAGNCAAAGTTCCAAAGACAGCAGA<br>AACTTTTCGTGCTTTGAGCACTGGGGAGAAAGGATTTGGCATATAAAGGGTTCTCTCTTTCACAG<br>AATTATTCCAGGATTCATGTGCCAGGGTGGTGAATTCACACGCCATAATGGCACTGGTGGCAAGT<br>CCATCTACGGAGAGAAATTTGAGGATGAGAACTTCATCTGAAAGCATAACAGTCTTGGCATCTTG<br>TCCATGGCAAATGCTGGACCAAAACACAATGGTTCCAGTTTTCATCTGCCTGCAAGACTGA<br>GTGGCTGGATGGCAAGCATGTGGTCTTTGGGAAGGTGAAAGAAGGCATGAGCATTGTGGAAGCCA<br>TGGAGCGTTTGGGTCCAGGAATGGCAAGACAGCAAGAAGATCACCATCTCCGACTGTGGACAA<br>CTCTAATTTCTTTGACTTGGCGGCATTTTACCCTCAAAACCATTCTCTGTAGCTCAGGAGAGC<br>ACCCCCACCANNNNNGNNATNA   |
| Thiol-specific<br>antioxidant (natural<br>killer cell-enhancing<br>factor B) | U06099   | TTCCAGTGTGATGGATATCTGCAGAATTNGCCCTTTCCGAAAGATAGGCTGCNAGGTGCTGGGAG<br>TGTCTGTGGACTCTCAGTTACCCACCTGGCCTGGATCAATACCCACGGAAGGAGGGAGGCTTG<br>GGCCCACTGAATATCCCTATGCTTGNATGTGACTAAAGCTTGTTCCAGAANTACGGCGTGT<br>GAAAAATGATGAGGGCATCGCTTACAGGGGCTNTTTATCATNGATGCCAAGGGTGTCTTCGCC<br>AGATCACAGTCAACGACCTACCTGTGGGACGCTCTGTANATGAGGCTCTCCGCTTGTCCAGGCC<br>TTTCAGTATACAGATGAGCATGGGGAAGTCTGTCTGCTGGCTGGAAGCCCGGCAGTGACACCAT<br>CAAAACCAATGTGGATGACAGCAAGGAATACTTCTCCNAACACAAGTGAAGTGGGTAAACATCGG<br>TAGCTGAATCCCGGATCTCACNTGCGCCCTTACCT   |
| Thiopurine<br>methyltransferase  | AF120100 | GAGACCCAAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTCCGC<br>CTTATCGCGGGATCCGACTGAGAGTGTTTTCCCGCTCTGTGGAAAGCCATTGAGATGAAATGG<br>TTCGACAGCCGGGGCCACACTGTAGTTGGTGTAGAAATCAGTGAAATTGGGATTCGGGAATTTT<br>TGCAGAACAGAATCTGTCTATACACAGAAGAACCGCTACCGAAATTGCTGGTGCCAAAGTGTTA<br>AGAGTTCTTCGGGAACATTTCTTATACTGTTGCAGCATTTTCGACCTTCCCAGAGCAACATC<br>GGCAAGTTTGACAGGATTTGGGATAGAGGAGCATTTGGTGGCTGTCAATCCAGGCGATCGTGACCG<br>CTATGCAGATATAACTGTCCCTGCTGAGAAGAGGGTATCACTACCTCCTGGTTGCTCTTCTT<br>ATGATCCAACAAAACACACAGGCCCGCCATTTTATGTTCCAGATGCTGAACCTTAAAAAGTTATTT<br>GGTACAAAATGCAACATGCAATGCCTTGAGGAGGTGGATGCTCTTGAAGAAAAGCTTGAAGGGCG<br>AATTCGATATCGCGGCCGCTCGAGCATGCATCTAGAGGGCCCTATTCTATAGTGTACCTAAATG<br>CTAGAGCTCGCTTGATCAACCTCGACT |
| Thioredoxin-1<br>(Trx1)  | X14878   | gncnaaaanggttataatgaaagttagtgaataatgataaaaaagggtanaattaatattttcatt<br>gtcatntataatcanaggcagttgggtatagactctcncncanttcattagntatttttgnaaan<br>taaaaaagnnacaggttttnacgnnnntggagctggttnncactttccagagcatgattagnenaac<br>tccgtaatagtggcttcagacttttcttctgttagcaccagagnactccccaaccttttgacctt<br>tanatananctgnaaggctcgcatgatttctcacagctcngcancaacatcctggcagtcattc<br>acgtggttacttcaagnaacaccacattggaatacngtccacagaggaatgaaagaagggttga<br>tcattttgcaagggtccacaccagctggcagagaagtccactaccacatagcttgtctcccgagc<br>ggccanggcctcctgaaaagcttcntgctctcgatcagcttcnccattttggctgttgccgggga<br>gggagccncacaggttttcggcagaaccgcatggaaatgg  |

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| Thioredoxin-2<br>(Trx2)      | U73525   | NACNTAANAANAANGAATAANGNGGGAAAGATCAATANNNGNCNNNNTTCCAGTNGATGGATAT<br>CNGCAGAATTGCGCCCTNTATCGCGGGATCTTCTGTCATCCCTCTGCTCAGACTGCCGGGAGATGGC<br>TNAGCGGCTTCTCCTGAGGAGGTTCTTGACCTCAGTCATCTCCAGGAAGCCTCCTCAGGGTGTGT<br>GGGCTTCCCTCACCCTCTACGAGCCTGCAGACCCCTCNGTACAATGCTGGTGGTCTAANNNGGAACA<br>CCCAGCCCTGCCCGGACATTTACGCCACCAGAGTCTGTTTCAACAACCTTTAACGTCCAGGATGG<br>ACCTGACTTTCAANACAGAGTTGTCAACAGTGAGACACCAGTTGTCTGTGGACTTTTCATGCACAGT<br>GGTATGGCCCCCTGCAAGATCCTAGGACCTCGGTGAGAGAAGATGGTAGCCAAACAGCACGGGAAG<br>GTGGTGATGGCCAAAGTGGACATTGACGATCACACAGACCTTGCCATTGAGTACGAGGTGTCTGC<br>TGTGCNTACCGNGCTGGCCATCAAGAACGGGGANGTGGGGACAAGTTTGTGGGATCAAGGCCAAG<br>NCCNNNGTNTCAA   |
| Thrombin receptor<br>(PAR-1) | M81642   | GCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTG<br>CCCTTATCGCGGGATCCACGTCTCTGATTGTGCACTACCTGCTCCTCTCCGACAGTCTGGCA<br>CAGAGACGGCCTATTTTGCTTACCTCCTCTGCGTCTGCGTGAGCAGCGTGAGCTGCTGCATCGAC<br>CCCTTGATTACTACTATGCCCTCTCCGAGTGCCAGAAGCACCTTTACAGCATTGTGTGCTGAG<br>AGAAAGCTCTGATTCCAACAGTTGCAACAGCACCGGCCAGCTGATGCCAGTAAGATGGATACCT<br>GCTCTAGCCACCTGAATAATAGCATATACAAAAGCTACTAGCTTAGGGAAGGGTGGCTGGAAG<br>GTTCCATGAAGAAAAGGTTGGAAAGTGAACAGCTGGGGAACCCCATCAGTCCCTGGCAAGAACT<br>GTATTGACTTCAACGCCCTTAAGAAAACCGCCAACGTCTGATTGTGCATGCATACTTCTTACAAGTG<br>CTATCAAGTGTATAGATTGGATAATCACCAGCAAGGTGATGGGAACGGAGTCAAGGTTTTCAGT<br>GTTAAGCTTGGGCCAAAGGGCCGAATTCCANCACTGGCGGGCGNTACTAGTGGGATCCGAGCT<br>CGGGACCN                                       |
| Thrombomodulin               | AF022743 | TTGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATT<br>CGCCCTTATCGCGGGATCCTGTGACCCCACTCCCAAGCTTTTGTCAATGCCCTGAGGGCTTCA<br>TCCTGGACGAGGGTTCCATATGCACAGACATTGATGAGTGCAGTCAAGGCGAATGCCTCACCAAT<br>GAATGTGCAAACTTCTGGCTCCTATGAGTGCATCTGCGGACCTGACACAGCCCTTGTGCTGCA<br>GATTAGCAAGGACTGTGACCCCATCCCTGTTCTGGAGGACTCAGAGGATGGTGGCTCTGGGAGC<br>ACCCATCAAGCAATCCGACGGTAGTCTCTTCGACAGTTCCTCTGCAAGACCAATGCATCT<br>GGTGTGCTCATTGGGATCTCCATTGCCAGCCTGTCCCTGGTGGTGGCGCTTTTGGCGCTTCTTTG<br>TCACCTGCGCAAGAAGCAGGGCACTGCTCGCGCAGAGCTGGAGTACAAGTGTACCTCTTCAGCCA<br>AGGAGGTAGTACTGCAGCACGTGAGGACTGATCGGACGCTGCAGACTCGGGGCAATAAGGGCGA<br>AATTCCANCACTGGCGGNCGTTACTAGTGGGA  |
| Thymidylate synthase         | L12138   | TTGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAAT<br>TCGCCCTTTCGCGGGATCCGACAGGAAGGAGACCTGGGCCAGTTTATGGATTCCAGTGGAGACAT<br>TTTGGAGCAGACTACAAAGATATGGATTACAGATTACTCGGGTCAAGGAGTAGACCAGCTGCAAAA<br>AGTGATTGACACCATCAAAACCAACCCCGATGACAGAAGAATCATATGTGTGCTGGAACCCAA<br>AAGATCTTCCCCTGATGGCACTGCCCTCTTGCCATGCCCTCTGTCAATTTTATGTGGTGAATGGG<br>GAGCTGTCTTGCCAGCTTTACCAGCGGTGAGGAGATATGGGTCTGGGTGTGCCCTTCAACATTGC<br>CAGCTATGCTCTGCTGACCTACATGATTGCACATATCACGGGCCGTCAGCCGGGTGATTTTGTCC<br>ATACTTTGGGAGATGCACACATTTATCTGAATCATATTGAGCCACTGAAAATTAGCTACGGCGA<br>GAACCAAGACCTTTCCCAAAGCTCAGAACTCTCCGAAAAGTTGAGACAATCGAAAGCTTGGCCAA<br>GGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGACTCGGTACCAAGCTTGTATGCAT<br>AGCTTGAGTATTCTATAGTGNACCTAAATAGCTTGN |
| Thymosin beta-10             | M17698   | NTTGTGGGAATTGTGAGCGGATACCATTTTCACACAGGAAACAGTTATGCCATGATTACGCCAAG<br>CTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCAAGCTTGGTACCGAGCTCGGATCCAC<br>TAGTAACGGCGCCAGTGTGCTGGAATTCGCCCTTCGCGGGATCCGGAGTACCTGGAGCGCGAGC<br>TCGGAACGAGAATCCACGAGTTGTAAGAAAATGGCAGACAAGCCGGACATGGGGGAAATCGCCAG<br>CTTCGATAAGGCCAAGCTGAAGAAAACCGGACGAGGAGAAGAACACCTTGCCGACCAAGAGA<br>CCATTGAACAGGAAAAGAGGAGTGAATCTCCTAAAAGCCTAGGAAGATTTCCCAACCCACCCC<br>TTCATCTCCGAGAACCCCTCGTGATGTGGAGGAAGAGCCACCTGCAAGATGGACGCGAGCCACA<br>AGCTGCACTGTGAACCCGGGCACTCCGCGCCGATGCCACCGGCCCGTGGGTCTCTGAAGGGGACC<br>CCCCACTAATCGGACTGCCAAATTTACCGGTTTGCCAGGGATATTATAAGCTTGGCCAAGGG<br>CGAATCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCAATTAC<br>NC   |

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| Tissue factor                                  | U07619    | CCAAGCTATTTAGGTGCACTATAGAATACTCAAGCTATGCATCAAGCTTGGTACCGAGCTCGGAT<br>CCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTATCGCGGGATCCGGGAACCTGTGGAGT<br>TTGCTCCTAGCTCAGAAAGACTCCCTTCATGGCCTGTCAITCCAGCTAATGCTTTGATTCCAACA<br>CTAGCATCTGTCACTTTAGGACATACTGAACGGTACAAATTGATCAACACTACAGCACCTTTTGC<br>ACAAAGCTTAAGATTGTGTATTCTACACGGCGGAAGACACTAGGTTGCCAGGCAAAGCCAGTGG<br>TCAGATGCCTTTCTATAACCTGGGTGGGCTTTTGGAGAACCCTTGAGGAGTGATGCCATAGGCT<br>CTAGAACAGGAAAGTGGGATTTGGGTGGACTTTTCCAACAGTTGTACTTTTCGTAAATCGGTATTT<br>GGGTTTGTGTTTTCTCTACTAGGTACTTTTGAAGTTCAAAGTAACTTGGCAAACCTGTATATG<br>TTAAATGCAGGATATTTCTGCTTGGGACATCCTTGTGATTTGTACTTTATTACAACCTAGCACTT<br>TAAC TGACAATGATGGGGATTGAACACTCGAGGGCAAGGGCGAATTCTGCAGATATCCATCACAC<br>TGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCAATTCCC      |
| Tissue inhibitor of metalloproteinases-1       | U06179    | CCAAGTGTGTTGGAATTCGCCCTTATCGCGGGATCCATCTCTGGCCTCTGGCATCCTCTTGTTCG<br>TATCATGTAGCTTCCAGTAAAGCCTGTAGCTGTGCCCAACCCACCCACAGACAGCTTTCTGC<br>AACTCGGACCTGGTTATAAGGGCTAAATTCATGGGTTCGCCAGAAATCATCGAGACCCTTATATA<br>CCAGCGTTATGAGATCAAGATGACTAAGATGCTCAAAGGATTTCGACGCTGTGGGAAATGCCACAG<br>GTTTCCGGTTCGCCCTACACCCAGCCATGGAGAGCCTCTGTGGATATGTCCACAAGTCCCAAGAAC<br>CGCAGCGAGGAGTTTCTCATCGCGGGCCGTTTAAAGAACGGAATTTGCACATCACTGCCCTGCAG<br>CTTCTTGGTTCCCTGGCATAATCTGAGCCCTGCTCAGCGAAAGGCCTTCGTAAAGACCTATAGTG<br>CTGGCTGTGGGGTGTGCACAGTGTTCCTGTTCAGCCATCCCTTGCAAACCTGGAGAGTGACAGT<br>CATTGCTTGTGGACAGATCAGATCCTCGTGGGCTCTGAGAAGGGCTACAGAGCGATCACTTTGC<br>CTGCGCTGCCACGGAATCCAGATTTGTAAGCTTGGCCAAAGGGCGAATTCTGCAGATATCCATCAC<br>ACTGGCGGCCGCTCGAGCATGCATCTAGAGGGCCCAATTCCG     |
| Transferrin                                    | NM_017055 | CTCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCCGCACGAGGGTGACCTGTGTATTGGCCAGCAAAATGTGCTCCGAACAACAGAGAGGGATAT<br>AATGGTTATACAGGGGCTTTCAGTGCTCGTTGAGAAGGGAGACGTAGCCTTTGTGAAGCACC<br>GACTGTCTTGGAAACACGAACGGAAAGAACACTGCTGCATGGGCTAAGGATCTGAAGCAGGAAG<br>ACTTCCAGCTGTGTGCCCTGATGTTACCAAGAAGCCTGTAACCGAGTTTCGCCACCTGCCACCTG<br>GCCAAGCTCCAAACCATGTTGTGTTCTCACGAAAAGAGAAGGCAGCCCGGTTAGCACTGTGCT<br>GACTGCCCAAGAGGATTTATTTTGGAAACGTGACAAGGACTGCACTGGCAATTTCTGTTGTTCC<br>GGTCTTCCACCAAGGACCTTCTGTTTCAGAGATGACACCAAGTGTGTTGACTAAACTTCCAGAAGGT<br>ACCACATATGAAGAGTACTTAGGAGCAGAGTACTTGAAGCTGTTGGAACATAAGGAAGTGTTC<br>AACCTCACGACTCCTAGAAGCCTGCCTTTCCACAAAAGTTAAATCCAAGAAGTGGGTGCCACT<br>GTGGTGGAGGAGGATGCCCCCGTGGATCCATGGGC                    |
| Transitional endoplasmic reticulum Atpase      | A1059675  | CNCAAAANNANANNNTTNGGNAACCCAGGGTTTTTNCNNNNCCNNNTTTTNAAAACCNNCC<br>NNGGCCNAANTAAAANTNACCCCCCNAAAANNAANNTNNGNCCCNNGGGGNTTTTTTTT<br>TTTTTTTTTTTCCNTTTNNCCCCANNNNTNTTNNNCNTTTTCNANAANTTTTTTTTTTTTTT<br>TTTGGTTTAGAACTGCTTATGATTAGTCTTCCAACAGTAACCTAAAAGCATGTAAAATAAAAAT<br>CAACCTACTTTCTATATAAACACCCAGAACTGAGGCCCTTGTCCACCTACCCAGGCTGGCTA<br>GAGGTAAGGGAGGGCTTGGACAGCATGAGTATAGATGCTTTACTGTGGTGATGGTGGGGGCGC<br>GCTCGGTTACACACACAGGTTACCTCTCGTCCGGAATCTTGGCCTCGAGGGCCAAATTCCTT<br>ATAGTGAGTCGTATTAATTCGTAATCATGTCATANC  |
| Tryptophan hydroxylase                         | X53501    | GANNGGCCCTCTAGATGCATGCTCGAGCGGCCGCGCAGTGTGATGGATATCTGCAGAATTCGCC<br>TTATCGCGGGATCCAGGATTGGAGCACGTGTGGTGTACAGAGTGTAGCCTTGGCATAAGCAGTTG<br>TATAAACTTTTCACTTGTAAACAAAGTGTACAGACATCAGCTTATAAAGAGGAAAAGTTTGT<br>TTTGGGTGTTATGGTCCATTAGACGCTGCTTCTGTGGTTTAAGCCAGTGGTGAAACAAGGCATGA<br>TGAGAGAATGTGGCAGAGCAACTTCTATAAAGGATGGAAGAGAGAAAAGTGAAGGGTTTAGAGAA<br>AGAAGAAGAGAGAGATGGAATGAGAGAGGAGAACACACACATGGGTACGCGCACACACACAC<br>AC<br>CAGAAAGATCCTACAGTACAGTTTAAAGTTTCAATTACCAGGGTAAGAGAGAGGGCTCAGAGTTA<br>AGAGTACTCGCTGCTTCCAGAGGACCTGCTTTGATTCCAGCACCCACACTGTAAGCTTGGC<br>CAAAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATNCGAGCTCGGNCCCAAGCTTG<br>ATGCATAGCTTGAGTATTCTATAGTGTACCTTAAATAGCTTTGGCGTAATCATTGGNCA |
| Ubiquitin conjugating enzyme (RAD 6 homologue) | M62388    | TTNGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCGCAGTGTGATGGATATCTGCAGAATT<br>CGCCCTTCGCGGGATCCGTAGGAGCTCATGCGGGATTCAAGCGATTGCAAGAGGACCCACCTG<br>TGGGGGTCACTGGTGCACCATCTGAAAACAACATCATGCAGTGGAAACGAGTTATATTGGACCA<br>GAAGGGACACCCCTTGAAGATGGTACTTTTAACTAGTAATAGAATTTCTGAAGAAATCCAAA<br>TAAACCACCAACCGTTAGGTTTTTATCCAAAATGTTTCAATCCAAATGTGTATGCTGACGGCAGA<br>TATGCTTAGACATCCTGCAGAACCGATGGAGCCCCACGTACGACGCTCTCTCCATCTTAACCTCA<br>ATTGAGTCTCTGTTGGATGAGCCGAATCCAAACAGTCCGCCAATAGCCAAGCAGCACAGCTTTA<br>TCAGGAAAACAAACGGGAGTATGAGAAGAGGGTTTCGGCCATTGTTGAGCAGAGCTGGAATGACT<br>CATAATAGACACCTGGTCTGTCCACCTTTCCATCGTCTGTTGTAAGCTTGGCCAAGGGCGAATTC<br>CAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGT<br>ATTCTATAGTGACCTAAATAGCTTGGCGTAA                     |



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| Ubiquitin D (Ubd)                        | NM_053299 | TCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGGCTACTCACATATAAGCAGACATGAGGACTCTTTTCTCACTCGGCCCTCTGACTGCAGACATGGCTTCCTGCGTCTGTGTTGTCCGTTTCGGAGCAATGGCCATTAATGACCTTTGACACACCATGAGTGACAAAGTGAAGAAAATCAATGAGCATATTAGGTCCCAAACCAAGGTCTCTGTGCAGGACCAGATCCTTCTGCTAGACTCCAAGATCCTCAAGCCCCATAGAGCGTTGTTCATCTTATGGGATTGACAAGGAAAACACTATCCACCTCACCTTAAAGGTGGTGAAGCCCAGTGATGAAGAGCTGCCCTTGTCTCTGTGGAGTCGGGCGACGAGGGGCAAGGCACCTCCTTCGAGTTCGAAGATCCAGCTCCGTGGCCCAGGTGAAGGAAATGATCGAGAATGTGACCGCTGTGCCTCCCAAGAAGCAGATCGTGAAATTGCAATGGAAGAGGCTGGAAGATGGAAGATCATGGCCGACTACAACATCAAGAGTGGTAGTTTGCTCTTTCTCACAGCGCACTGCATTGGGGGGTGACTACGGGAGTGGGGTGGATGAGAACTCCAAAACCCGACTTCCTTAATCAATTACCAATTGCATCTCTTGATGATATAAAAAATAATGAN |
| UDP-glucuronosyltransferase              | Y00156    | ANNNNNNNNNNTNCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAAATTCGGCAGGAGCTAAACCCTTGCCCAAGGATATGGAAGATTTGTCCAGAGCTCTGGAGAGCATGGCGTGGTGGTGTCTTCTCTGGGGTCAATGGTCAGCAGCATGACAGAAGAAAAGCCCAATGCAATTGCATGGCCCTTGCCCGAGATTCCACAAAAGGTTCCTTGGAATTTGATGGCAAACCCCAAGCAACCTTAGGACCCAATACCAGAGTCTACAAGTGGCTTCCCCAGAAATGACCTCCTTGTCATCCAAAACCAAGCCTTTGTAACTCATGGTGGAGCCAAATGGTGTCTATGAGGCCATCTATCATGGAATCCCTATGGTTGGCATTCTATGTTTGGAGAATACATGATAACATGCCCCACATGGTGGCCAAAGGAGCAGCTGTACATGAATATCAGGACAATGTCAAAGTCAGATTTGTTCATGCACATAAGGAAATAATAAACAATCCATTCTATAAAAAAATGCTGTGTGGTGTCAACCATTCACCATGACCAACCTATGAAGCCCCGACAAAGGCTGTCTCTGGATTGAGTTTGTCTATGCGC  |
| Uncoupling protein 2                     | AB005613  | NGGGGAATTTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTCGCGGAATTCGCGAGGAGCACCACAGGTGCCCTGGCTGTGGCTGTGGCCCAACCTACAGATGTGGTAAAGGTCCGCTTCAGGCCAGGCCCGGGCTGGCGGTGGTTCGGAGATACCAGAGCATGTGTCGAAGCTTACAAGACCATTCACGAGAGGAAGGATCCGGGGCCTCTGGAAGGGACCTCTCCCAATGTTGCCGAAATGCCATTGTCAACTGTACTGAGCTGGTGACCTATGACCTCATCAAAGATACTCTCCTGAAAGCCAACCTCATGACAGACGACCTCCCTTGCCACTTCACTTCTGCCTTCGGGGCGGGCTTCTGCACCACCGCTCATGCTCCCTCCCATGATGTGGTCAAGACGAGATATATGAACCTGCTTGGGCCAGTACCACAGCGCCGGCCACTGTGCCCTGACCATGCTCCGGAAGGAGGGGCCCGAGCCTTCTACAAGGGGTTTCATGCCCTTCCCTTCCCTCGCTTGGGATCCTGGAACGTAAAGCTTGGCCAAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGACCAACTTGATGCAATACTTGAGTATTCTATAGTGGCA                                      |
| Urokinase plasminogen activator receptor | AF007789  | GCGAATTTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTATCGCGGATCCACCACCGAATGGCTTCCAATGTTACAGCTGTGAGGGGAACAGCACCTTTGGATGTTCTTACGAAGAGACGTCCCTCATTGACTGCCGGGGACCAATGAATCAGTGTCTGGAGGCTACAGGCTTAGATGTGCTGGGAAACCGGAGTTACACCGTAAGAGGCTGCGCCACGGCTTCTTGGTGCCAAGGTTCCACGTTGGCCGACTCCATCCAGACCCACGTCAACCTCTCTATCTCTCTGCTGTAAATGGCAGTGGCTGTAAACCGCCCTACAGGGGGCGCCCCGGGCCAGGCCCTGCTCATCTTATCCTCAATGGCTCCCTGCTCCTGACCCTCAGACTGTGGGGCATCCCTCTCTGGACCTGAATCCTGAGCCGTCTGCCCTGGCTGGACCCAGGGACTTTTGACCTCCTCCCTCTGCTCCATCTTTGAGGACAGGCGTGCTGTATTGCTTTCTTGGGGCTCAAGAACTGGAAGAGAATGAGAAAAGGGCTGCGGGAAGCTTGCCAAAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAACTTGATGCATAGCTTGAGTATTCTATAGTGNCACTAAATACTTGN                  |
| Vacuole membrane protein 1               | AF411216  | TATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAAATAAGCAGAGAGTTTATATGTCAGAAGTTAGCGTGGTGGAGCCTGCCCTTACATCGGGAGGGCTCTCACAGGAAGGAAGATCCCCATTTCCAACCTGTACTGATTTTAAACATTTCTCCCTGAAAGCAGTTTGTCCACATTTTACACTGACATACCTTTGCTTTCTTTGTTAAGGTAAGGTCTCCACCCCTCGATTCAATCCACATTGTATTCTTAGGGTGGATATGATGTTCTGCTGCAAACTTAACAAAACCTGGCCTTCTGACACTTTCACAGGGCCACATGGTCCAACCTGGAGAACCTCGGCCACACAGAACCCTTCTGACGTATGTTAAATATGCCAGGCTTTTCAGGCTTGTACAAATGATTGGTTTTCTTAAGTACCAAATGTATATAAGTTATATATGTTGGATAGCAGTCTTGATGCTCCATCATGGAACAATGTAATATGCTTCTTTCCACCCCTCAAAAAGGCCATTTTATGATGCATTGCACACCCCTCTGGGAAATGATCTTTTAAATTTTGAAGACAGTATAAGGAAATCTGGTTGGTGTCTCACAAATGGAGTACGCCATTTTTTATCTGTATATTTAGAATGAAGTCCGTGGAAAA                       |



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| Vascular cell adhesion molecule 1 (VCAM-1) | M84488   | GAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCCCC<br>TTCGCGGGATCCGAACTGCAGCCTCTTTCTCAAAATACAACACTCTCCTTCATGGCTACAAAAAT<br>GGAAGATTCCGGCATTTATGTATGTGAAGGGATTAATGAGGCTGGAATTAGCAAAAAATCAGTTG<br>AACTGATTATCCAAGGCTCTTCGAAGGACATACAGCTTACAGCCTTCCCATCTAAGAGCGTCAAA<br>GAGGGAGACACTGTCAATTATCTCCTGTACTTGTGGAAGTGTGCCCCGAAATATGGATAATTCTGAA<br>AAAGAAAGTCAAGACAGGAGACATGGTGCTAAAGTCTGTTAATGGCTCGTACACCATCCGCAAGG<br>CACAGCTGCAGGATGCCGGAGTATACGAGTGTGAATCGTAAACCGAAGTTCGCTCGAGTTGCCGA<br>AGTTTAAACACTTGATGTGAAGGAAAAAGAAATAACAAGGACTATTTTCCCTGAACTCCTTGC<br>ACTCTACTTTGCATCCTCCTTGGTAATACCCGCCATTGGGATGATCATTTAAGCTTGGCCAAGGG<br>CGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGACCAAGNTGNTGCATAGCT<br>TGAGTATTCTATAGTGNACCTAAA                         |
| Vascular endothelial growth factor         | AF062644 | GCGAATTGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTGCG<br>CCTTATCGCGGGATCCAGAGATGAGCTTCTGCGCATAGCAGATGTGAATGCAGACCAAGAAAA<br>GATAGAACAAAGCCAGAAAATCACTGTGAGCCTTGTTTCAGAGCGGAGAAAGCATTTGTTTGTCCA<br>AGATCCCGCAGACGTGTAAATGTTCTGCAAAAACACAGACTCGCGTTGCAAGCGGAGGCAGCTTG<br>AGTTAAACGAACGTACTTGCAGATGTGACAGCCAAAGGCGGTGAGCCAGGCTGCAGGAAGGAGCC<br>TCCCTCAGGGTTTCGGGAAGTACACCTCTCACCGGAAAGACCGATTAAACCATGTCACCACCACAC<br>CACCATCGTCACCGTCGACAGAACAGTCCCTTAATCCAGAAAGCCTGACATGAAGGGAGAGGAAGC<br>TTGGCCAAAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAA<br>GCTTGATGCATAGCTTGAGTATTCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTCATAG<br>CTGTTTCTGTGTGAATTTGTTATCCGCTCACAATCCACACAACATACGAGCCGGAAGCATAAA<br>GTGTAAGCCTGGGGTGCCCTAATGAGTGAGCTAACTCACATTAATTGCGT |
| Very long-chain acyl-CoA synthetase        | D85100   | TCCTCATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGA<br>ATTCCGGCACGAGGTAGATTTGTTGAAGAAAGTGAATGTTTACGGTGTGCCCGTGCCAGGTCATGA<br>AGGTCCGATCGGGATGGCCTCGATCAAGATGAAAGAAAACACGAGTTCAATGGAAGAAACTCT<br>TTCAGCACATCTCGGAGTACCTGCCAGTTACTCGAGGCTCGGTTCTGAGAATACAAGATACC<br>ATTGAGATCACCGGGACTTTTAAACACCGCAAGTGACCTGATGGAAGAGGGCTTTAACCCCTC<br>AGTCATCAAGATACCTTGTATTTTATGATGACACAGAAAAACATACGTGCCCATGACTGAGG<br>ACATTTATAATGCCATAATTGATAAGACTCTGAAGCTCTGAATGTTGCTGGCTCCTAACACTTC<br>CAGAAAGAAACACAATAGGCCTAGCATAGCCCTTCACATGTGTAATCCAACCTTAACCTGATTA<br>AAGGTTATAGGTGTGATTTTTCCTAGGAAATATTCAATTTAAAGGACAATTGTTTGTGTTTGT<br>TTGGTTTTTATTAATTACACCAGAAGCTTTGCAAGTAAAAGATTTAAGTCACCTATTTTTTCAA<br>TGTGCACCTGCCATTTGTCTTGCAAACTTAACTTCTTGGAGAGAG                 |
| Vesicular monoamine transporter (VMAT)     | L00603   | TGATTACCCCCAAGCTATTTAGGTGCCCTATAGAATACTCAAGCTATGCATCAAGCTTGGTACCG<br>AGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTATCGCGGGATCCGGCAG<br>AGGAGAGAATCCAAATGCTGCTTTCTTTTATATAAATGCTTGATGGTCTTCTTGGGTGAGAACAA<br>AACGTTATGCACTTTAAACAGTCAAGGTAAAGTATGATGTGGTTTATCAAATCCGGCTCATGTTT<br>TAGAAAACAAGGCTATCAAGCTGCTATAATGTGAAAAATCAAACATACATCTCCACCTGCTT<br>CAGGTCACTGAGTGTTTTTCTAGAGATTGTTAATTTGAGTTGCTGTTATTTTPTAGACTCC<br>TAAAAGGTTGTTTATATCAATGTAGAAATGAGTTTACGCAAGATGGATGCAATGAAACTGCCC<br>GTGCTAGCACAGTAATGTTCAAGGTAATGGAGTGGTCCGGACACCTTCCCTTTCTGAAGCAGAG<br>AAAACCATCTACAAGCGTGTGTGTTACTGCATCATCTGTGCGCTGGTAGAACAATGTTTCTTAA<br>GCACGACAACACTGATCGATAAGCTTGGCCAAAGGGCGAATCTGCAGATATCCATCACACTGGC<br>GGCCGCTCGAGCATGCATCTAGAGGGCCCAATTC                          |
| VL30 element                               | M91235   | TCCTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAA<br>TTCGGCACGAGGGTGTTTTTTTTTTTTTTTCAGTCTCTCTGCATCTTCTTTCAGTGGACCTCTC<br>TCTCTAGATTCCCTTCTTGTTTTCTCACCATCCCACGTGAGATGCTTGTAGTAAGTGTACAG<br>ATCTTCTTTACCCTGAGGAAAGACAGAATCCTGCTAGAGGCCAGAAAGAAATGTTCCAGACATGG<br>ATGGAAGGCTCCTGACTGTGACTTCAATGCCCCGTAAGGTAGGGAGTGTCTCAGGTCTGCCCCC<br>AGGCTCCGAGGGTGGGTCTCCTAGGGGCTGAAAAATGCCCCACCAATCTGGCTAAGATAAGGAAA<br>GGATATGAAGAGAAAGTTACAGAACTTGAAGGGTAAAGCTAAGTCACTGAGAGAGTTATTGTAA<br>GTTGCAGAGAAAAAATAGTTGATGCGTGGTTTACGGGTCTGTGCAGAAAAGTGGACAGCACCTAATA<br>GCTGTAGAAGAAGATGCAGAGAGACTGAAAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA<br>GACAGGAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA<br>TTTACTTGGCNCCTGGNCGCGTTTTTCAACGTCGTGACTGGG               |

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| Voltage-dependent<br>anion channel 2<br>(Vdac2) | NM_031354 | CTATGACATGATTACGAATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATT<br>CGGCACGAGGGTCTCCTTCACCTTCGCCCTCCAGCCGCGGTGGCTGCAGCGCAACTTCCAGATAGC<br>GGAGTGGCCTCAGCTGCGAGCCGAGCGGTGGCGGCAGCGCCCTCAGGACACCCGCAGATCACCT<br>TTTCCCCGCGACTTCGCCATGGCTGAATGTTGTGTACCGGTATGCCAACGGCCAATTTGTATCCC<br>TCCACCCATATGCTGACCTTGGCAAAGCTGCCAGAGATATTTCAACAAAGGATTTGGTTTGGGT<br>TGGTAAAGCTGGATGTGAAAACGAAGTCATGCAGTGGTGTGGAATTTTCAACATCTGGCTCATCT<br>AATACAGACACTGGTAAAGTCAGTGGGACCTTGGAGACCAAGTACAAATGGTGTGAGTATGGTCT<br>GACTTTCACAGAGAAATGGAACACTGACAACACTCTGGGGACGGAGATTGCAATTGAAGACCAGA<br>TTTGTCAAGGTTTGAACTGACCTTTGACACCACGTTTTTCACCAAACACAGGAAAGAAAAGTGGT<br>AAAATCAAGTCTGCTTACAAGANGGAATGTATAAACCTTGGCTGTGATGTTGATTTGATTTTGC<br>TGGGACCTGCCATCCATGGGTCAACCGTNTTTGGNTACGGGGGGGGGGGGGNG |
| zinc finger protein                             | AF001417  | AGGTGTGNAATGACCGAGGAACCTCAGATTTCTTGAATTGACTAAGACTTCACCAATGGGGTCAG<br>AGGTAAACTTTGGTCTGGGCGAAAGTTCNTCCGAACCTGCTGAAGATTCGCTGCTGACATCAGA<br>GTTTCAGGCTATTGGTCTCTAAGTTATAATTAAAGCCGGAGCTGATCAGAGAGTCCCTCTGGGGGAC<br>TAGAAGAAATCTTCAGTCTGATTCCCTCCTCTCCCGTGCTAGAATGATTTTGGTCCACAGG<br>TCTTCTCGGTTGTCAAATTTTATCTCAGAGGCTGACACGTAGCAGGGCTCACTCTGAAGATAGCG<br>TTCCAACTCCAGGCAGGTCTGTTGCCAATATTCTCCAGGGACGGCAGAGCCGAGAAGTAGCCCG<br>TTTCGTGCACAATCTGTAGTTCTTGGGAAGATGCTACACATTGGGAGCACATCCATGTCCGGTTGG<br>AAAAGACAGTCCCGCTGTCGGGAAAACAGGGAGGTGAACGATCAGGAGTCGGAGCAGAACTGT<br>TCCCGGGAGCGCAGGTGAAAGTTTCATGCAAACCTGGATGGCGCTGCAATCGGACGCCGGGTCCGG<br>ACCCCTCCCGCAGCCCGCAGCGCGCCGAGCCACGCAATATTTCCTCGTGCCGAATTTCTGCCT<br>CGAGGGCCAAATTCCTATAGTGAGTCGTATTAAATTCGTAATCATGTCATANNNG   |